

```

CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/192.943
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/936.422
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 137/241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-192-943-14

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Alignment Scores:
Pred. No.: 9.02e+03 14
Score: 4.00 4
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 2.02% 0
DB: 4 0

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US-09-966-880A-8 (1-198) x US-08-192-943-14 (1-14)

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Qy 104 LeuSerLeuArg 107
Db 12 CCGCTCTGCGC 1

RESULT 272
US-09-647-344A-45/c
Sequence 45, Application US/09647344A
Patent No. 6586180
GENERAL INFORMATION:
APPLICANT: Ruffner, Duane E.
APPLICANT: Pierce, Michael L.
APPLICANT: Chen, Zhidong
TITLE OF INVENTION: Directed Antisense Libraries
FILE REFERENCE: T6678.PCT.US
CURRENT APPLICATION NUMBER: US/09/647,344A
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/US99/06742
PRIOR FILING DATE: 1999-03-28
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 45
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A sequence flanking a chloramphenicol (CAT) gene and containing a
US-09-647-344A-45
Alignment Scores:

```

```

Pred. No.: 9.02e+03 14
Score: 4.00 4
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 2.02% 0
DB: 4 0

US-09-966-880A-8 (1-198) x US-09-647-344A-45 (1-14)

Qy 171 ArgLeuSerArg 174
Db 12 CCGCTCTGCGC 1

RESULT 273
US-09-401-063-1779/c
Sequence 1779, Application US/09401063
Patent No. 6623962
GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2086
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1779:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-401-063-1779
Alignment Scores:
Pred. No.: 9.02e+03 14
Score: 4.00 4
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 2.02% 0
DB: 4 0

```

US-09-966-880A-8 (1-198) x US-09-401-063-1779 (1-14)

QY 130 HisargAlagly 133
DB 13 CACAGGCGAGG 2

RESULT 274

US-09-401-063-1821
; Sequence 1821, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1821:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-401-063-1821
Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-401-063-1821 (1-14)

QY 134 ValGlnIleAla 137
DB 1 GUGCAGGCGCA 12

RESULT 275

US-09-874-601-17
; Sequence 17, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:

; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHO
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01

; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()

; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-17
Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-874-601-17 (1-14)

QY 83 SerTtpSerPro 86
DB 1 UGUGUGUCCCU 12

RESULT 276

PCT-US94-04496-16/c
; Sequence 16, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca Esq., Mark

REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: JUJ-1242
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: No
PCT-US94-04496-16

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US94-04496-16 (1-14)

QY 46 PheGlyTyrLeu 49
Db 13 TTTGGGTACCTT 2

RESULT 277
5166057-8/c
Patent No. 5166057
APPLICANT: FALISE, PETER; PARVIN, JEFFREY D.; KRYSTAL, MARK
TITLE OF INVENTION: RECOMBIANT NEGATIVE STRAND RNA VIRUS
EXPRESSION-SYSTEMS
NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/527,237
FILING DATE: 22-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,053
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 399,728
FILING DATE: 28-AUG-1989
SEQ ID NO: 8:
LENGTH: 14
5166057-8

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x 5166057-8 (1-14)

QY 59 LeuLeuPheLeu 62
Db 14 CTCGTGTTCTA 3

RESULT 278
US-07-990-297-21/c
Sequence 21, Application US/07990297
Patent No. 5340728
GENERAL INFORMATION:
APPLICANT: GROSZ, RON
TITLE OF INVENTION: IMPROVED METHOD FOR
TITLE OF INVENTION: AMPLIFICATION OF TARGETED
TITLE OF INVENTION: SEGMENTS OF NUCLEIC ACID USING
TITLE OF INVENTION: NESTED POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/990,297
FILING DATE: 19921209
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: MD-0103
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-990-297-21

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-990-297-21 (1-15)

QY 86 ProCysTyrAsp 89
Db 15 CTTGTGTACGAC 4

RESULT 279
US-07-962-569A-1
Sequence 1, Application US/07962569A
Patent No. 5391497
GENERAL INFORMATION:
APPLICANT: MENON, RAVI S.
APPLICANT: JEFFERS, KATHLEEN F.
APPLICANT: CHANG, YING-FON
APPLICANT: HAM, RICHARD G.
TITLE OF INVENTION: HUMAN K-CASEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH.D.
STREET: 11545 W. BERNARDO COURT, STE. 302
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92127

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/962,569A
FILING DATE: 19921013
CLASSIFICATION: 435

```

; ATTORNEY/AGENT INFORMATION:
; NAME: PEPPER PH.D., FREDERICK W.
; REGISTRATION NUMBER: 31,286
; REFERENCE/DOCKET NUMBER: 920224.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 451-1120
; TELEFAX: (619) 451-9628
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; US-07-962-569A-1

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-962-569A-1 (1-15)
QY 83 SerTipSerPro 86
Db 4 TCCTGGAGCCG 15

RESULT 280
US-08-365-189-10/c
; Sequence 10, Application US/08365189
; Patent No. 5514576
; GENERAL INFORMATION:
; APPLICANT: Bower, Patricia A.
; TITLE OF INVENTION: Cloned Pullulanase
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,189
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/132,648
; FILING DATE: October 5, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryser, David G.
; REGISTRATION NUMBER: 36,407
; REFERENCE/DOCKET NUMBER: 66-005-9367-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5717
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

; ATTORNEY/AGENT INFORMATION:
; NAME: PEPPER PH.D., FREDERICK W.
; REGISTRATION NUMBER: 31,286
; REFERENCE/DOCKET NUMBER: 920224.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 451-1120
; TELEFAX: (619) 451-9628
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-145-704-45

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; US-08-365-189-10

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-365-189-10 (1-15)
QY 41 SerPheserleu 44
Db 12 AGCTTCAGCCTC 1

RESULT 281
US-08-145-704-45
; Sequence 45, Application US/08145704
; Patent No. 5567604
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Pennewald, Susan
; APPLICANT: Zendegeui, Joseph G.
; APPLICANT: Joshua O. Ojwang
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,704
; FILING DATE: 28-OCT-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-145-704-45

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0

```

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DB:                                     0
US-09-966-880A-8 (1-198) x US-08-145-704-45 (1-15)
QY 33 VallysAICAG 36
Db 1 GTAAACGACGG 12

RESULT 282
US-08-242-664-27/c
; Sequence 27, Application US/08242664
; Patent No. 5571937
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,664
; FILING DATE: May 12, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-242-664-27

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-242-664-27 (1-15)
QY 59 LeuLeuPheLeu 62
Db 13 TTGCTCTTCCTC 2

RESULT 283
US-08-311-760A-32
; Sequence 32, Application US/08311760A
; Patent No. 5599706
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy

```

```

; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,760A
; FILING DATE: September 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-311-760A-32

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-311-760A-32 (1-15)
QY 180 LeuLeuProLeu 183
Db 3 CUACUACCAUUA 14

RESULT 284
US-08-311-760A-187
; Sequence 187, Application US/08311760A
; Patent No. 5599706
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

```

; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,760A
; FILING DATE: September 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 187:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-311-760A-187

```

```

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

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US-09-966-880A-8 (1-198) x US-08-311-760A-187 (1-15)

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Qy 180 LeuLeuProLeu 183
Db 3 CUACUACCAUUA 14

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RESULT 285
US-08-182-968A-60
; Sequence 60, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:

```

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; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA: 07/882,888
; APPLICATION NUMBER:
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-60

```

```

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

```

```
US-09-966-880A-8 (1-198) x US-08-182-968A-60 (1-15)

```

```

Qy 59 LeuLeuPheLeu 62
Db 3 UUGCUCUUCUC 14

```

```

RESULT 286
US-08-182-968A-175
; Sequence 175, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

```

; INFORMATION FOR SEQ ID NO: 175:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-182-968A-175

Alignment Scores:

Pred. NO.: 9.65e+03

Score: 4.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.02%

DB: 1

Length: 15

Matches: 4

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-175 (1-15)

QY 164 GlyLeuHisGlu 167

DB 3 GGCCUUCAGAA 14

RESULT 287

US-08-182-968A-176

; Sequence 176, Application US/08182968A

; Patent No. 5610054

; GENERAL INFORMATION:

; APPLICANT: Draper, Kenneth G.

; TITLE OF INVENTION: METHOD AND REAGENT FOR

; TITLE OF INVENTION: INHIBITING HEPATITIS C

; NUMBER OF SEQUENCES: 497

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/182,968A

; FILING DATE: 13-JANUARY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/882,888

; FILING DATE: 14-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 205/277

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 176:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-182-968A-176

Alignment Scores:

Pred. NO.: 9.65e+03

Score: 4.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.02%

DB: 1

Length: 15

Matches: 4

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

Query Match:

DB: 2.02%

US-09-966-880A-8 (1-198) x US-08-182-968A-176 (1-15)

QY 164 GlyLeuHisGlu 167

DB 2 GGCCUUCAGAA 13

RESULT 288

US-08-182-968A-224/c

; Sequence 224, Application US/08182968A

; Patent No. 5610054

; GENERAL INFORMATION:

; APPLICANT: Draper, Kenneth G.

; TITLE OF INVENTION: METHOD AND REAGENT FOR

; TITLE OF INVENTION: INHIBITING HEPATITIS C

; NUMBER OF SEQUENCES: 497

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/182,968A

; FILING DATE: 13-JANUARY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/882,888

; FILING DATE: 14-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 205/277

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 224:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-182-968A-224

Alignment Scores:

Pred. NO.: 9.65e+03

Score: 4.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.02%

DB: 1

Length: 15

Matches: 4

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-224 (1-15)

QY 72 ProGlyArgCys 75

DB 15 CCCGGAAGATGC 4

RESULT 289

US-08-182-968A-225/c

; Sequence 225, Application US/08182968A

; Patent No. 5610054


```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 205/277
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 227:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-182-968A-227
Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-227 (1-15)
QY 125 GlyLeuATGAG 128
Db 4 GGGUUGCGAGG 15

RESULT 292
US-08-182-968A-299/c
; Sequence 299, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 299:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-182-968A-299
Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-299 (1-15)
QY 123 ProGluGlyLeu 126
Db 12 CCGAAGGCCTC 1

RESULT 293
US-08-182-968A-347
; Sequence 347, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 347:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-182-968A-347
Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-347 (1-15)
```

```

QY      128 ArgLeuHisArg 131
DB      4 CGGUGACAGG 15

RESULT 294
US-08-182-968A-459
; Sequence 459, Application US/08182968A
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 459:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-968A-459

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-459 (1-15)
QY      2 AspSerLeuLeu 5
DB      4 GACUCACUCUU 15

RESULT 295
US-08-319-492B-57
; Sequence 57, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

```

; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
; PRIOR APPLICATION DATA:
; APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-319-492B-57

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-319-492B-57 (1-15)
QY      103 AsnLeuSerLeu 106
DB      4 AACUGUGCCUUA 15

RESULT 296
US-08-319-492B-58
; Sequence 58, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

Two

STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/319,492B
 FILING DATE: October 7, 1994

PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below:
 APPLICATION NUMBER: 08/008,895
 FILING DATE: January 19, 1993
 APPLICATION NUMBER: 07/989,849
 FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 209/276
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 117:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-319-492B-117

Alignment Scores:
 Pred. No.: 9.65e+03 Length: 15
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-319-492B-58 (1-15)

QY 103 AsnLeuSerLeu 106
 DB 1 AACUUGUCCUUA 12

RESULT 297
 US-08-319-492B-117
 Sequence 117, Application US/08319492B
 Patent No. 5616488
 GENERAL INFORMATION:
 APPLICANT: Sullivan, Sean M.
 APPLICANT: Draper, Kenneth G.
 APPLICANT: McSwiggen, James
 APPLICANT: Stinchcomb, Dan T.
 TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
 TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
 NUMBER OF SEQUENCES: 751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/319,492B
 FILING DATE: October 7, 1994

PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below:
 APPLICATION NUMBER: 08/008,895
 FILING DATE: January 19, 1993
 APPLICATION NUMBER: 07/989,849
 FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 209/276
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-319-492B-58

Alignment Scores:
 Pred. No.: 9.65e+03 Length: 15
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-319-492B-117 (1-15)

QY 64 TyrlleSerAsp 67
 DB 3 UAUUUUUCAGAU 14

RESULT 298
 US-08-319-492B-118
 Sequence 118, Application US/08319492B
 Patent No. 5616488
 GENERAL INFORMATION:
 APPLICANT: Sullivan, Sean M.
 APPLICANT: Draper, Kenneth G.
 APPLICANT: McSwiggen, James
 APPLICANT: Stinchcomb, Dan T.
 TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
 TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
 NUMBER OF SEQUENCES: 751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/319,492B
;; FILING DATE: October 7, 1994
;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below:
;; APPLICATION NUMBER: 08/008,895
;; FILING DATE: January 19, 1993
;; APPLICATION NUMBER: 07/989,849
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 209/276
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 118:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-319-492B-118
Alignment Scores:
Pred. No.: 9.65e-03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-319-492B-118 (1-15)
QY 64 TyrlSerAsp 67
Db 2 UAUUUUUCAGAU 13
RESULT 299
US-08-319-492B-119
; Sequence 119, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard

Two

;; APPLICATION NUMBER: 08/008,895
;; FILING DATE: January 19, 1993
;; APPLICATION NUMBER: 07/989,849
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 209/276
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 119:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-319-492B-119
Alignment Scores:
Pred. No.: 9.65e-03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-319-492B-119 (1-15)
QY 64 TyrlSerAsp 67
Db 1 UAUUUUUCAGAU 12
RESULT 300
US-08-319-492B-173
; Sequence 173, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard

Two

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-319-492B-173

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-319-492B-173 (1-15)

OY 30 CyeTyValval 33
Db 4 UGUUAUGUGUG 15

Search completed: March 5, 2004, 02:20:47
Job time : 87 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 4, 2004, 23:31:58 ; Search time 397 Seconds
(without alignments)
2118.749 Million cell updates/sec

Title: US-09-966-880A-8

Perfect score: 198

Sequence: 1 MDSLLMNRKFLYQFNVRW.....ILLPLYEVDLRLDAFRTGL 198

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1688237

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09966880/runat_04032004_083152_22377/app_query.fasta_1.391
-DB=N Geneseq 29Jan04 -QFMT=fastap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=300 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20
-USER=US09966880@cgn_1_1_470@runat_04032004_083152_22377 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	3.0	18	3 AAZ77408	Human bia
2	6	3.0	19	3 AAZ73262	Human bia
3	6	3.0	20	2 AAV09175	Phosphoro
4	6	3.0	20	2 AAX96050	PCR prime
5	6	3.0	20	3 AAZ74954	Human bia
6	6	3.0	20	6 ABS73437	Chimeric
7	6	3.0	20	9 ACF36600	RXR-beta
8	5	2.5	15	2 AAX31672	Tag seque

C	9	5	2.5	15	4	AAF52623	IGF-I oli
	10	5	2.5	15	4	AAF53096	IGF-I oli
	11	5	2.5	15	6	ABK32626	Human pan
	12	5	2.5	15	7	ACD56498	HBV enzym
	13	5	2.5	15	9	ADD28710	Escherich
C	14	5	2.5	15	9	ADD28861	Escherich
	15	5	2.5	15	9	ADD28860	Escherich
C	16	5	2.5	15	9	ADD28711	Escherich
C	17	5	2.5	16	2	AAQ81257	Ribozyme
C	18	5	2.5	16	6	ABL52895	Mutant cu
	19	5	2.5	17	2	AAAT53462	Rat ICAM
	20	5	2.5	17	2	AAAT53758	Rat ICAM
	21	5	2.5	17	2	AAAT53666	Rat ICAM
	22	5	2.5	17	2	AAAT53748	Rat ICAM
	23	5	2.5	17	2	AAAT53431	Rat ICAM
	24	5	2.5	17	2	AAAT74553	Mouse flt
	25	5	2.5	17	2	AAAT74554	Mouse flt
	26	5	2.5	17	2	AAAT71605	Human KDR
	27	5	2.5	17	2	AAAT69260	Human flt
	28	5	2.5	17	2	AAAT71604	Human KDR
	29	5	2.5	17	2	AAAT71606	Human KDR
	30	5	2.5	17	2	AAAT69261	Human flt
C	31	5	2.5	17	2	AAV94862	Mouse IL-
C	32	5	2.5	17	2	AAV94863	Mouse IL-
C	33	5	2.5	17	2	AAAT20716	Integrin
C	34	5	2.5	17	2	AAV91119	Human C-r
C	35	5	2.5	17	2	AAV93554	Human B-r
C	36	5	2.5	17	2	AAV92402	Human A-R
C	37	5	2.5	17	2	AAAT54363	NK-KB ant
C	38	5	2.5	17	3	AAA33807	Low adeno
C	39	5	2.5	17	3	AAA36106	Human gen
C	40	5	2.5	17	3	AAAF19929	Human NF-
	41	5	2.5	17	3	AAA25939	Oestrogen
	42	5	2.5	17	3	AAA24771	Oestrogen
C	43	5	2.5	17	3	AAAF04476	Hammerhea
C	44	5	2.5	17	4	ABK01373	Human NOG
C	45	5	2.5	17	4	ABK00382	Human NOG

ALIGNMENTS

RESULT 1

ID AAZ77408
XX AAZ77408 standard; DNA; 18 BP.
AC AAZ77408;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:11764.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
DR

XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.

XX Claim 9; Page 2738; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention

XX SQ Sequence 18 BP; 3 A; 9 C; 0 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	914	Length:	18
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	3	Gaps:	0

US-09-966-880A-8 (1-198) x AAZ77408 (1-18)

QY 179 IleleuLeuProLeuTYR 1784

DB 1 ATCTTCTCCCACTTAC 18

RESULT 2

AAZ73262/c

ID AAZ73262 standard; DNA; 19 BP.

XX AC AAZ73262;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker upstream amplification primer SEQ ID NO:7618.

XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.

XX Claim 9; Page 1855; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention

XX SQ Sequence 19 BP; 4 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	960	Length:	19
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	3	Gaps:	0

US-09-966-880A-8 (1-198) x AAZ73262 (1-19)

QY 167 GluAenSerValArgLeu 172

DB 19 GAAATAGTGTAAAGCTC 2

RESULT 3

AAV09175

ID AAV09175 standard; DNA; 20 BP.

XX AC AAV09175;

XX 09-JUN-1998 (first entry)

XX Phosphorothioate oligonucleotide sequence 8054 targeting IL1R mRNA.

XX Type I interleukin-1 receptor; IL1R; human; IL1 protein; hybridisation;
KW inflammation; ss; 5' Cap region; phosphorothioate linkage.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /note= "Phosphorothioate internucleotide linkage"

XX WO9744656-A1.

XX 27-NOV-1997.

XX 12-MAY-1997; 97WO-US007147.

XX 21-MAY-1996; 96US-00651692.

XX (ISIS-) ISIS PHARM INC.

XX Miraglia L, Bennett CF, Dean N, Geiger T;

XX WPI; 1998-018646/02.

XX 2'-substituted oligonucleotide(s) specific for interleukin-1 receptor
PT type I - used to modulate expression and detect overexpression of the
PT receptor.

XX Example 5; Page 19; 63pp; English.

PS This is a novel oligomer comprising 20 covalently linked nucleotides

CC which bind to the 5' Cap region of the interleukin-1 receptor (IL1R)

CC mRNA. Expression of IL1R, in cells and tissues can be modulated by

CC compositions comprising oligomers which are able to specifically

CC hybridise with target areas of its encoding sequence. The composition can

CC be used for treatment of disease in humans caused by excessive receptor

CC expression, e.g. inflammation. When labelled they can be used

CC diagnostically to determine overexpression of IL1R, also to determine

CC localisation and distribution of this expression for research, diagnostic

CC or therapeutic purposes

XX Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.01e+03	Length:	20
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x AAV09175 (1-20)

Qy 125 GlyLeuArgArgLeuHis 130

Db 2 GGGCTCGCGCGCTCCAC 19

RESULT 4

AAZ96050

ID AAZ96050 standard; DNA; 20 BP.

XX AC AAZ96050;

XX 13-SEP-1999 (first entry)

XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;

XX neutralising epitope; PCR primer; ss.

XX Synthetic.

OS Chlamydothila pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

XX 21-NOV-1997; 97FR-00014673.

XX 04-NOV-1998; 98US-0107078P.

XX (GEST) GENSET.

XX Griffais R;

XX WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae.

XX Page 1795; Disclosure; 1912pp; English.

XX AAX91991-X97517 represent PCR primers used to amplify open reading frames

CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae

CC (see AAX91990). C. pneumoniae causes respiratory disease such as

CC pneumonia and bronchitis and is thought to be a contributing factor in

CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema

CC nodosum or pharyngitis. The polypeptides encoded by the open reading

CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used

CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae

CC nucleotide sequences can also be used as immunogenic compositions,

CC especially where the vector directs the expression of a neutralising

CC epitope of C. pneumoniae

XX Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.01e+03	Length:	20
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x AAX96050 (1-20)

Qy 167 GluAsnSerValArgLeu 172

Db 1 GAGAACTCGGTGCGGCTG 18

RESULT 5

AAZ74954

ID AAZ74954 standard; DNA; 20 BP.

XX AC AAZ74954;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID NO:9310.

XX Human genome; biallelic marker; high density disequilibrium map;

XX genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX haplotyping; hybridisation; identification; characterisation;

XX amplification; single nucleotide polymorphism; SNP; PCR primer;

XX diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium

XX map of the human genome.

XX Claim 8; Page 2215; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention
 SQ Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.01e+03 Length: 20
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.03% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ74954 (1-20)

OY 40 ThrSerPheserLeuAsp 45
 DB 2 ACAAGTTTCTCATTAGAC 19

RESULT 6
 ABS73437/c
 ID ABS73437 standard; DNA; 20 BP.
 XX AC ABS73437;
 XX DT 03-DEC-2002 (first entry)
 DE Chimeric phosphorothioate oligonucleotide #18.

XX Human; glioma-associated oncogene-2; antisense compound; infection;
 KW inflammation; tumour formation; antiinflammatory; antitumour;
 KW inhibitor of human glioma-associated oncogene-2 expression;
 KW antisense gene therapy; phosphorothioate; ss.

XX Homo sapiens.
 OS Synthetic.
 OS Chimeric.

XX US6440739-B1.

XX 27-AUG-2002.

XX 17-JUL-2001; 2001US-00907843.

XX 17-JUL-2001; 2001US-00907843.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Freier SM;

XX WPI; 2002-697096/75.

XX Novel antisense compound that hybridizes and inhibits nucleic acid
 PT encoding human glioma-associated oncogene-2, useful for treatment of
 PT diseases associated with human glioma-associated oncogene-2.

XX Claim 3; Col 45; 43pp; English.

XX The present invention relates to a new antisense compound targeted to
 CC human glioma-associated oncogene-2. The invention is useful for
 CC inhibiting the expression of human glioma-associated oncogene-2 in cells
 CC or tissues. The invention is also useful for treatment of diseases
 CC associated with human glioma-associated oncogene-2. The invention is
 CC further useful for diagnostics, therapeutics, prophylaxis, as research
 CC reagents and kits, for distinguishing functions of various members of a
 CC biological pathway, and in antisense gene therapy. The invention is also
 CC useful prophylactically, e.g., to prevent or delay infection,
 CC inflammation or tumour formation. The present nucleic acid sequence
 CC represents an oligonucleotide that was used in the methods of the
 CC invention to inhibit human glioma-associated oncogene-2

SQ Sequence 20 BP; 2 A; 9 C; 7 G; 2 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.01e+03 Length: 20
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 3.03% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABS73437 (1-20)

OY 122 GluProGluGlyLeuArg 127
 DB 18 GAGCCTGAGGGCCTGGCG 1

RESULT 7
 ACF36600/c
 ID ACF36600 standard; DNA; 20 BP.
 XX AC ACF36600;
 XX DT 18-DEC-2003 (first entry)

XX RXR-beta cDNA amplifying RT-PCR primer RXR-1.
 DE RXR-beta cDNA amplifying RT-PCR primer RXR-1.
 KW KRAB; repressor fusion protein; Kruppel-associated box; KAP1; RXR-beta;
 KW cloned cell production; drug screening; luciferase; RT-PCR; primer; ss.

XX Synthetic.

XX WO2003072788-A1.

XX 04-SEP-2003.

XX 20-FEB-2003; 2003WO-US005347.

XX 21-FEB-2002; 2002US-0358599P.

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX Rauscher FJ, Ayyanathan K, Schultz DC;

XX WPI; 2003-712733/67.

XX Producing a cloned cell containing a stably silenced target gene, useful
 PT in research and drug screening, comprises introducing a nucleic acid
 PT molecule expressing a chimeric repressor fusion protein into a parent
 PT cell.

XX Example 7; Page 54; 113pp; English.

XX The invention relates to producing a cloned cell containing a stably
 CC silenced target gene. The method involves introducing a nucleic acid
 CC molecule expressing a chimeric repressor fusion protein into a parent
 CC cell. The repressor fusion protein comprises a first amino acid sequence
 CC comprising a Kruppel-Associated Box (KRAB) domain or its variant that
 CC binds to the protein KAP1 and has DNA-dependent repressor activity fused
 CC to a second amino acid targeting sequence that binds to the target gene,
 CC fused to a switch component, that, in the presence of a ligand or
 CC inducer, permits the second amino acid sequence to bind to the target
 CC gene, where the fusion protein is under the control of regulatory
 CC sequences capable of directing its expression in the parent cell. The
 CC methods are useful for producing cloned cells that are particularly
 CC useful in research and drug screening, e.g., identifying a test molecule
 CC that activates the expression of a stably silenced target gene, or
 CC manipulating expression of target gene in a cell. Sequences ACF36600-01
 CC represent primers used in a RT-PCR assay for detecting levels of RXR-beta
 CC mRNA in NIH3T3 cells

SQ Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.01e+03 Length: 20
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0


```

Db      15 GAGGACTCAGGAGA 1
RESULT 10
AAAF53096
ID      AAF53096 standard; DNA; 15 BP.
XX
AC      AAF53096;
XX
DT      30-MAR-2001 (first entry)
XX
DE      IGF-I oligonucleotide #4056.
XX
KW      Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW      cystostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
KW      skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pteryriasis;
KW      IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW      growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW      keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW      hyperneovascular condition; hyperplasia; kidney disease;
KW      neovascular condition of the retina; ss.
XX
OS      Homo sapiens.
XX
PN      WO200078341-A1.
XX
PD      28-DEC-2000.
XX
PF      21-JUN-2000; 2000WO-AU000693.
XX
PR      21-JUN-1999; 99US-0140345P.
XX
PA      (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI      Wright CJ, Werther GA, Edmondson SR;
XX
DR      WPI; 2001-041421/05.
XX
PT      Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT      UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT      inhibits or reduces growth factor mediated cell proliferation and/or
PT      inflammation.
XX
PS      Example 8; Page 87; 201pp; English.
XX
CC      The present invention relates to a method for ameliorating the effects of
CC      skin disorders. The method comprises contacting the skin with an
CC      antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC      receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC      inhibiting or reducing growth factor mediated cell proliferation,
CC      inflammation and/or other disorders. The present sequence is an
CC      oligonucleotide which can be used to design the antisense
CC      oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC      F45161). The method is useful for ameliorating the effects of psoriasis,
CC      ichthyosis, pteryriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC      neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC      hyperneovascular condition such as a neovascular condition of the retina,
CC      brain or skin, growth factor-mediated malignancies, other sclerotic
CC      disease, kidney disease, hyperproliferation of the inside of blood
CC      vessels or any other hyperplasia
XX
SQ      Sequence 15 BP; 3 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      7.25e+03      Length:      15
Score:          5.00          Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    2.53%          Indels:      0
DB:             4             Gaps:       0

US-09-966-880A-8 (1-198) x AAF53096 (1-15)

QY      93 HisValAlaAcopPhe 97
Db      1 CATGTTGCTGACTTT 15

RESULT 12
ACD56498
ID      ACD56498 standard; RNA; 15 BP.
XX
AC      ACD56498;
XX
DT      24-SEP-2003 (first entry)
XX
DE      HBV enzymatic nucleic acid substrate sequence #179.
XX

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```

QY      174 ArgGlnLeuArgArg 178
Db      1 CGCCAGCTTCGACGA 15

RESULT 11
ABK32626
ID      ABK32626 standard; DNA; 15 BP.
XX
AC      ABK32626;
XX
DT      23-APR-2002 (first entry)
XX
DE      Human pancreatic cancer SAGE tag #178.
XX
KW      Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW      serial analysis of gene expression; diagnostic; prognostic; probe;
KW      cancer marker; ss.
XX
OS      Homo sapiens.
XX
PN      US6333152-B1.
XX
PD      25-DEC-2001.
XX
PF      20-MAY-1998; 98US-00081646.
XX
PR      20-MAY-1998; 98US-00081646.
XX
PA      (UYJO ) UNIV JOHNS HOPKINS.
XX
PI      Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX
DR      WPI; 2002-153821/20.
XX
PT      New human nucleic acid containing specific SAGE tags, useful as
PT      diagnostic markers for cancer, also derived probes.
XX
PS      Disclosure; Col 82; 161pp; English.
XX
CC      The invention relates to an isolated, purified human nucleic acid (I)
CC      that has the same sequence as a mRNA found in humans and is a SAGE
CC      (serial analysis of gene expression) tag comprising a single stranded
CC      probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC      diagnostic and prognostic markers of cancer, especially of the colon and
CC      pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC      SAGE tags of the invention
XX
SQ      Sequence 15 BP; 2 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      7.25e+03      Length:      15
Score:          5.00          Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    2.53%          Indels:      0
DB:             6             Gaps:       0

US-09-966-880A-8 (1-198) x ABK32626 (1-15)

QY      93 HisValAlaAcopPhe 97
Db      1 CATGTTGCTGACTTT 15

RESULT 12
ACD56498
ID      ACD56498 standard; RNA; 15 BP.
XX
AC      ACD56498;
XX
DT      24-SEP-2003 (first entry)
XX
DE      HBV enzymatic nucleic acid substrate sequence #179.
XX

```

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNase; inozyme; zinzyme;
 KW ambrzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW viricide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 FN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US09187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SLAV/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORE/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Example 1; Page 221; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, ambrzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC enzymatic nucleic acid sequences disclosed in the present invention
 XX
 SQ Sequence 15 BP; 2 A; 6 C; 1 G; 0 T; 6 U; 0 Other;
 Alignment Scores:
 Pred. No.: 7.25e+03 Length: 15
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACD56498 (1-15)

172 LeuSerArgGlnLeu 176
 |||||
 1 CUUUUCGCGCACUU 15
 |||||
 RESULT 13
 ADD28710
 ID ADD28710 standard; DNA; 15 BP.
 XX
 AC ADD28710;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Escherichia coli 0157:H7 VNTR amplicon sequence SEQ ID NO:325.
 XX
 KW molecular sub-typing system; Escherichia coli;
 KW variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; gene; ds.
 XX
 OS Escherichia coli.
 XX
 FN WO2003050269-A2.
 XX
 PD 19-JUN-2003.
 XX
 PF 11-DEC-2002; 2002WO-US039914.
 XX
 PR 11-DEC-2001; 2001US-0339687P.
 XX
 PA (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P.
 PA (KEYS/) KEYS C.
 XX
 PI Keim P, Keys C;
 XX
 DR WPI; 2003-864934/80.
 XX
 PT Molecular sub-typing system for Escherichia coli, comprises observing and
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA
 PT sample.
 XX
 PS Claim 7; SEQ ID NO 325; 166pp; English.
 XX
 CC The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (I) for sub-typing E. coli O157:H7; (2) primers
 CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails
 CC (III) for multiplex amplification of (I) comprising two or more primers
 CC of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
 CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC coli O157:H7 strains by multiplex, comprising (III), and amplifying in a
 CC reagents for maintaining hybridisation and amplification condition in a
 CC multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub
 CC typing (M1) an E. coli strain, comprising: (a) obtaining one or more
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
 CC producing discrete genetic data for an epidemiological database. (I) is
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an E. coli VNTR loci related
 CC amplicon sequence which is used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 15 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
 CC producing discrete genetic data for an epidemiological database. (1) is
 CC useful as a research tool. (5) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an oligonucleotide which is used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Alignment Scores: Length: 15
 Pred. No.: 7.25e+03 Matches: 5
 Score: 5.00 Conservatives: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 9

US-09-966-880A-8 (1-198) x ADD28861 (1-15)

Qy 72 ProGlyArgCysTyr 76
 Db 15 CCTGGACGGTGCTAC 1

RESULT 15
 ADD28860
 ID ADD28860 standard; DNA; 15 BP.
 AC ADD28860;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX Escherichia coli 0157:H7 VNTR related oligonucleotide SEQ ID NO:479.
 DE molecular sub-typing system; Escherichia coli;
 XX variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; ss.
 XX
 XX Synthetic.
 OS Escherichia coli.
 XX
 XX WO2003050269-A2.
 PN
 XX 19-JUN-2003.
 PD
 XX
 XX 11-DEC-2002; 2002WO-US039914.
 PF
 XX 11-DEC-2001; 2001US-0339687P.
 PR
 XX (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P.
 PA (KEYS/) KEYS C.
 XX
 XX Keim P, Keys C;
 PI
 XX WPI; 2003-864934/80.
 DR
 XX Molecular sub-typing system for Escherichia coli, comprises observing and
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA
 PT sample.
 XX
 PS Disclosure; SEQ ID NO 479; 166pp; English.

The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (1) for sub-typing E. coli 0157:H7; (2) primers
 CC (II) for amplifying (1); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli 0157:H7; (4) multiplex cocktails
 CC (III) for multiplex amplification of (1) comprising two or more primers
 CC of (II); (5) kits for molecular sub-typing of E. coli 0157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for

Alignment Scores: Length: 15
 Pred. No.: 7.25e+03 Matches: 5
 Score: 5.00 Conservatives: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 9

US-09-966-880A-8 (1-198) x ADD28710 (1-15)

Qy 72 ProGlyArgCysTyr 76
 Db 1 CCTGGACGGTGCTAC 15

RESULT 14
 ADD28861/C
 ID ADD28861 standard; DNA; 15 BP.
 XX
 AC ADD28861;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX Escherichia coli 0157:H7 VNTR related oligonucleotide SEQ ID NO:480.
 DE molecular sub-typing system; Escherichia coli;
 KW variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; ss.
 XX
 XX Synthetic.
 OS Escherichia coli.
 XX
 XX WO2003050269-A2.
 PN
 XX 19-JUN-2003.
 PD
 XX
 XX 11-DEC-2002; 2002WO-US039914.
 PF
 XX 11-DEC-2001; 2001US-0339687P.
 PR
 XX (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P.
 PA (KEYS/) KEYS C.
 XX
 XX Keim P, Keys C;
 PI
 XX WPI; 2003-864934/80.
 DR
 XX Molecular sub-typing system for Escherichia coli, comprises observing and
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA
 PT sample.
 XX
 PS Disclosure; SEQ ID NO 480; 166pp; English.

The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (1) for sub-typing E. coli 0157:H7; (2) primers
 CC (II) for amplifying (1); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli 0157:H7; (4) multiplex cocktails
 CC (III) for multiplex amplification of (1) comprising two or more primers
 CC of (II); (5) kits for molecular sub-typing of E. coli 0157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
 CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC coli 0157:H7 strains by multiplex, comprising (III), and amplifying
 CC reagents for maintaining hybridisation and amplification condition in a
 CC multiplex instrument with DNA from an E. coli 0157:H7 strain; and (7) sub
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a

CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC coli O157:H7 strains by multiplex, comprising (iii), and amplifying
 CC reagents for maintaining hybridisation and amplification condition in a
 CC multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub
 CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
 CC producing discrete genetic data for an epidemiological database. (1) is
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an oligonucleotide which is used in
 CC the exemplification of the present invention.

SQ Sequence 15 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores: Length: 15
 Pred. No.: 7.25e+03 Matches: 5
 Score: 5.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD28860 (1-15)

QY 72 ProGlyArgCysTyr 76
 Db 1 CCTGGACGGTGCTAC 15

RESULT 16

ADD28711/c
 ID ADD28711 standard; DNA; 15 BP.

AC ADD28711;

XX 15-JAN-2004 (first entry)

DE Escherichia coli O157:H7 VNTR amplicon sequence SEQ ID NO:326.

XX molecular sub-typing system; Escherichia coli;
 KW variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; gene; ds.
 XX Escherichia coli.

OS Escherichia coli.

XX W02003050269-A2.

XX 19-JUN-2003.

XX 11-DEC-2002; 2002WO-US039914.

XX 11-DEC-2001; 2001US-0339687P.

XX (UYAR-) UNIV ARIZONA.

PA (KEIM/) KEIM P.

PA (KEYS/) KEYS C.

XX Keim P, Keys C;

XX WPI; 2003-864934/80.

XX Molecular sub-typing system for Escherichia coli, comprises observing and
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA
 PT sample.

XX Claim 7; SEQ ID NO 326; 166pp; English.

XX

CC The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (I) for sub-typing E. coli O157:H7; (2) primers
 CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails
 CC (III) for multiplex amplification of (I) comprising two or more primers
 CC of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
 CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC coli O157:H7 strains by multiplex, comprising (iii), and amplifying
 CC reagents for maintaining hybridisation and amplification condition in a
 CC multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub
 CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
 CC producing discrete genetic data for an epidemiological database. (1) is
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an E. coli VNTR loci related
 CC amplicon sequence which is used in the exemplification of the present
 CC invention.

SQ Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Alignment Scores: Length: 15
 Pred. No.: 7.25e+03 Matches: 5
 Score: 5.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD28711 (1-15)

QY 72 ProGlyArgCysTyr 76

Db 15 CCTGGACGGTGCTAC 1

RESULT 17

AAQ81257/c

ID AAQ81257 standard; mRNA; 16 BP.

XX AAQ81257;

XX 25-MAR-2003 (revised)

DT 07-SEP-1995 (first entry)

XX Ribozyne target sequence in TGF-beta mRNA (bases 735-750).

XX Target site; ribozyme; hammerhead; hairpin; hepatitis delta virus;
 KW group 1 intron; RNasep RNA motif; transforming growth factor-beta;
 KW TGF-beta; fibrous; connective; tissue disease; TGF-alpha; inhibin;
 KW epidermal growth factor; EGF; activin; amphiregulin; insulin;
 KW bone morphogenic protein; fibroblast growth factor; relaxin; as.

XX Homo sapiens.

XX W09429452-A2.

XX 22-DEC-1994.

XX 02-JUN-1994; 94WO-US006331.

XX 09-JUN-1993; 93US-00074343.

XX (RIBO-) RIBOZYME PHARM INC.

XX Draper KG;
 XX WPI; 1995-051612/07.
 XX
 XX Enzymatic RNA molecule with, e.g. a hammerhead or hairpin motif - cleaves
 PT mRNA associated with fibrous or connective tissue disease, and is useful
 PT for treatment or prophylaxis of such diseases.
 XX
 XX Claim 3; Page 4; 63pp; English.
 XX
 XX The sequences (AA081238-1304) represent the target sites where a ribozyme
 CC (hammerhead, hairpin, hepatitis delta virus, group 1 intron or RNaseP RNA
 CC motif) cleaves the mRNA of the transforming growth factor-beta (TGF-beta)
 CC gene. This sequence corresponds to bases 735-750 of the TGF-beta mRNA.
 CC The ribozymes can also target the mRNAs of genes associated with the
 CC development or maintenance of fibrous or connective tissue disease in
 CC order to prevent or treat these diseases. Such genes include TGF-alpha or
 CC beta, epidermal growth factor, inhibitors, activins, amphiregulin, bone
 CC morphogenic proteins, fibroblast growth factors a and b, insulin growth
 CC factor 1 or 2, insulin or relaxin. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 16 BP; 1 A; 8 C; 1 G; 0 T; 6 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 7.69e+03 Length: 16
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAQ81257 (1-16)
 QY 21 AlalysGlyArgArg 25
 Db 15 GCARAAAGGTAGGAGG 1
 RESULT 18
 ABL52895/c
 ID ABL52895 standard; DNA; 16 BP.
 AC ABL52895;
 XX
 XX 25-JUN-2002 (first entry)
 DT
 DE Mutant cutinase PCR primer Dop2-R.
 XX
 XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; PCR; primer; ss.
 KW
 OS Synthetic.
 XX
 XX WO200192502-A1.
 PN
 XX
 XX 06-DEC-2001.
 PD
 XX
 XX 22-MAY-2001; 2001WO-DK000350.
 PF
 XX
 XX 02-JUN-2000; 2000DK-00000861.
 PR
 XX 23-OCT-2000; 2000DK-00001577.
 PR
 XX 24-NOV-2000; 2000DK-00001772.
 PR
 XX 19-JAN-2001; 2001DK-00000100.
 PR
 XX (NOVO) NOVOZYMES AS.
 PA
 XX
 XX Svendsen A, Glad SOS, Fukuyama S, Matsui T;
 FI
 XX WPI; 2002-216714/27.
 DR
 XX
 XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
 PT oligomers of poly(ethylene terephthalate) comprises a substitution of
 PT amino acid residues corresponding to positions of Humicola insolens

PT cutinase.
 XX
 XX Example 1; Page 37; 41pp; English.
 XX
 XX The present invention relates to wild-type mature cutinase from Humicola
 CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
 CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
 CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases
 CC have improved thermostability, and are used for enzymatic hydrolysis of
 CC cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing
 CC of yarn or fabric from poly(ethylene terephthalate) fibers. The present
 CC sequence is a PCR primer, which was used during the construction of the
 CC cutinase mutants
 XX
 XX Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 7.69e+03 Length: 16
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0
 US-09-966-880A-8 (1-198) x ABL52895 (1-16)
 QY 70 LeuAspProGlyArg 74
 Db 16 CTGGATCCAGGGCGT 2
 RESULT 19
 AAT53462
 ID AAT53462 standard; RNA; 17 BP.
 AC AAT53462;
 XX
 XX 25-MAR-2003 (revised)
 DT
 XX 27-MAR-1997 (first entry)
 DE
 DE Rat ICAM hammerhead ribozyme target sequence (nt. position 668).
 XX
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.
 XX
 XX Rattus rattus.
 OS
 XX WO9523225-A2.
 PN
 XX
 XX 31-AUG-1995.
 PD
 XX
 XX 23-FEB-1995; 95WO-IB000156.
 PF
 XX
 XX 23-FEB-1994; 94US-00201109.
 PR
 XX 29-MAR-1994; 94US-00218934.
 PR
 XX 04-APR-1994; 94US-00222795.
 PR
 XX 07-APR-1994; 94US-00224483.
 PR
 XX 15-APR-1994; 94US-00227958.
 PR
 XX 15-APR-1994; 94US-00228041.
 PR
 XX 18-MAY-1994; 94US-00245736.
 PR
 XX 06-JUL-1994; 94US-00271280.
 PR
 XX 15-AUG-1994; 94US-00291932.
 PR
 XX 16-AUG-1994; 94US-00291433.
 PR
 XX 17-AUG-1994; 94US-00292620.
 PR
 XX 19-AUG-1994; 94US-00293520.

PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kistich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX
 DR WPI; 1995-351090/45.
 XX
 XX Ribozymes having modified bases and methods for producing them - for use
 PT in inhibiting disease related genes.
 PT
 PS Claim 2; Page 201; 407pp; English.
 XX
 CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
 CC nucleotide base position indicated in the DE line. Regions of the mRNA
 CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 CC inhibit ICAM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 SQ Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT53462 (1-17)

QY 58 GluLeuLeuPheLeu 62
 Db 1 GRACUGCUCUCCUC 15
 RESULT 20
 AAT53758
 ID AAT53758 standard; RNA; 17 BP.
 XX
 AC AAT53758;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-APR-1997 (first entry)
 XX
 DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2909).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;

KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 ss.

XX Rattus rattus.
 XX
 XX WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 XX 23-FEB-1995; 95WO-IB000156.
 XX
 PR 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kistich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX
 DR WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them - for use
 in inhibiting disease related genes.

Claim 2; Page 204; 407pp; English.

The present sequence represents a preferred target sequence for an
 enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
 nucleotide base position indicated in the DE line. Regions of the mRNA
 that do not form secondary folding structures and that contain potential
 hammerhead and hairpin ribozyme cleavage sites were identified by
 computer analysis. Ribozymes directed against these mRNA sequences were
 designed and synthesised with modifications that improve their nuclease
 resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 inhibit ICAM-1 expression, making them useful for reducing transplant
 rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)

SQ Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT53758 (1-17)

QY 58 GluteLeuPheLeu 62
 DB 1 GAACUGCUCUCCUC 15

RESULT 21

AAT53666
 ID AAT53666 standard; RNA; 17 BP.

XX AAT53666;

XX 25-MAR-2003 (revised)

DT 27-MAR-1997 (first entry)

XX Rat ICAM hammerhead ribozyme target sequence (nt. position 2376).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.

XX Rattus rattus.

OS
 XX WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB000156.

XX 23-FEB-1994; 94US-00201109.

XX 29-MAR-1994; 94US-00218934.

XX 04-APR-1994; 94US-00222795.

XX 07-APR-1994; 94US-00224483.

XX 15-APR-1994; 94US-00227958.

XX 15-APR-1994; 94US-00228041.

XX 18-MAY-1994; 94US-00245736.

XX 06-JUL-1994; 94US-00271280.

XX 15-AUG-1994; 94US-00291932.

XX 16-AUG-1994; 94US-00291433.

XX 17-AUG-1994; 94US-00292620.

XX 19-AUG-1994; 94US-00293520.

XX 02-SEP-1994; 94US-00300000.

XX 08-SEP-1994; 94US-00303039.

XX 23-SEP-1994; 94US-00311486.

XX 28-SEP-1994; 94US-00311749.

XX 03-OCT-1994; 94US-00314397.

XX 07-OCT-1994; 94US-00316771.

XX 11-OCT-1994; 94US-00319492.

XX 04-NOV-1994; 94US-00321993.

XX 10-NOV-1994; 94US-00334847.

XX 28-NOV-1994; 94US-00337608.

XX 16-DEC-1994; 94US-00345516.

XX 23-DEC-1994; 94US-00357577.

XX 30-JAN-1995; 94US-00363233.

XX (RIBO-) RIBOZYME PHARM INC.

PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudydz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Ueman N, Wincott PE, Woolf T;
 XX WPI; 1995-351090/45.

XX Ribozymes having modified bases and methods for producing them - for use
 in inhibiting disease related genes.

XX Claim 2; Page 203; 407pp; English.

XX The present sequence represents a preferred target sequence for an
 enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
 nucleotide base position indicated in the DE line. Regions of the mRNA
 that do not form secondary folding structures and that contain potential
 hammerhead and hairpin ribozyme cleavage sites were identified by
 computer analysis. Ribozymes directed against these mRNA sequences were
 designed and synthesised with modifications that improve their nuclease
 resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 inhibit ICAM-1 expression, making them useful for reducing transplant
 rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 correct PI field.)

SQ Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT53666 (1-17)

QY 58 GluteLeuPheLeu 62

DB 1 GAACUGCUCUCCUC 15

RESULT 22

AAT53748

ID AAT53748 standard; RNA; 17 BP.

XX AAT53748;

XX 25-MAR-2003 (revised)

DT 03-APR-1997 (first entry)

XX Rat ICAM hammerhead ribozyme target sequence (nt. position 2904).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.

XX Rattus rattus.

XX WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB000156.

XX 23-FEB-1994; 94US-00201109.


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PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 18-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00311749.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX
XX RIBozymes having modified bases and methods for producing them - for use
XX in inhibiting disease related genes.
XX
XX Claim 2; Page 204; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by
XX computer analysis. Ribozymes directed against these mRNA sequences were
XX designed and synthesised with modifications that improve their nuclease
XX resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
XX inhibit ICAM-1 expression, making them useful for reducing transplant
XX rejection and alleviating symptoms in patients with rheumatoid arthritis,
XX asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
XX correct PI field.)
XX
XX Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.13e+03 Length: 17
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAT53748 (1-17)
XX
XX QY 58 GluLeuLeuPheLeu 62
XX |||||
XX 1 GAACUGCUCUCCUC 15
XX
XX RESULT 23
XX AAT53431
XX ID AAT53431 standard; RNA; 17 BP.
XX

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AC AAT53431;
XX
XX 25-MAR-2003 (revised)
XX 27-MAR-1997 (first entry)
XX
XX Rat ICAM hammerhead ribozyme target sequence (nt. position 26).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX intercellular adhesion molecule; rel A; tumour necrosis factor;
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX translocation; chronic myelogenous leukaemia; CML; cancer;
XX Philadelphia chromosome; inflammation; autoimmune disease;
XX atherosclerosis; myocardial infarction; stroke; restenosis;
XX transplant rejection; rheumatoid arthritis; psoriasis;
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX ss.
XX
XX Rattus rattus.
XX
XX W09523225-A2.
XX
XX 31-AUG-1995.
XX
XX 23-FEB-1995; 95WO-IB000156.
XX
XX 23-FEB-1994; 94US-00201109.
XX 29-MAR-1994; 94US-00218934.
XX 04-APR-1994; 94US-00222795.
XX 07-APR-1994; 94US-00224483.
XX 15-APR-1994; 94US-00227958.
XX 15-APR-1994; 94US-00228041.
XX 18-MAY-1994; 94US-00245736.
XX 06-JUL-1994; 94US-00271280.
XX 15-AUG-1994; 94US-00291932.
XX 16-AUG-1994; 94US-00291433.
XX 17-AUG-1994; 94US-00292620.
XX 19-AUG-1994; 94US-00293520.
XX 02-SEP-1994; 94US-00300000.
XX 08-SEP-1994; 94US-00303039.
XX 23-SEP-1994; 94US-00311486.
XX 23-SEP-1994; 94US-00311749.
XX 28-SEP-1994; 94US-00314397.
XX 03-OCT-1994; 94US-00316771.
XX 07-OCT-1994; 94US-00319492.
XX 11-OCT-1994; 94US-00321993.
XX 04-NOV-1994; 94US-00334847.
XX 10-NOV-1994; 94US-00337608.
XX 28-NOV-1994; 94US-00345516.
XX 16-DEC-1994; 94US-00357577.
XX 23-DEC-1994; 94US-00363233.
XX 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
XX Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
XX Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
XX in inhibiting disease related genes.
XX
XX Claim 2; Page 201; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by

```

CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAW-1 target sequences and thereby
 CC inhibit ICAW-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)

SQ Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT53431 (1-17)

Qy 58 GluLeuLeuPheLeu 62
 ID AAX74553 standard; RNA; 17 BP.
 Db 1 GAACUCUCUCCUC 15

RESULT 24

AAX74553
 ID AAX74553 standard; RNA; 17 BP.

XX AC AAX74553;

XX DT 28-JUL-1999 (first entry)

XX DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #81.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.

XX OS Mus sp.

XX PN WO9715662-A2.

XX PD 01-MAY-1997.

XX PF 25-OCT-1996; 96WO-US017480.

XX PR 26-OCT-1995; 95US-0005974P.

XX PR 11-JAN-1996; 96US-00584040.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (CHIR) CHIRON CORP.

XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 157; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples

CC of nucleic acid molecules from the present invention
 XX Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX74553 (1-17)

Qy 179 IleLeuLeuProLeu 183
 ID AAX74554 standard; RNA; 17 BP.
 Db 2 AUAACUCUACCCUC 16

RESULT 25

AAX74554

ID AAX74554 standard; RNA; 17 BP.

XX AC AAX74554;

XX DT 28-JUL-1999 (first entry)

XX DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #82.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.

XX OS Mus sp.

XX PN WO9715662-A2.

XX PD 01-MAY-1997.

XX PF 25-OCT-1996; 96WO-US017480.

XX PR 26-OCT-1995; 95US-0005974P.

XX PR 11-JAN-1996; 96US-00584040.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (CHIR) CHIRON CORP.

XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 157; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention

SQ Sequence 17 BP; 4 A; 6 C; 1 G; 0 T; 6 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX74554 (1-17)

QY 179 IleLeuLeuProLeu 183

Db 1 AUACUCUUAACCCUG 15

RESULT 26

AAX71605

ID AAX71605 standard; RNA; 17 BP.

XX

AC AAX71605;

XX

DT 28-JUL-1999 (first entry)

XX

DE Human KDR VEGF receptor hammerhead ribozyme substrate #617.

XX

KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.

XX

OS Homo sapiens.

XX

PN WO9715662-A2.

XX

PD 01-MAY-1997.

XX

PF 25-OCT-1996; 96WO-US017480.

XX

PR 26-OCT-1995; 95US-0005974P.

XX

PR 11-JAN-1996; 96US-00584040.

XX

XX (RIBO-) RIBOZYME PHARM INC.

PA

PA (CHIR) CHIRON CORP.

XX

PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX

WI; 1997-259017/23.

XX

CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

PT

PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,

PT

PT rheumatoid arthritis, etc., in a human patient.

XX

PS Claim 4; Page 115; 218pp; English.

XX

CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX57275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention

XX

SQ Sequence 17 BP; 6 A; 3 C; 3 G; 0 T; 5 U; 0 Other;

Alignment Scores:

Pred. No.:

Score: 8.13e+03 Length: 17

Percent Similarity: 100.00% Matches: 5

Best Local Similarity: 100.00% Conservative: 0

Query Match: 2.53% Mismatches: 0

Indels: 0

Gaps: 2

DB:

US-09-966-880A-8 (1-198) x AAX71605 (1-17)

QY 157 ArgThrPhelysAla 161

Db 2 AGAACUUUAAAGCU 16

RESULT 27

AAX69260

ID AAX69260 standard; RNA; 17 BP.

XX

AC AAX69260;

XX

DT 28-JUL-1999 (first entry)

XX

DE Human flt1 VEGF receptor hammerhead ribozyme substrate #555.

XX

KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.

XX

OS Homo sapiens.

XX

PN WO9715662-A2.

XX

PD 01-MAY-1997.

XX

PF 25-OCT-1996; 96WO-US017480.

XX

PR 26-OCT-1995; 95US-0005974P.

XX

PR 11-JAN-1996; 96US-00584040.

XX

XX (RIBO-) RIBOZYME PHARM INC.

PA

PA (CHIR) CHIRON CORP.

XX

PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX

WI; 1997-259017/23.

XX

CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

PT

PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,

PT

PT rheumatoid arthritis, etc., in a human patient.

XX

PS Claim 4; Page 63; 218pp; English.

XX

CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX57275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention

XX

SQ Sequence 17 BP; 3 A; 5 C; 2 G; 0 T; 7 U; 0 Other;

Alignment Scores:

Pred. No.:

Score: 8.13e+03 Length: 17

Percent Similarity: 100.00% Matches: 5

Best Local Similarity: 100.00% Conservative: 0

Query Match: 2.53% Mismatches: 0

Indels: 0

Gaps: 2

DB:

US-09-966-880A-8 (1-198) x AAX69260 (1-17)

QY 102 ProhsLeuSerIeu 106

Db 3 CCGAAUCUACUCUUG 17

```

RESULT 28
AAX71604
ID AAX71604 standard; RNA; 17 BP.
XX
AC AAX71604;
XX
28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hammerhead ribozyme substrate #616.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 115; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 6 A; 3 C; 3 G; 0 T; 5 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e-03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX71604 (1-17)

QY 157 ArgThrPhelysAla 161
| | | | | | | | | |
Db 3 AGAACUUUUAAGCU 17

RESULT 29
AAX71606
ID AAX71606 standard; RNA; 17 BP.
XX
AC AAX71606;
XX
28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #556.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX
DE Human KDR VEGF receptor hammerhead ribozyme substrate #618.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 115; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 7 A; 2 C; 3 G; 0 T; 5 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e-03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX71606 (1-17)

QY 157 ArgThrPhelysAla 161
| | | | | | | | | |
Db 1 AGAACUUUUAAGCU 15

RESULT 30
AAX69261
ID AAX69261 standard; RNA; 17 BP.
XX
AC AAX69261;
XX
28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #556.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

```

KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 XX 25-OCT-1996; 96WO-US017480.
 XX
 XX 26-OCT-1995; 95US-0005974P.
 PR
 PR 11-JAN-1996; 96US-00584040.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 PI WPI; 1997-259017/23.
 XX
 DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 63; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;
 XX

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX69261 (1-17)
 QY 102 ProAsnLeuSerLeu 106
 Db 1 CCGAUCUAUCUUG 15
 RESULT 31
 AAV94862/c
 ID AAV94862 standard; RNA; 17 BP.
 XX
 XX AAV94862;
 AC
 XX 24-FEB-1999 (first entry)
 DE Mouse IL-2 receptor g-chain substrate position 42.
 XX
 XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
 KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
 KW autoimmune disease; psoriasis; allergy; inflammatory disease;
 KW graft rejection; ss.
 XX
 OS Mus sp.
 XX
 PN WO9824913-A2.
 XX
 PD 11-JUN-1998.
 XX
 XX 02-DEC-1997; 97WO-US021748.
 PF
 PR 03-DEC-1996; 96US-00758306.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Stinchcomb DT, Mcswiggen JA;
 PI WPI; 1998-333332/29.
 DR

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV94862 (1-17)
 QY 124 GluGlyLeuArgArg 128
 Db 17 GGAGGACTTAGAGG 3
 RESULT 32
 AAV94863/c
 ID AAV94863 standard; RNA; 17 BP.
 XX
 XX AAV94863;
 AC
 XX 24-FEB-1999 (first entry)
 DE Mouse IL-2 receptor g-chain substrate position 43.
 XX
 XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
 KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
 KW autoimmune disease; psoriasis; allergy; inflammatory disease;
 KW graft rejection; ss.
 XX
 OS Mus sp.
 XX
 PN WO9824913-A2.
 XX
 PD 11-JUN-1998.
 XX
 XX 02-DEC-1997; 97WO-US021748.
 PF
 PR 03-DEC-1996; 96US-00758306.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Stinchcomb DT, Mcswiggen JA;
 PI WPI; 1998-333332/29.
 DR

XX 11-JUN-1998.
 PD
 XX 02-DEC-1997; 97WO-US021748.
 PF
 XX 03-DEC-1996; 96US-00758306.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Stinchcomb DT, Mcswiggen JA;
 PI WPI; 1998-333332/29.
 DR
 XX Ribozymes targeted to interleukin 2 - useful for treating e.g. cancer,
 PT autoimmune disease and allergies.
 XX
 PS Claim 4; Page 40; 61pp; English.
 XX
 CC The present sequence invention describes ribozymes targeted to modulate
 CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.
 CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and
 CC AAV94575 to AAV95260 represent specifically claimed substrate sequences
 CC from the present invention. The ribozymes can be used for the treatment
 CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy
 CC and other inflammatory conditions. The ribozymes are also used to induce
 CC tolerance in a recipient to alloantigen from a donor
 XX
 SQ Sequence 17 BP; 2 A; 6 C; 1 G; 0 T; 8 U; 0 Other;
 XX

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV94862 (1-17)
 QY 124 GluGlyLeuArgArg 128
 Db 17 GGAGGACTTAGAGG 3
 RESULT 32
 AAV94863/c
 ID AAV94863 standard; RNA; 17 BP.
 XX
 XX AAV94863;
 AC
 XX 24-FEB-1999 (first entry)
 DE Mouse IL-2 receptor g-chain substrate position 43.
 XX
 XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
 KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
 KW autoimmune disease; psoriasis; allergy; inflammatory disease;
 KW graft rejection; ss.
 XX
 OS Mus sp.
 XX
 PN WO9824913-A2.
 XX
 PD 11-JUN-1998.
 XX
 XX 02-DEC-1997; 97WO-US021748.
 PF
 PR 03-DEC-1996; 96US-00758306.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Stinchcomb DT, Mcswiggen JA;
 PI WPI; 1998-333332/29.
 DR

XX Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer,
PT autoimmune disease and allergies.
XX
PS Claim 4; Page 40; 6lpp; English.
XX
CC The present sequence invention describes ribozymes targetted to modulate
CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.
CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and
CC AAV94575 to AAV95260 represent specifically claimed substrate sequences
CC from the present invention. The ribozymes can be used for the treatment
CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy
CC and other inflammatory conditions. The ribozymes are also used to induce
CC tolerance in a recipient to alloantigen from a donor
XX
SQ Sequence 17 BP; 2 A; 6 C; 1 G; 0 T; 8 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAV94863 (1-17)

Qy 124 GluclyLeuArg 128
Db 16 GAAGGACTAAGAAGG 2

RESULT 33
AA20716
ID AA20716 standard; RNA; 17 BP.
AC
AC AA20716;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:3942.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiobroma;
KW tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9950403-A2.
PN
XX
XX 07-OCT-1999.
PD
XX
XX 24-MAR-1999; 99WO-US006507.
PF
XX
XX 27-MAR-1998; 98US-0079678P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
PI
XX
XX WPI; 1999-591315/50.
DR
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
PT
XX
XX Claim 55; Page 163; 305pp; English.
PS
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA

CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tubercous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 6 A; 1 C; 4 G; 0 T; 6 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAA20716 (1-17)

Qy 177 ArgArgileLeuLeu 181
Db 1 AGAAGGAUUGUCU 15

RESULT 34
AAV91119/c
ID AAV91119 standard; RNA; 17 BP.
XX
XX AAV91119;
AC
XX
XX 18-FEB-1999 (first entry)
DT
XX
XX Human C-raf target site nucleotide position 1251.
DE
XX
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9850530-A2.
PN
XX
XX 12-NOV-1998.
PD
XX
XX 05-MAY-1998; 98WO-US009249.
PF
XX
XX 09-MAY-1997; 97US-0046059P.
PR
XX
XX 09-JUN-1997; 97US-0049002P.
PR
XX
XX 03-JUL-1997; 97US-0051718P.
PR
XX
XX 22-AUG-1997; 97US-0056808P.
PR
XX
XX 02-OCT-1997; 97US-0061321P.
PR
XX
XX 02-OCT-1997; 97US-0061324P.
PR
XX
XX 05-NOV-1997; 97US-0064868P.
PR
XX
XX 19-DEC-1997; 97US-0068212P.

```

XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
XX PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
XX PI Thompson J, Workman CT, Beaudry A, Svedler D;
XX PI WPI; 1999-009494/01.
XX DR Identifying new catalytic nucleic acid that modulates selected processes
XX PT - especially ribozymes that cleave Raf RNA for treating cancer,
XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates
XX PT used as antiviral agents and synthons.
XX PS Claim 177; Page 149; 259pp; English.
XX CC A method has been developed for the identification of a nucleic acid
XX CC capable of modulating a process in a biological system. The method
XX CC comprises: (a) introducing into the system a random library of nucleic
XX CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
XX CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
XX CC in systems where modulation has occurred and/or determining the sequence
XX CC of at least part of the SBDs in such systems. Nucleic acid molecules with
XX CC endonuclease activity and catalytic activity, from the present invention,
XX CC are used to modulate gene expression in plant and mammalian cells and to
XX CC cleave target nucleic acid, particularly for treating systemic diseases
XX CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
XX CC ascites and infection. They may also be used to detect genetic drift and
XX CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
XX CC with RNA-cleaving activity that modulate expression of the Raf gene, are
XX CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX CC generally any condition associated with the level of c-raf. Introduction
XX CC of sugar/phosphate modifications increases stability against nuclease and
XX CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
XX CC method, specifically for modulating the expression of a Raf gene
XX SQ Sequence 17 BP; 5 A; 3 C; 4 G; 0 T; 5 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV91119 (1-17)

QY 107 ArgilePheThrAla 111
Db 17 AGGATCTTACTGCA 3

RESULT 35
AAV93554/C
ID AAV93554 standard; RNA; 17 BP.
XX AC AAV93554;
XX AC 18-FEB-1999 (first entry)
XX DT Human B-raf substrate nucleotide position 1662.
XX DE
XX KW Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
XX KW screening; identification; synthesis; deprotection; purification; cancer;
XX KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
XX KW restenosis; rheumatoid arthritis; ss.
XX OS Homo sapiens.
XX XX WO9850530-A2.
XX PN
XX XX 12-NOV-1998.
XX PD

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XX PF 05-MAY-1998; 98WO-US009249.
XX PR 09-MAY-1997; 97US-0046059P.
XX PR 09-JUN-1997; 97US-0049002P.
XX PR 03-JUL-1997; 97US-0051718P.
XX PR 22-AUG-1997; 97US-0056808P.
XX PR 02-OCT-1997; 97US-0061321P.
XX PR 02-OCT-1997; 97US-0061324P.
XX PR 05-NOV-1997; 97US-0064866P.
XX PR 19-DEC-1997; 97US-0068212P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
XX PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
XX PI Thompson J, Workman CT, Beaudry A, Svedler D;
XX PI WPI; 1999-009494/01.
XX DR Identifying new catalytic nucleic acid that modulates selected processes
XX PT - especially ribozymes that cleave Raf RNA for treating cancer,
XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates
XX PT used as antiviral agents and synthons.
XX PS Claim 177; Page 170; 259pp; English.
XX CC A method has been developed for the identification of a nucleic acid
XX CC capable of modulating a process in a biological system. The method
XX CC comprises: (a) introducing into the system a random library of nucleic
XX CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
XX CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
XX CC in systems where modulation has occurred and/or determining the sequence
XX CC of at least part of the SBDs in such systems. Nucleic acid molecules with
XX CC endonuclease activity and catalytic activity, from the present invention,
XX CC are used to modulate gene expression in plant and mammalian cells and to
XX CC cleave target nucleic acid, particularly for treating systemic diseases
XX CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
XX CC ascites and infection. They may also be used to detect genetic drift and
XX CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
XX CC with RNA-cleaving activity that modulate expression of the Raf gene, are
XX CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX CC generally any condition associated with the level of c-raf. Introduction
XX CC of sugar/phosphate modifications increases stability against nuclease and
XX CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
XX CC method, specifically for modulating the expression of a Raf gene
XX SQ Sequence 17 BP; 2 A; 4 C; 6 G; 0 T; 5 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV93554 (1-17)

QY 82 ThrSerTrpSerPro 86
Db 17 ACAGCTGGAGCCCT 3

RESULT 36
AAV92402
ID AAV92402 standard; RNA; 17 BP.
XX AC AAV92402;
XX AC 18-FEB-1999 (first entry)
XX DT Human A-Raf substrate position 327.
XX DE
XX XX

```

KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.

XX Homo sapiens.
 XX WO9850530-A2.
 XX 12-NOV-1998.
 XX 05-MAY-1998; 98WO-US009249.
 XX 09-MAY-1997; 97US-0046059P.
 XX 09-JUN-1997; 97US-0049002P.
 XX 22-AUG-1997; 97US-0051718P.
 XX 22-AUG-1997; 97US-0056808P.
 XX 02-OCT-1997; 97US-0061321P.
 XX 02-OCT-1997; 97US-0061324P.
 XX 05-NOV-1997; 97US-0064866P.
 XX 19-DEC-1997; 97US-0068212P.
 XX (RIBO-) RIBOZYME PHARM INC.

XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX WPI; 1999-009494/01.

XX Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer,
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 PT used as antiviral agents and synthons.

XX Claim 177; Page 157; 259pp; English.

XX A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene

XX Sequence 17 BP; 6 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps:

US-09-966-880A-8 (1-198) x AAV92402 (1-17)

Qy 171 ArgLeuSerArgGln 175

Db 2 CGACUCUCUAGACAA 16

RESULT 37
 AAX54363/c
 ID AAX54363 standard; DNA; 17 BP.

XX AAX54363;
 XX 05-JUL-1999 (first entry)
 XX NK-kB antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.

XX Synthetic.

XX WO9913886-A1.

XX 25-MAR-1999.

XX 17-SEP-1998; 98WO-US019419.

XX 17-SEP-1997; 97US-0059160P.

XX 09-JUN-1998; 98US-00093972.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 1999-229400/19.

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction.

XX Disclosure; Page 63; 120pp; English.

XX The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene initiation
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
 CC end and the juxta-section between coding and non-coding regions and all
 CC segments of RNAs encoding proteins associated with one or more diseases,
 CC conditions or mixtures. The antisense oligonucleotides may be derived
 CC from sequences AAX5272-74. These multiple target oligonucleotides
 CC (specifically AAX5180-271) can be used for the antisense treatment of
 CC diseases and conditions. Typical diseases and conditions are those
 CC associated with impaired respiration and inflammation, including lung
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 CC acute asthma, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer

XX Sequence 17 BP; 0 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAx54363 (1-17)

Qy 36 ArgAspSerAlaThr 40

Db 15 CCGGACAGCGCCACC 1

RESULT 38

AAA33807/c

ID AAA33807 standard; DNA; 17 BP.

XX AC AAA33807;

XX 28-JUL-2000 (first entry)

XX Low adenosine antisense oligonucleotide SEQ ID NO:1496.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;

KW phosphothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;

KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS WO200009525-A2.

PN 24-FEB-2000.

PD 03-AUG-1999; 99WO-US017712.

PF 03-AUG-1998; 98US-0095212P.

PR (UYEC-) UNIV EAST CAROLINA.

PA Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary

PT vasoconstriction, inflammation, allergies, asthma, hypertension,

PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers.

XX Claim 18; Page 451; 1343pp; English.

XX The present invention describes a new composition comprising an antisense

CC oligonucleotide (ON) with low adenosine (up to 15%), which targets

CC nucleic acids involved in bronchoconstriction, allergies, and/or

CC inflammation. The ON can have antiinflammatory, antiallergic,

CC antiasthmatic, cytostatic and analgesic activities. The compositions are

CC useful for the treatment of diseases associated with inflammation,

CC impaired airways, including lung disease and diseases whose secondary

CC effects afflict the lungs of a subject. They can be used for treating

CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,

CC impeded respiration, respiratory distress syndrome, pain, cystic

CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive

CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,

CC carcinomas, and cancers which may metastasise to the lungs, including

CC breast and prostate cancer. The reduction of the adenosine content of the

CC ONs reduces side effects. The A-containing ONs break down with the

CC release of deoxyadenosine which activates adenosine receptors causing

CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the

CC nucleotide sequences given in the sequence listing from the present

CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185

CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ

CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to

CC AAA33992) are specifically claimed ONs from the present invention. N.B.

CC Sequences given in the disclosure of the present invention do not match

CC up with their corresponding SEQ ID NO: sequences given in the sequence

CC listing

SQ Sequence 17 BP; 0 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA33807 (1-17)

Qy 36 ArgAspSerAlaThr 40

Db 15 CCGGACAGCGCCACC 1

RESULT 39

AAA36106

ID AAA36106 standard; DNA; 17 BP.

XX AC AAA36106;

XX 26-JUL-2000 (first entry)

XX Human genomic SNP allele specific oligonucleotide SEQ ID NO:163.

XX Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;

KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;

KW genomic classification; identification; DNA fingerprinting;

KW tumour characterisation; hybridisation; ss.

XX Homo sapiens.

OS WO200018960-A2.

PN 06-APR-2000.

PD 24-SEP-1999; 99WO-US022283.

PF 25-SEP-1998; 98US-0101757P.

PR (MASI) MASSACHUSETTS INST TECHNOLOGY.

PA Landers JB, Jordan B, Housman DE, Charest A;

PI WPI; 2000-293181/25.

XX Detection of single nucleotide polymorphisms in genomes by preparation

PT and analysis of reduced complexity genomes, useful for genotyping,

PT fingerprinting and determining allele frequency of SNPs.

XX Disclosure; Page 58; 111pp; English.

XX A method has been developed for detecting the presence or absence of a

CC single nucleotide polymorphism (SNP) allele in a genomic sample. The

CC method comprises preparing a reduced complexity genome (RCG) from the

CC genomic sample and analysing the RCG for the presence or absence of a SNP

CC allele. The method can be used to characterise a tumour, to generate a

CC genomic pattern for an individual genome or to generate a genomic

CC classification code for a genome. The method can be used to assess

CC whether a subject is at risk for developing a disease or to identify a

CC set of SNP alleles associated with a disease. The method can also be used

CC to perform linkage analysis. AAA35944 to AAA35947 represent sequences

CC used in the exemplification of the present invention. AAA35948 to

CC AAA36632 represent nucleotide sequences containing SNPs

XX Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA36106 (1-17)

Qy 169 SerValArgLeuser 173

Db 3 AGCGTCGGTTAAGT 17

RESULT 40

AAAF19929/c

ID AAAF19929 standard; DNA; 17 BP.

XX AAF19929;

DT 14-MAR-2001 (first entry)

XX Human NF-kB polynucleotide fragment #1496.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

XX Homo sapiens.

OS W0200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PI Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.

XX Claim 14; Page 257; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The

CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention

SQ Sequence 17 BP; 0 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAF19929 (1-17)

Qy 36 ArgAspSerAlaThr 40

Db 15 CGGACAGCGCCACC 1

RESULT 41

AAA25939

ID AAA25939 standard; DNA; 17 BP.

XX AAA25939;

XX 19-JUL-2000 (first entry)

DT Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2437.

DE Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.

XX Homo sapiens.

XX W09954459-A2.

XX 28-OCT-1999.

XX 19-APR-1999; 99WO-US008547.

XX 20-APR-1998; 98US-0082404P.

XX 23-JUN-1998; 98US-00103636.

XX (RIBO-) RIBOZYME PHARM INC.

XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

PI Matulic-Adamic J;

XX WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target sequences,

PT used to treat cancer.

XX Claim 77; Page 95; 149pp; English.

XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorothioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A), that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),

CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype.
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA25993 to AAA26105 represent their corresponding target sequences.
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 17 BP; 3 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0
 US-09-966-880A-8 (1-198) x AAA25939 (1-17)
 QY 57 ValGluLeuLeuPhe 61
 Db 1 GTAGAGCTCTGTTT 15
 RESULT 42
 AAA24771
 ID AAA24771 standard; DNA; 17 BP.
 XX
 AC AAA24771;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1369.
 XX
 KW Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9954459-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 19-APR-1999; 99WO-US008547.
 XX
 PR 20-APR-1998; 98US-0082404P.
 PR 23-JUN-1998; 98US-00103636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
 PI Matulic-Adamic J;
 XX
 DR WPI; 2000-013248/01.
 XX
 PT New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.
 XX
 PS Claim 77; Page 57; 148pp; English.
 XX
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphoro(dil)thioate

CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent their corresponding target sequences.
 CC sequences, and AAA26107 to AAA26218 represent other ribozyme sequences
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 17 BP; 2 A; 8 C; 5 G; 2 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0
 US-09-966-880A-8 (1-198) x AAA24771 (1-17)
 QY 127 ArgArgLeuHisArg 131
 Db 1 CGCCGGCTTCACCGG 15
 RESULT 43
 AAUF04476/c
 ID AAUF04476 standard; DNA; 17 BP.
 XX
 AC AAUF04476;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #1992.
 XX
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2000061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 PI WPI; 2000-647423/62.
 XX
 DR Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 4; Page 101; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-1F-1, the GATA transcription

CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 8 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e-03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAP04476 (1-17)

QY 11 PreLeuTyGlnPhe 15
 DB 15 TTTCTCTATCAGTTC 1

RESULT 44

ABK01373/c

ID ABK01373 standard; RNA; 17 BP.

XX ABK01373;

AC ABK01373;

DT 12-MAR-2002 (first entry)

XX Human NOGO Inozyme #643.

DE Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

XX cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNazyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-0185516P.

XX 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

PI WPI; 2001-607195/69.

DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

XX constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

XX central nervous system injury.

XX Claim 88; Page 88; 200pp; English.

PS

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with an NNN motif) or
 CC an amberszyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC of CD20. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention

SQ Sequence 17 BP; 6 A; 4 C; 2 G; 0 T; 5 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e-03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK01373 (1-17)

QY 194 ArgThrLeuGlyLeu 198

DB 17 AGAACITTTGGTTTA 3

RESULT 45

ABK00382/c

ID ABK00382 standard; RNA; 17 BP.

XX ABK00382;

AC ABK00382;

DT 12-MAR-2002 (first entry)

XX Human NOGO Hammerhead Ribozyme #382.

DE Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

XX cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNazyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS

OS Synthetic.
 XX WO200159103-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004273.
 XX 11-FEB-2000; 2000US-0181797P.
 XX 28-FEB-2000; 2000US-0185516P.
 XX 06-MAR-2000; 2000US-0187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX Claim 88; Page 72; 200pp; English.
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg^{2+} .
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of the
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a hammerhead ribozyme of the invention
 XX
 SQ Sequence 17 BP; 7 A; 3 C; 4 G; 0 T; 3 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0
 US-09-966-880A-8 (1-198) x ABK00382 (1-17)
 QY 169 SerValArgLeuSer 173

Db RESULT 46
 ASK01374/c
 ID ABK01374 standard; RNA; 17 BP.
 XX
 AC ABK01374;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Inozyme #644.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberzyme; zynzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004273.
 XX 11-FEB-2000; 2000US-0181797P.
 XX 28-FEB-2000; 2000US-0185516P.
 XX 06-MAR-2000; 2000US-0187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX Claim 88; Page 88; 200pp; English.
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg^{2+} .
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of the
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a hammerhead ribozyme of the invention

CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jacob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention
 XX
 SQ Sequence 17 BP; 6 A; 4 C; 1 G; 0 T; 6 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK01374 (1-17)

QY 194 ArgThrLeuGlyLeu 198

DB 16 AGAACTTGGGTTA 2

RESULT 47

ABK02555/c

ID ABK02555 standard; RNA; 17 BP.

AC ABK02555;

DT 12-MAR-2002 (first entry)

DE Human NOGO Amberzyme #227.

XX Human; ss; antisense therapy; cyostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jacob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-0185516P.

XX 08-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

XX

DR WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.

XX Claim 88; Page 135; 200pp; English.

PS The invention relates to a nucleic acid molecule which down regulates
 XX expression of a CD20 gene and a nucleic acid molecule which down
 XX regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCR motif), a G-cleaver (cleaving RNA with a NIN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jacob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an amberzyme molecule of the invention

SQ Sequence 17 BP; 8 A; 4 C; 3 G; 0 T; 2 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK02555 (1-17)

QY 58 GluLeuLeuPheLeu 62

DB 15 GAGCTTCTGTTCTT 1

RESULT 48

ABK02240

ID ABK02240 standard; RNA; 17 BP.

XX ABK02240;

DT 12-MAR-2002 (first entry)

DE Human NOGO DNazyme #152.

XX Human; ss; antisense therapy; cyostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.

PN 15-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

PI Blatt L, Mcswiggen J, Chowrira BM;

XX MPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.

XX Claim 88; Page 115; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytooma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a DNzyme molecule of the invention

XX Sequence 17 BP; 6 A; 2 C; 4 G; 0 T; 5 U; 0 Other;

Alignment Scores:

Pred. No.: 8 13e+03 Length: 17
 Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK02240 (1-17)

Qy 8 ArgArgGlyGlyPheLeu 12
 Db 1 AGGAGAAAUAUCCUU 15

RESULT 49

ABK01263/C

ID ABK01263 standard; RNA; 17 BP.

XX ABK01263;

DT 12-MAR-2002 (first entry)

DE Human NOGO Inozyme #533.

Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian; ribozyme;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

PI Blatt L, Mcswiggen J, Chowrira BM;

XX MPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 constructs, which down regulate expression of a CD20 gene or neurite
 growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 central nervous system injury.

XX Claim 88; Page 86; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention

SQ Sequence 17 BP; 7 A; 3 C; 4 G; 0 T; 3 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK01263 (1-17)

Qy 169 SerValArgLeuSer 173

Db 15 TCAGTGAGACTTCT 1

RESULT 50

ABK01219/c
 ID ABK01219 standard; RNA; 17 BP.

XX AC ABK01219;

DT 12-MAR-2002 (first entry)

XX DE Human NOGO Inozyme #489.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

PD 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWEIRA B M.

XX Blatt L, Mcswiggen J, Chowaira BM;

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

XX constructs, which down regulate expression of a CD20 gene or neurite

XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

XX central nervous system injury.

XX Claim 88; Page 85; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg^{2+} .
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention

SQ Sequence 17 BP; 8 A; 5 C; 3 G; 0 T; 1 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK01219 (1-17)

Qy 58 GluLeuPheLeu 62

Db 16 GAGCTTCGTCTTCT 2

RESULT 51

ABA80972/c

ID ABA80972 standard; DNA; 17 BP.

XX AC

XX ABA80972;

DT 24-JAN-2002 (first entry)

XX

DE	LDLR mutation correcting oligonucleotide SEQ ID NO: 3818.	XX	LDLR mutation correcting oligonucleotide SEQ ID NO: 3819.
XX	Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss.	XX	Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss.
OS	Homo sapiens.	OS	Homo sapiens.
XX	WO2001/73002-A2.	XX	WO2001/73002-A2.
XX	04-OCT-2001.	XX	04-OCT-2001.
XX	27-MAR-2001; 2001WO-US009761.	XX	27-MAR-2001; 2001WO-US009761.
XX	27-MAR-2000; 2000US-0192176P.	XX	27-MAR-2000; 2000US-0192176P.
XX	27-MAR-2000; 2000US-0192179P.	XX	27-MAR-2000; 2000US-0192179P.
XX	01-JUN-2000; 2000US-0208538P.	XX	01-JUN-2000; 2000US-0208538P.
XX	30-OCT-2000; 2000US-0244989P.	XX	30-OCT-2000; 2000US-0244989P.
XX	(UYDE) UNIV DELAWARE.	XX	(UYDE) UNIV DELAWARE.
XX	Kmiec EB, Gamper HB, Rice MC;	XX	Kmiec EB, Gamper HB, Rice MC;
XX	WPI; 2001-639230/73.	XX	WPI; 2001-639230/73.
XX	Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.	XX	Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.
XX	Claim 7; Page 251; 294pp; English.	XX	Claim 7; Page 251; 294pp; English.
XX	The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and presenilin-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention	XX	The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and presenilin-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention
SQ	Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other;	SQ	Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
XX	Alignment Scores:	XX	Alignment Scores:
XX	Pred. No.: 8.13e+03	XX	Pred. No.: 8.13e+03
XX	Score: 5.00	XX	Score: 5.00
XX	Percent Similarity: 100.00%	XX	Percent Similarity: 100.00%
XX	Best Local Similarity: 100.00%	XX	Best Local Similarity: 100.00%
XX	Query Match: 2.53%	XX	Query Match: 2.53%
XX	Indels: 4	XX	Indels: 4
XX	Gaps: 0	XX	Gaps: 0
XX	DB: 93 HisVallalaApphe 97	XX	DB: 93 HisVallalaApphe 97
XX	15 CATGTTGCAGCTTT 1	XX	15 CATGTTGCAGCTTT 1
XX	RESULT 52	XX	RESULT 52
XX	ABA80973	XX	ABA80973

QY	93 HisValAlaAspPhe 97 3 CATGTGCAGACTTT 17
DB:	
Best Local Similarity:	100.00%
Query Match:	2.53%
Mismatches:	0
Indels:	0
Gaps:	0

US-09-966-880A-8 (1-198) x ABA78569 (1-17)

QY 123 LeuHisArgAlaGly 133
|||||||
Db 2 CTGCACCGGGCGGG 16

RESULT 54
ABA78570/C
ID ABA78570 standard; DNA; 17 BP.
XX AC ABA78570;
XX DT 24-JAN-2002 (first entry)
XX DE CDKN2A mutation correcting oligonucleotide SEQ ID NO: 1416.

Human, gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1; Alzheimer's disease; cytostatic; antickling; antiataemic; haemostatic; antiileptic; ss.

OS Homo sapiens.
XX WO200173002-A2.
XX PN 27-MAR-2001; 2001WO-US009761.
XX PD 27-MAR-2000; 2000US-0192176P.
XX PR 27-MAR-2000; 2000US-0192179P.
XX PR 01-JUN-2000; 2000US-0208538P.
XX PR 30-OCT-2000; 2000US-0244989P.
XX PA (UYDE) UNIV DELAWARE.
XX PI Kmiec EB, Camper HB, Rice MC;
XX PS WPI; 2001-639230/73.
XX DR Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.
XX DS Claim 7; Page 130; 294pp; English.

The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention

SQ Sequence 17 BP; 1 A; 6 C; 9 G; 1 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Consensus: 100.00%

SQ Sequence 17 BP; 1 A; 9 C; 6 G; 1 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.13e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x ABA78570 (1-17)

QY 129 LeuHisArgAlaGly 133

Db 16 CTGCACCGGCGGG 2

RESULT 55

AAH43675

ID AAH43675 standard; DNA; 17 BP.

XX AC AAH43675;

DT 21-JAN-2002 (first entry)

XX DE Primer RCpyrG5.

XX KW A. fumigatus; pyrG; mutant bank; mutation; inducible; haploid; PCR;

XX KW diploid; phenotype; amplify; polymerase chain reaction; primer; ss.

XX OS Synthetic.

XX PN WO200177295-A1.

XX PD 18-OCT-2001.

XX PF 11-APR-2001; 2001WO-GB001626.

XX PR 11-APR-2000; 2000GB-00008748.

XX PA (TWO-) F2G LTD.

XX PI Denning DW, Brookman JL, Rickers A, Birch M;

XX DR WPI; 2001-657169/75.

XX PT Mutant bank of diploid microorganisms for identifying genes which

PT contribute to a chosen phenotype, has population of mutant cells in which

PT at least one cell has a random mutation which disrupts the activity of a

PT gene.

XX PS Example 1; Page 32; 64pp; English.

XX CC The sequences given in AAH43675-80 are primers which were used to isolate

CC the mutated pyrG gene in plasmid pMB3 linearised with XbaI. The isolated

CC sequence was used in the method of the invention in the production of a

CC mutant bank of diploid microorganisms which comprises a population of

CC mutant cells in which at least one cell has a mutation that disrupts the

CC activity of a gene, and which is inducible into haploid form. The mutant

CC bank is useful for identifying genes in a microorganism which contribute

CC to a chosen phenotype. The method comprises exposing the diploid

CC microorganisms, where the population collectively have a mutation in

CC every gene within the genome, to an agent that induces the microorganisms

CC into haploid form, separating and culturing the haploid microorganism as

CC single clones, and selecting clones or colonies for which the chosen

CC phenotype is altered relative to a wild type microorganisms, and

CC identifying the mutated gene in each of the selected clones. The complete

CC diploid population may be cultured under suitable conditions. This is

CC possible because the wild type copy of the gene will rescue any

CC individual that may otherwise grow poorly, or even not be viable, should

CC the mutant copy of the gene predominate. Thus, the diploid mutant bank

CC may comprise a population of mutant, viable cells in which essentially

CC the activity of every gene within the genome is disrupted rather than an

CC incomplete population comprising non-lethal mutants

XX SQ Sequence 17 BP; 3 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.13e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x AAH43675 (1-17)

QY 176 LeuArgArgileLeu 180

Db 3 TTGAGGCGAATTC 17

RESULT 56

ABN09591/C

ID ABN09591 standard; DNA; 17 BP.

XX AC ABN09591;

XX DT 29-MAY-2002 (first entry)

XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9583.

XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;

XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

XX KW skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.

XX PN WO200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0256860P.

XX (ABOM-) ABOmica INC.

XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,

PT or as specific biomolecule capture probes for surface-enhanced laser

PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX PS Disclosure; SEQ ID NO 9583; 214pp; English.

XX CC The present invention describes a human genome-derived myosin-like

CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1

CC nucleic acids can be used as probes to detect, characterise and quantify

CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMPLP-1

CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABN09591 (1-17)

Qy 41 SerPheSerLeuArg 45
 Db 15 AGCTTTTCCCTCGAC 1

RESULT 57
 ABN09638
 ID ABN09638 standard; DNA; 17 BP.
 XX
 AC ABN09638;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9630.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 FA (ABOM-) AFOMICA INC.
 XX

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon MB;
 XX WPI; 2002-179446/23.
 DR
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 9630; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 3 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABN09638 (1-17)

Qy 124 GluGlyLeuArgArg 128
 Db 3 GAAGGGCTCCGGAGG 17

RESULT 58
 ABN09773
 ID ABN09773 standard; DNA; 17 BP.
 XX
 AC ABN09773;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9765.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR

PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 9765; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880a-8 (1-198) x ABN09773 (1-17)

Qy 103 AsnLeuSerLeuArg 107
 |||||
 Db 3 AACCTTCGCTGAGG 17

RESULT 59

ABN09639

ID ABN09639 standard; DNA; 17 BP.

XX AC ABN09639;

XX DT 29-MAY-2002 (first entry)

XX

DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9631.
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
 PA
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 9631; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 4 A; 3 C; 9 G; 1 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABN09639 (1-17)

QY 124 GluglyLeuArgArg 128
|||||

DB 2 GAAGGCTCCGGAGG 16

RESULT 60
ABN09774
ID ABN09774 standard; DNA; 17 BP.
AC ABN09774;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9766.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
XX WC200192524-A2.
DN
XX
PD 06-DEC-2001.
XX
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR
PR 21-SEP-2000; 2000US-0234587P.
PR
PR 27-SEP-2000; 2000US-0236359P.
PR
PR 04-OCT-2000; 2000GB-00024263.
PR
PR 30-JAN-2001; 2001WO-US000661.
PR
PR 30-JAN-2001; 2001WO-US000662.
PR
PR 30-JAN-2001; 2001WO-US000663.
PR
PR 30-JAN-2001; 2001WO-US000664.
PR
PR 30-JAN-2001; 2001WO-US000665.
PR
PR 30-JAN-2001; 2001WO-US000666.
PR
PR 30-JAN-2001; 2001WO-US000667.
PR
PR 30-JAN-2001; 2001WO-US000668.
PR
PR 30-JAN-2001; 2001WO-US000669.
PR
PR 30-JAN-2001; 2001WO-US000670.
PR
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (ABOM-) AEOMICA INC.
PA
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 9766; 214pp; English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-1 can be used in gene therapy and vaccine production. The hGDMPLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMPLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMPLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMPLP-1 proteins as standards in assays used to determine the concentration and/or amount specifically of hGDMPLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionization, as therapeutic supplement in patients having specific deficiency in hGDMPLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABN09774 (1-17)

Qy 103 AsnLeuSerLeuArg 107
|||||
Db 2 AACCTCTCGTGAGG 16

RESULT 61

ABN09590/C

ID ABN09590 standard; DNA; 17 BP.

XX AC ABN09590;

XX 29-MAY-2002 (first entry)

DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9582.

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.

FN WC200192524-A2.

PD 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234587P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 05-FEB-2001; 2001US-0266860P.

XX (ABOM-) AEOMICA INC.

PA Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 9582; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABN09590 (1-17)

QY 41 SerPreSerLeuasp 45
Db 16 AGCTTTTCCTCGAC 2

RESULT 62
ABN09640
ID ABN09640 standard; DNA; 17 BP.
XX
AC ABN09640;
XX
XX 29-MAY-2002 (first entry)
DT
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9632.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
XX WO200192524-A2.
PN
PD 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
PF
XX
XX 26-MAY-2000; 2000US-0207456P.
PR
PR 21-SEP-2000; 2000US-0234687P.
PR
PR 27-SEP-2000; 2000US-0236359P.
PR
PR 04-OCT-2000; 2000GB-00024263.
PR
PR 30-JAN-2001; 2001WO-US000661.
PR
PR 30-JAN-2001; 2001WO-US000662.
PR
PR 30-JAN-2001; 2001WO-US000663.
PR
PR 30-JAN-2001; 2001WO-US000664.
PR
PR 30-JAN-2001; 2001WO-US000665.
PR
PR 30-JAN-2001; 2001WO-US000665.
PR
PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (ABOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
FI WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
PT
PT Disclosure; SEQ ID NO 9632; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABN09640 (1-17)

QY 124 GluGlyLeuArgArg 128
Db 1 GAAGGGCTCGAGG 15

RESULT 63
ABN09775
ID ABN09775 standard; DNA; 17 BP.
XX
XX ABN09775;
XX
XX 29-MAY-2002 (first entry)
DT
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9767.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
XX WO200192524-A2.
PN

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PF 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 05-FEB-2001; 2001US-0266860P.

XX PF (AEOM-) AEOMICA INC.

XX PA Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX PI WPI; 2002-179446/23.

XX DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,

XX PT or as specific biomolecule capture probes for surface-enhanced laser

XX PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX PS Disclosure; SEQ ID NO 9767; 214pp; English.

XX CC The present invention describes a human genome-derived myosin-like

XX CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

XX CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1

XX CC nucleic acids can be used as probes to detect, characterize and quantify

XX CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

XX CC provide initial substrates for the recombinant engineering of hGDMPLP-1

XX CC protein variants having desired phenotypic improvements, and for

XX CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be

XX CC used as immunogens to raise antibodies that specifically recognise hGDMPLP

XX CC -1 proteins, as standards in assays used to determine the concentration

XX CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule

XX CC capture probes for surface-enhanced laser desorption ionisation, as

XX CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

XX CC production, and in vaccines or for replacement therapy. The

XX CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

XX CC disorder associated with the expression of hGDMPLP-1, in particular heart

XX CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

XX CC The present sequence represents an oligomer used in the screening of the

XX CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.

XX CC The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequence

XX SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.13e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	6	Gaps:	0

US-09-966-880A-8 (1-198) x ABN09775 (1-17)

QY 103 AsnLeuSerLeuArg 107

Db 1 AACCTCTCGCTGAGG 15

RESULT 64

ABN09589/c

ID ABN09589 standard; DNA; 17 BP.

XX AC AEN09589;

XX DT 29-MAY-2002 (first entry)

XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9581.

XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;

XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

XX KW skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.

XX PN WO200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 05-FEB-2001; 2001US-0266860P.

XX PF (AEOM-) AEOMICA INC.

XX PA Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX PI WPI; 2002-179446/23.

XX DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,

XX PT or as specific biomolecule capture probes for surface-enhanced laser

XX PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX PS Disclosure; SEQ ID NO 9581; 214pp; English.

XX CC The present invention describes a human genome-derived myosin-like

XX CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

XX CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1

XX CC nucleic acids can be used as probes to detect, characterize and quantify

XX CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

XX CC provide initial substrates for the recombinant engineering of hGDMPLP-1

XX CC protein variants having desired phenotypic improvements, and for

XX CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be

XX CC used as immunogens to raise antibodies that specifically recognise hGDMPLP

XX CC -1 proteins, as standards in assays used to determine the concentration

XX CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule

XX CC capture probes for surface-enhanced laser desorption ionisation, as

XX CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

XX CC production, and in vaccines or for replacement therapy. The

XX CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

XX CC disorder associated with the expression of hGDMPLP-1, in particular heart

XX CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

XX CC The present sequence represents an oligomer used in the screening of the

XX CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.

XX CC The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequence

XX SQ Sequence 17 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

PT creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.

PS Claim 7; Page 103; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention

SQ Sequence 17 BP; 5 A; 5 C; 1 G; 6 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK25647 (1-17)

QY 32 ValVallysArgArg 36
 DB 15 GTTGTCAAAAGGAGA 1

RESULT 67

ABK25648
 ID ABK25648 standard; DNA; 17 BP.

XX AC ABK25648;

XX XX 09-APR-2002 (first entry)

XX DE Stress tolerance conferring genome altering oligonucleotide #116.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; LNA modification; phosphorothioate linkage;
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW modified fatty acid content; reduced palmitate production; albino plant;
 KW increased stearate production; reduced linolenic acid production;
 KW photosynthetic process.

XX Arabidopsis thaliana.

OS Synthetic.

XX XX WO200192512-A2.

XX PN

PD 06-DEC-2001.

XX PF 01-JUN-2001; 2001WO-US017672.

XX PR 01-JUN-2000; 2000US-0208938P.

XX PR 30-OCT-2000; 2000US-0244989P.

XX PR 27-MAR-2001; 2001US-00818875.

XX PA (UVDE) UNIV DELAWARE.

XX PI Kmiec EB, Gamper HB, Rice MC, Kim J;

XX WPI; 2002-106307/14.

DR New oligonucleotides with modified nuclease-resistant termini, useful for
 XX creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.

XX Claim 7; Page 103; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention

SQ Sequence 17 BP; 6 A; 1 C; 5 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK25648 (1-17)

QY 32 ValVallysArgArg 36
 DB 3 GTTGTCAAAAGGAGA 17

RESULT 68

ABK25911

ID ABK25911 standard; DNA; 17 BP.

XX AC ABK25911;

XX XX 09-APR-2002 (first entry)

XX XX Albino plant producing genome altering oligonucleotide #83.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;

XX o-methyl modification; LNA modification; phosphorothioate linkage;

KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;

KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulfonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW modified fatty acid content; reduced palmitate production; albino plant;
 KW increased stearate production; reduced linolenic acid production;
 KW photosynthetic process.

XX Triticum aestivum.
 OS Synthetic.
 XX WO200192512-A2.
 XX 06-DEC-2001.
 XX 01-JUN-2001; 2001WO-US017672.
 XX 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-024989P.
 PR 27-MAR-2001; 2001US-00818875.
 XX (UYDE) UNIV DELAWARE.
 PA Kmiec EB, Gamper HB, Rice MC, Kim J;
 PI WPI; 2002-106307/14.
 DR New oligonucleotides with modified nuclease-resistant termini, useful for
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.

XX Claim 7; Page 119; 220pp; English.
 PS The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of O-methyl modification, an RNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulfonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention

XX SQ Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. NO.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK25911 (1-17)

OY 171 ArgLeuSerArgGln 175

|||||

Db 3 CGACTGAGTCGTCAG 17
 RESULT 69
 AAL48300
 ID AAL48300 standard; DNA; 17 BP.
 XX AAL48300;
 AC AAL48300;
 XX 03-OCT-2002 (first entry)
 DT HPV ribozyme cleavage site #14.
 DE Ribozyme; catalytic nucleic acid; infection; PCR; target site; ss.
 XX Human papillomavirus.
 OS WO200246449-A2.
 PN 13-JUN-2002.
 PD 07-DEC-2001; 2001WO-US046178.
 PF 07-DEC-2000; 2000US-0251810P.
 PR (UYPE-) UNIV PENNSYLVANIA STATE.
 PA Clawson G, Pan W;
 XX WPI; 2002-519672/55.
 DR Identifying cleavage sites of a target RNA, by adding target RNA to
 PT library of nucleic acids e.g. ribozyme, which comprise catalytic core
 PT flanked by random nucleotides and isolating nucleic acid that cleave
 PT target RNA.

XX Example 5; Page 52; 79pp; English.
 PS The present invention relates to a method of identifying cleavage sites
 CC in a target RNA which are accessible to a ribozyme comprising a catalytic
 CC core flanked by random nucleotides. A target RNA is added to the library
 CC of nucleic acids and nucleic acids that bind to and/or cleave the target
 CC RNA are isolated. The method is useful for identifying ribozyme cleavage
 CC sites in sequences and in real time PCR assays. The present sequence is a
 CC ribozyme target site described in the exemplification of the invention
 XX SQ Sequence 17 BP; 8 A; 3 C; 5 G; 0 T; 1 U; 0 Other;
 Alignment Scores:
 Pred. NO.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AAL48300 (1-17)
 OY 174 ArgGlnLeuArgArg 178
 |||||
 Db 3 AGACAGCUCAGAGA 17
 RESULT 70
 ABV79962
 ID ABV79962 standard; DNA; 17 BP.
 XX ABV79962;
 AC ABV79962;
 XX 03-JAN-2003 (first entry)
 DT Human HTPL scanning oligonucleotide SEQ ID 1208.
 DE Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 XX human testis expressed Patched like protein; testis; adrenal; liver;
 KW

Db 3 CTTCCAGACAACTG 17

RESULT 72
ABV79961

ID ABV79961 standard; DNA; 17 BP.

XX AC ABV79961;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 1207.

XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

XX KW human testis expressed patched like protein; testis; adrenal; liver;

XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EP1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX DR WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful

XX PT for identifying agonist and antagonist and specific binding partners, and

XX PT for treating subjects having defects in HTPL.

XX PS Example 2; Page 222; 718pp; English.

XX CC The present invention relates to human testis expressed patched like

XX CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL

XX CC has two isoforms, with a few single base pair differences between the

XX CC two. One of the single base pair changes introduces a premature stop

XX CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL

XX CC shares an overall structure organisation with the Patched protein. The

XX CC shared structural features strongly imply that HTPL plays a role similar

XX CC to that of Patched and is a potential tumour suppressor. HTPL is

XX CC important in regulating male germ cell development, and the HTPL gene was

XX CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are

XX CC useful for diagnosing a disorder caused by mutation in HTPL, and in

XX CC therapy and manufacture of a medicament for treatment or prevention of

XX CC such disorder associated with decreased expression or activity of human

XX CC HTPL. Such disorders include disorders of testis, or adrenal, adult and

XX CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,

XX CC skeletal muscle or colon function. HTPL proteins and nucleic acids are

XX CC clinically useful diagnostic markers and potential therapeutic agents for

XX CC male infertility and cancer. The present oligonucleotide was used in an

XX CC example from the invention

XX SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.13e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABV79961 (1-17)

Qy 172 LeuSerArgGlnIeu 176

Db 2 CTTCCAGACAACTG 16

RESULT 73
AAS99517/c

ID AAS99517 standard; DNA; 17 BP.

XX AC AAS99517;

XX DT 07-AUG-2003 (revised)

XX DT 12-MAR-2002 (first entry)

XX DE Mycobacterium species identification additional probe #2.

XX KW Drug resistance detection; mycobacterial species identification; probe;

XX KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;

XX KW primer.

XX OS Mycobacterium fortuitum.

XX OS Mycobacterium flavescens.

XX PN WO200192573-A1.

XX PD 06-DEC-2001.

XX PF 30-MAY-2001; 2001WO-KR000904.

XX PR 30-MAY-2000; 2000KR-00029369.

XX PA (BIOM-) BIOMEDLAB CO LTD.

XX PI Kim H, Kim N, Yoon S, Kim J, Park M;

XX DR WPI; 2002-075472/10.

XX PT Kit for mycobacterial species identification and drug resistance

XX PT detection, has oligonucleotide chip with species identification probe, a

XX PT mycobacterial drug-resistance detection probe, and its contrast group

XX PT probe.

XX PS Disclosure; Page 12; 74pp; English.

XX CC The invention relates to a diagnostic kit for mycobacterial species

XX CC identification and drug resistance detection comprising an

XX CC oligonucleotide chip including a species identification probe, a

XX CC mycobacterial drug-resistance detection probe, a contrast group probe

XX CC corresponding to each drug resistance detection probe, and a marker for

XX CC detecting a hybridisation of the oligonucleotide chip and a specimen. The

XX CC identification probe is comprised of species-specific DNA sequences of

XX CC mycobacterial rpoB gene and the detection probe is comprised of one or

XX CC more modified codons of mycobacterial rpoB gene. The method involves

XX CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction

XX CC (PCR) and discriminating species by fluorescent intensity corresponding

XX CC to a particular species. The specimen is preferably uncultured sputum,

XX CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AA99569

XX CC represent mycobacterium species identification probes and primers of the

XX CC invention. (Updated on 07-AUG-2003 to correct OS field.)

XX SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.13e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AAS99517 (1-17)

Qy 174 ArgGlnLeuArgArg 178
Db 17 CGACAGCTGCGAGT 3

RESULT 74

ABV90749
ID ABV90749 standard; DNA; 17 BP.

XX AC ABV90749;

XX DT 23-DEC-2002 (first entry)

XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1462.

XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.

XX OS Homo sapiens.

XX PN EP1239051-A2.

XX PD 11-SEP-2002.

XX PF 28-JAN-2002; 2002EP-00001165.

XX PR 30-JAN-2001; 2001WO-US0000663.

XX PR 30-JAN-2001; 2001WO-US0000664.

XX PR 30-JAN-2001; 2001WO-US0000665.

XX PR 30-JAN-2001; 2001WO-US0000666.

XX PR 30-JAN-2001; 2001WO-US0000667.

XX PR 30-JAN-2001; 2001WO-US0000668.

XX PR 30-JAN-2001; 2001WO-US0000669.

XX PR 30-JAN-2001; 2001WO-US0000670.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 10-OCT-2001; 2001US-0328205P.

XX PA (AEOM-) AEOMICA INC.

XX PI Shannon M;

XX WPI; 2002-684061/74.

XX DR Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL

XX PT -1, useful for treating disorders associated with decreased expression or

XX PT activity of human POSHL1.

XX PS Example 2; SEQ ID NO 1462; 60pp + Sequence Listing; English.

XX CC The invention relates to an isolated SH3 domain (POSH)-like signalling
XX CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
XX CC (SI) having 95% deviations, especially conservative substitutions or a
XX CC fragment of the sequences comprising at least 8 contiguous amino acids.
XX CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX CC adaptor protein that interacts with Rho family small GTPases as well as
XX CC downstream components of the signal transduction pathway. (I) is useful
XX CC for identifying a specific binding partner. (I) and nucleic acids (II)
XX CC encoding (I) are useful for diagnosing, monitoring disease and treating
XX CC caused by altered expression of human POSHL1 including diagnosing and
XX CC treating cancer, they useful in the development of vaccines and (II) is
XX CC useful in gene therapy. (II) is useful for constructing microarrays which
XX CC are useful for measuring and for surveying gene expression and creating
XX CC transgenic non-human animals capable of producing the proteins. The
XX CC present sequence is that of a scanning oligonucleotide useful in examples
XX CC of the invention. Note: The present sequence did not form part of the
XX CC printed specification, but is based on sequence information supplied to
XX CC Derwent by the European Patent Office

XX SQ Sequence 17 BP; 7 A; 2 C; 8 G; 0 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABV90749 (1-17)

Qy 21 AlaLysGlyArgArg 25

Db 1 GCAAAGGAGAGG 15

RESULT 75

ABV90748

ID ABV90748 standard; DNA; 17 BP.

XX AC ABV90748;

XX DT 23-DEC-2002 (first entry)

XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1461.

XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.

XX OS Homo sapiens.

XX PN EP1239051-A2.

XX PD 11-SEP-2002.

XX PF 28-JAN-2002; 2002EP-00001165.

XX PR 30-JAN-2001; 2001WO-US0000663.

XX PR 30-JAN-2001; 2001WO-US0000664.

XX PR 30-JAN-2001; 2001WO-US0000665.

XX PR 30-JAN-2001; 2001WO-US0000666.

XX PR 30-JAN-2001; 2001WO-US0000667.

XX PR 30-JAN-2001; 2001WO-US0000668.

XX PR 30-JAN-2001; 2001WO-US0000669.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 10-OCT-2001; 2001US-0328205P.

XX PA (AEOM-) AEOMICA INC.

XX PI Shannon M;

XX WPI; 2002-684061/74.

XX DR Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL

XX PT -1, useful for treating disorders associated with decreased expression or

XX PT activity of human POSHL1.

XX PS Example 2; SEQ ID NO 1461; 60pp + Sequence Listing; English.

XX CC The invention relates to an isolated SH3 domain (POSH)-like signalling
XX CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
XX CC (SI) having 95% deviations, especially conservative substitutions or a
XX CC fragment of the sequences comprising at least 8 contiguous amino acids.
XX CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX CC adaptor protein that interacts with Rho family small GTPases as well as
XX CC downstream components of the signal transduction pathway. (I) is useful
XX CC for identifying a specific binding partner. (I) and nucleic acids (II)
XX CC encoding (I) are useful for diagnosing, monitoring disease and treating
XX CC caused by altered expression of human POSHL1 including diagnosing and
XX CC treating cancer, they useful in the development of vaccines and (II) is
XX CC useful in gene therapy. (II) is useful for constructing microarrays which

CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Alignment Scores: 8.13e+03 Length: 17
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6

US-09-966-880A-8 (1-198) x ABV90748 (1-17)

Qy 21 AlalysGlyArg 25
Db 2 GCAAAAGGGAGAGG 16

RESULT 76
ABV90747
ID ABV90747 standard; DNA; 17 BP.
AC ABV90747;
XX
XX 23-DEC-2002 (first entry)
DT
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1460.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI239051-A2.
PN
XX
XX 11-SEP-2002.
PD
XX
XX 28-JAN-2002; 2002EP-00001165.
PF
XX
XX 30-JAN-2001; 2001WO-US000663.
PR
XX 30-JAN-2001; 2001WO-US000664.
PR
XX 30-JAN-2001; 2001WO-US000665.
PR
XX 30-JAN-2001; 2001WO-US000666.
PR
XX 30-JAN-2001; 2001WO-US000667.
PR
XX 30-JAN-2001; 2001WO-US000668.
PR
XX 30-JAN-2001; 2001WO-US000669.
PR
XX 30-JAN-2001; 2001WO-US000670.
PR
XX 23-MAY-2001; 2001US-00864761.
PR
XX 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M;
PI
XX
XX WPI; 2002-684061/74.
DR
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX
XX Example 2; SEQ ID NO 1460; 60pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, ABB3999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.

CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Alignment Scores: 8.13e+03 Length: 17
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6

US-09-966-880A-8 (1-198) x ABV90747 (1-17)

Qy 21 AlalysGlyArg 25
Db 3 GCAAAAGGGAGAGG 17

RESULT 77
ABL31617/c
ID ABL31617 standard; DNA; 17 BP.
XX
XX ABL31617;
AC
XX
XX 21-MAR-2002 (first entry)
DT
XX
XX Human HLA genotyping oligonucleotide SEQ ID NO 1106.
DE
XX
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200192572-A1.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 01-JUN-2001; 2001WO-JP004662.
PF
XX
XX 01-JUN-2000; 2000JP-00164798.
PR
XX
XX (NISN) NISSHINBO IND INC.
PA
XX
XX (SYST-) SYSTEM RES INC.
XX
XX
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
PI
XX
XX WPI; 2002-122074/16.
DR
XX
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT individuals e.g. by determining immunogenetic differences when
PT transplanting between them.
PT
XX
XX Claim 10; Page 303; 345pp; Japanese.
PS
XX
XX The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene

CC polymorphisms. The method is useful for judging HLA genotypes of
 CC individuals by determining immunogenetic differences before transplanting
 CC between them, providing genetic information to decide compatibility of
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
 CC pancreas, langerhans islet in pancreas and cornea, susceptibility
 CC diagnosis of genetic diseases and identifying individuals
 CC
 XX Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
 SQ

Alignment Scores: 8.13e+03 Length: 17
 Pred. No.: 5.00 Matches: 5
 Score: 100.00% Conservativity: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 6

US-09-966-880A-8 (1-198) x ABL31617 (1-17)

Qy 112 ArgLeuTy-PheCys 116

Db 15 CGCTTGACTCTGT 1

RESULT 78

ABK57787/c

ID ABK57787 standard; RNA; 17 BP.

XX AC ABK57787;

XX 02-JUL-2002 (first entry)

XX Human CLCA1 gene enzymatic nucleic acid #2159.

XX Human, chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.

XX Homo sapiens.

XX WO200211674-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US024970.

XX 09-AUG-2000; 2000US-0224383P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTAX USA LLC.

PA (THOM) THOMPSON J.

XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

XX Grupe A;

XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX Claim 4; Page 136; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition

CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 XX
 SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Alignment Scores: 8.13e+03 Length: 17
 Pred. No.: 5.00 Matches: 5
 Score: 100.00% Conservativity: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 6

US-09-966-880A-8 (1-198) x ABK57787 (1-17)

Qy 103 AsnLeuSerLeuArg 107

Db 16 AACTTGCTCTGAGA 2

RESULT 79

ABK5838/c

ID ABK5838 standard; RNA; 17 BP.

XX AC ABK5838;

XX 02-JUL-2002 (first entry)

XX Human CLCA1 gene enzymatic nucleic acid #209.

XX Human, chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.

XX Homo sapiens.

XX WO200211674-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US024970.

XX 09-AUG-2000; 2000US-0224383P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTAX USA LLC.

PA (THOM) THOMPSON J.

XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

XX Grupe A;

XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX Claim 4; Page 56; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC that are related to or will respond to the levels of CLCA1 in a cell or

CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 XX
 SQ Sequence 17 BP; 6 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

Alignment Scores: Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK55838 (1-17)

Qy 126 LeuArgLeuHis 130

Db 15 CTTGGAGATTGCAT 2

RESULT 80

ABK56396/c

ID ABK56396 standard; RNA; 17 BP.

AC ABK56396;

XX 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #767.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.

XX Homo sapiens.

XX WC200211674-A2.

PN 14-FEB-2002.

PD 09-AUG-2001; 2001WO-US024970.

PF 09-AUG-2000; 2000US-0224383P.

PR (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTAX USA LLC.

PA (THOM/) THOMPSON J.

XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grupe A;

XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX Claim 4; Page 69; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic

CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 XX

SQ Sequence 17 BP; 6 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

Alignment Scores: Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK56396 (1-17)

Qy 126 LeuArgLeuHis 130

Db 15 CTTGGAGATTGCAT 1

RESULT 81

ABK57455/c

ID ABK57455 standard; RNA; 17 BP.

XX AC ABK57455;

XX 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #1826.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.

XX Homo sapiens.

XX WO200211674-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US024970.

XX 09-AUG-2000; 2000US-0224383P.

PR (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTAX USA LLC.

PA (THOM/) THOMPSON J.

XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grupe A;

XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX Claim 4; Page 113; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are

CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 XX
 SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Alignment Scores: Length: 17
 Pred. No.: 8.13e+03 Matches: 5
 Score: 5.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK57455 (1-17)

Qy 103 AsnLeuSerLeuArg 107
 Db 15 AACTTGTCTCTGAGA 1

RESULT 82
 ABZ95623/c
 ID ABZ95623 standard; DNA; 17 BP.

AC ABZ95623;

XX 17-OCT-2003 (first entry)

DE Human NF-kappaB antisense fragment no.1487.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Disclosure; SEQ ID NO 10865; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 17 BP; 0 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Alignment Scores: Length: 17
 Pred. No.: 8.13e+03 Matches: 5
 Score: 5.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABZ95623 (1-17)

Qy 36 ArgAspSerAlaThr 40

Db 15 CGGCACAGCGCCACC 1

RESULT 83

ACC52922

ID ACC52922 standard; DNA; 17 BP.

XX ACC52922;

XX 27-JUN-2003 (first entry)

XX Human tumour suppressor sequence #1689.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 KW tumour regression; apoptosis; virus resistance; diagnosis;
 KW cellular degeneration.

XX Homo sapiens.

XX FR2826373-A1.

XX 27-DEC-2002.

XX 20-JUN-2001; 2001FR-00008139.

XX 20-JUN-2001; 2001FR-00008139.

XX (MOLE-) MOLECULAR ENGINES LAB SA.

XX Tuijnder M, Telerman A, Amson R;

XX WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumor suppression, regression,
 PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 430; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated

CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 XX
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC52922 (1-17)

QY 169 SerValArgLeuSer 173
 |||||
 Db 3 TCCGTCGCTCAGC 17

RESULT 84

ACC53318
 ID ACC53318 standard; DNA; 17 BP.

XX AC ACC53318;

XX DT 27-JUN-2003 (first entry)

XX DE Human tumour suppressor sequence #2085.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 KW tumour regression; apoptosis; virus resistance; diagnosis;
 KW cellular degeneration.

XX OS Homo sapiens.

XX PN FR2826373-A1.

XX PD 27-DEC-2002.

XX PF 20-JUN-2001; 2001FR-00008139.

XX PR 20-JUN-2001; 2001FR-00008139.

XX PA (MOLE-) MOLECULAR ENGINES LAB SA.

XX PI Tuijnder M, Telerman A, Amson R;

XX DR WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumour suppression, regression,
 PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.

XX PS Claim 1; Page 521; 79pp; French.

XX CC This sequence represents an isolated nucleic acid sequence associated
 CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 XX

SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC53318 (1-17)

QY 118 AspArgLysAlaGlu 122
 |||||
 Db 1 GATCGCAAGCTGAG 15

RESULT 85

ACC52814
 ID ACC52814 standard; DNA; 17 BP.

XX AC ACC52814;

XX DT 27-JUN-2003 (first entry)

XX DE Human tumour suppressor sequence #1581.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 KW tumour regression; apoptosis; virus resistance; diagnosis;
 KW cellular degeneration.

XX OS Homo sapiens.

XX PN FR2826373-A1.

XX PD 27-DEC-2002.

XX PF 20-JUN-2001; 2001FR-00008139.

XX PR 20-JUN-2001; 2001FR-00008139.

XX PA (MOLE-) MOLECULAR ENGINES LAB SA.

XX PI Tuijnder M, Telerman A, Amson R;

XX DR WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumour suppression, regression,
 PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.

XX PS Claim 1; Page 405; 79pp; French.

XX CC This sequence represents an isolated nucleic acid sequence associated
 CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 XX

SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC52814 (1-17)

QY 43 SerLeuApphGly 47
 |||||
 Db 3 TCCCTGGACTTGGG 17

RESULT 86

ACC51417
 ID ACC51417 standard; DNA; 17 BP.

XX AC C51417;
 XX 27-JUN-2003 (first entry)
 XX Human tumour suppressor sequence #184.
 XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 XX tumour regression; apoptosis; virus resistance; diagnosis;
 XX cellular degeneration.
 XX Homo sapiens.
 XX FR2826373-A1.
 XX 27-DEC-2002.
 XX 20-JUN-2001; 2001FR-00008139.
 XX 20-JUN-2001; 2001FR-00008139.
 XX (MOLE-) MOLECULAR ENGINES LAB SA.
 XX Tuijnder M, Telerman A, Amson R;
 XX WPI; 2003-250498/25.
 XX New nucleic acid sequences associated with tumor suppression, regression,
 XX apoptosis or virus resistance are useful to diagnose and treat viral
 XX disease, development of tumor cells and cell degeneration.
 XX Claim 1; Page 82; 798pp; French.
 XX This sequence represents an isolated nucleic acid sequence associated
 XX with tumour suppression or regression, apoptosis or virus resistance. The
 XX invention relates to these sequences or sequences having at least 80%
 XX identity to them, and polypeptides encoded by the sequences or
 XX polypeptides having 80% identity to the polypeptide sequences. The
 XX invention is used to diagnose or treat viral disease or disease
 XX characterized by development of tumour cells or cellular degeneration
 XX Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0
 US-09-966-880A-8 (1-198) x ACC51417 (1-17)
 Qy 173 SerArgGlnLeuArg 177
 Db 3 TCACGGCAGCTGAGA 17
 RESULT 87
 ACC53675/C
 ID ACC53675 standard; DNA; 17 BP.
 XX ACC53675;
 XX 27-JUN-2003 (first entry)
 XX Human tumour suppressor sequence #2442.
 XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 XX tumour regression; apoptosis; virus resistance; diagnosis;
 XX cellular degeneration.
 XX Homo sapiens.

PN FR2826373-A1.
 XX 27-DEC-2002.
 XX 20-JUN-2001; 2001FR-00008139.
 XX 20-JUN-2001; 2001FR-00008139.
 XX (MOLE-) MOLECULAR ENGINES LAB SA.
 XX Tuijnder M, Telerman A, Amson R;
 XX WPI; 2003-250498/25.
 XX New nucleic acid sequences associated with tumor suppression, regression,
 XX apoptosis or virus resistance are useful to diagnose and treat viral
 XX disease, development of tumor cells and cell degeneration.
 XX Claim 1; Page 604; 798pp; French.
 XX This sequence represents an isolated nucleic acid sequence associated
 XX with tumour suppression or regression, apoptosis or virus resistance. The
 XX invention relates to these sequences or sequences having at least 80%
 XX identity to them, and polypeptides encoded by the sequences or
 XX polypeptides having 80% identity to the polypeptide sequences. The
 XX invention is used to diagnose or treat viral disease or disease
 XX characterized by development of tumour cells or cellular degeneration
 XX Sequence 17 BP; 9 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0
 US-09-966-880A-8 (1-198) x ACC53675 (1-17)
 Qy 59 LeuLeupheLeuArg 63
 Db 17 CTCTCTGTTTGTGAGA 3
 RESULT 88
 ACC54176
 ID ACC54176 standard; DNA; 17 BP.
 XX ACC54176;
 XX 27-JUN-2003 (first entry)
 XX Human tumour suppressor sequence #2943.
 XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 XX tumour regression; apoptosis; virus resistance; diagnosis;
 XX cellular degeneration.
 XX Homo sapiens.
 XX FR2826373-A1.
 XX 27-DEC-2002.
 XX 20-JUN-2001; 2001FR-00008139.
 XX 20-JUN-2001; 2001FR-00008139.
 XX (MOLE-) MOLECULAR ENGINES LAB SA.
 XX Tuijnder M, Telerman A, Amson R;
 XX WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX Claim 1; Page 719; 798pp; French.
XX
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumor suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumor cells or cellular degeneration
XX
SQ Sequence 17 BP; 2 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC54176 (1-17)

QY 169 SerValArgLeuSer 173
Db 3 TCCTGTCGGCTCAGC 17

RESULT 89
ABT36841/c
ID ABT36841 standard; DNA; 17 BP.
XX
XX AC ABT36841;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 2478.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001PR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 322; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement

CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABT36841 (1-17)

QY 132 AlaGlyValGlnIle 136
Db 15 GCTGGAGTGCAGATC 1

RESULT 90
ABT37905
ID ABT37905 standard; DNA; 17 BP.
XX
XX AC ABT37905;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 3542.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001PR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 448; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive

CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABT37905 (1-17)

OY 118 AspArgLysAlaGlu 122
DB 1 GATCGCAAGGCTGAG 15

RESULT 91
ABT34570
ID ABT34570 standard; DNA; 17 BP.

AC ABT34570;

XX 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 207.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.

XX Homo sapiens.

OS WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004208.

XX 17-SEP-2001; 2001FR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX

PS Disclosure; Page 58; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX

SQ Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABT34570 (1-17)

OY 83 SerTyrSerProCys 87
DB 3 TCTCGAGGCCCTGT 17

RESULT 92
ABZ64654

ID ABZ64654 standard; RNA; 17 BP.

XX ABZ64654;

XX 21-MAR-2003 (first entry)

XX Human HER2 DNAzyme substrate #111.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

OS WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US016840.

XX 29-MAY-2001; 2001US-0294140P.

PR 06-JUN-2001; 2001US-0296249P.

PR 10-SEP-2001; 2001US-0318471P.

XX (RIBO-) RIBOZYME PHARM INC.

XX McSwiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 4; Page 135; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, AIDS. The sequences
CC shown in ABZ59889 - ABZ62315, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 3 A; 4 C; 7 G; 0 T; 3 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABZ64654 (1-17)

Qy 89 AspCysAlaArgHis 93
Db 3 GAUUGUGCGAGGCAC 17

RESULT 93
ACD59843
ID ACD59843 standard; RNA; 17 BP.
XX
AC ACD59843;
XX
XX 24-SEP-2003 (first entry)
DT
XX HCV DNazyme substrate sequence #1533.
DE
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
XX amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX Hepatitis C virus.
XX
XX WO200281494-A1.
XX
XX 17-OCT-2002.
PD
XX
XX 26-MAR-2002; 2002WO-US009187.
PF
XX
XX 26-MAR-2001; 2001US-00817879.
PR
XX 08-JUN-2001; 2001US-00877478.
PR
XX 08-JUN-2001; 2001US-0296876P.
PR
XX 24-OCT-2001; 2001US-0335059P.
PR
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (NACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.

PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
XX WPI; 2003-229207/22.
DR
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 261; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNazyme or minus strand DNazyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 0 T; 3 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACD59843 (1-17)

Qy 126 LeuArgArgLeuHis 130
Db 1 CUGAGGAGGCGUCCAU 15

RESULT 94
ACD53202
ID ACD53202 standard; RNA; 17 BP.
XX
AC ACD53202;
XX
XX 24-SEP-2003 (first entry)
DT
XX HBV G-cleaver substrate sequence #39.
DE
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
XX amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX Hepatitis B virus.
XX
XX WO200281494-A1.
XX

PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 XX WPI; 2003-229207/22.
 DR
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 PT
 XX Example 1; Page 165; 387pp; English.
 PS
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberszymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HCV. The compounds
 CC that modulate the expression and/or replication of HCV. The compounds
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberszyme sequences
 CC disclosed in the present invention
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 1 G; 0 T; 6 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0
 US-09-966-880a-8 (1-198) x ACD53302 (1-17)
 Qy 172 LeuSerArgGlnLeu 176
 Db 2 CUUUCUGCCCAACU 16
 RESULT 95
 ACD50977
 ID ACD50977 standard; RNA; 17 BP.
 XX
 AC ACD50977;
 XX
 XX 23-SEP-2003 (first entry)

XX
 DE HBV hammerhead ribozyme substrate sequence #341.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberszyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 XX WO200281494-A1.
 PN
 XX
 XX 17-OCT-2002.
 DD
 XX
 XX 26-MAR-2002; 2002WO-US009187.
 PF
 XX
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 XX WPI; 2003-229207/22.
 DR
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 PT
 XX Example 1; Page 142; 387pp; English.
 PS
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberszymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberszyme sequences
 CC disclosed in the present invention
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 4 G; 0 T; 6 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x ACD50977 (1-17)

QY 194 ArgThrLeuGlyLeu 198
|||||

DB 1 AGGACUCUGGACUU 15

RESULT 96
ACD50781
ID ACD50781 standard; RNA; 17 BP.
XX
AC ACD50781;
XX
DT 23-SEP-2003 (first entry)
XX
DE HBV hammerhead ribozyme substrate sequence #247.
XX

Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
RNA stability; RNA expression; RNA synthesis; antisense;
enzymatic nucleic acid; hammerhead ribozyme; DNazyme; zinzyme;
amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
HBV reverse transcriptase; Enhancer I region; viral replication;
degenerative; disease state; HBV infection; HCV infection; cirrhosis;
liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
virucide; antiinflammatory; substrate; ss.

Hepatitis B virus.
WO200281494-A1.
17-OCT-2002.
26-MAR-2002; 2002WO-US009187.
26-MAR-2001; 2001US-00817879.
08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0330505P.
05-DEC-2001; 2001US-0337055P.
(RIBO-) RIBOZYME PHARM INC.
(BLAT/) BLATT L.
(MACE/) MACEJAK D.
(MCSW/) MCSWIGGEN J.
(MORR/) MORRISSEY D.
(PAVC/) PAVCO P.
(LEEP/) LEE P.
(DRAP/) DRAPER K.
(ROBE/) ROBERTS E.

Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
Draper K, Roberts E;
WPI; 2003-229207/22.

Novel compound useful for treating cirrhosis, liver failure,
hepatocellular carcinoma, or condition associated with hepatitis C virus
infection.

Example 1; Page 140; 387pp; English.

The present invention relates to nucleic acid molecules which modulate
the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
are nucleic acid decoy molecules and aptamers that bind to HBV reverse
transcriptase and/or HBV reverse transcriptase primer sequences, as well
as oligonucleotides that specifically bind the Enhancer I region of HBV
DNA. The nucleic acids may be used to modulate the expression of HBV
genes and HBV viral replication. Also disclosed is a method for screening

CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
CC disclosed in the present invention
XX
SQ Sequence 17 BP; 3 A; 6 C; 1 G; 0 T; 7 U; 0 Other;
XX

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x ACD50781 (1-17)

QY 172 LeuSerArgGlnLeu 176
|||||

DB 3 CUUUCUGGCCACUU 17

RESULT 97
ACD50976
ID ACD50976 standard; RNA; 17 BP.
XX
AC ACD50976;
XX
DT 23-SEP-2003 (first entry)
XX
DE HBV hammerhead ribozyme substrate sequence #340.
XX

Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
RNA stability; RNA expression; RNA synthesis; antisense;
enzymatic nucleic acid; hammerhead ribozyme; DNazyme; zinzyme;
amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
HBV reverse transcriptase; Enhancer I region; viral replication;
degenerative; disease state; HBV infection; HCV infection; cirrhosis;
liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
virucide; antiinflammatory; substrate; ss.

Hepatitis B virus.
WO200281494-A1.
17-OCT-2002.
26-MAR-2002; 2002WO-US009187.
26-MAR-2001; 2001US-00817879.
08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0330505P.
05-DEC-2001; 2001US-0337055P.
(RIBO-) RIBOZYME PHARM INC.
(BLAT/) BLATT L.
(MACE/) MACEJAK D.
(MCSW/) MCSWIGGEN J.
(MORR/) MORRISSEY D.
(PAVC/) PAVCO P.
(LEEP/) LEE P.
(DRAP/) DRAPER K.
(ROBE/) ROBERTS E.

Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
Draper K, Roberts E;
WPI; 2003-229207/22.

Novel compound useful for treating cirrhosis, liver failure,
hepatocellular carcinoma, or condition associated with hepatitis C virus
infection.

Example 1; Page 140; 387pp; English.

The present invention relates to nucleic acid molecules which modulate
the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
are nucleic acid decoy molecules and aptamers that bind to HBV reverse
transcriptase and/or HBV reverse transcriptase primer sequences, as well
as oligonucleotides that specifically bind the Enhancer I region of HBV
DNA. The nucleic acids may be used to modulate the expression of HBV
genes and HBV viral replication. Also disclosed is a method for screening

PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.

XX Example 1; Page 142; 387pp; English.

CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberyzyme sequences
CC disclosed in the present invention

SQ Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACD50976 (1-17)

Qy 194 ArgThrLeuGlyLeu 198
Db 3 AGGACUUCUGGACUU 17

RESULT 98
ACD52479
ID ACD52479 standard; RNA; 17 BP.

AC ACD52479;
XX 24-SEP-2003 (first entry)
DE HBV inozyme substrate sequence #405.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW amberyzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.

XX Hepatitis B virus.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296876P.

XX 24-OCT-2001; 2001US-0335059P.

XX 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI; 2003-229207/22.

PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.

XX Example 1; Page 158; 387pp; English.

CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberyzyme sequences
CC disclosed in the present invention

SQ Sequence 17 BP; 3 A; 3 C; 5 G; 0 T; 6 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACD52479 (1-17)

Qy 194 ArgThrLeuGlyLeu 198
Db 2 AGGACUUCUGGACUU 16

RESULT 99
ACD68084
ID ACC68084 standard; DNA; 17 BP.

XX ACC68084;

XX 01-JUL-2003 (first entry)

XX Murine oligonucleotide associated with tumour supression, SEQ ID 5331.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;

XX tumour suppression; tumour reversion; apoptosis; virus resistance;

XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;

XX schizophrrenia; ss.

XX Mus musculus.

XX PN WO2003025176-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004210.
XX PR 17-SEP-2001; 2001FR-00011979.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-333167/31.
XX PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
XX PS Disclosure; Page 654; 738pp; French.
XX CC The present invention relates to murine oligonucleotides (ACC62754-ACC6806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip; in vitro as (anti)sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia
XX SQ Sequence 17 BP; 2 A; 8 C; 1 G; 6 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0
US-09-966-880A-8 (1-198) x ACC68084 (1-17)
QY 179 ILeuLeuProLeu 183
DB 2 ATCTTCTCCCACTC 16
RESULT 100
ACC63683
ID ACC63683 standard; DNA; 17 BP.
XX AC ACC63683;
XX DT 01-JUL-2003 (first entry)
XX DE Murine oligonucleotide associated with tumour suppression, SEQ ID 930.
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; ss.
XX OS Mus musculus.
XX PN WO2003025176-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004210.
XX PR 17-SEP-2001; 2001FR-00011979.
XX PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

PA (MOLE-) MOLECULAR ENGINES LAB.
XX Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-333167/31.
XX PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
XX PS Disclosure; Page 139; 738pp; French.
XX CC The present invention relates to murine oligonucleotides (ACC62754-ACC6806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip; in vitro as (anti)sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia
XX SQ Sequence 17 BP; 3 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0
US-09-966-880A-8 (1-198) x ACC63683 (1-17)
QY 71 AspProGlyArgCys 75
DB 1 GATCAGGCGAGGTGT 15
RESULT 101
ACC65317
ID ACC65317 standard; DNA; 17 BP.
XX AC ACC65317;
XX DT 01-JUL-2003 (first entry)
XX DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2564.
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; ss.
XX OS Mus musculus.
XX PN WO2003025176-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004210.
XX PR 17-SEP-2001; 2001FR-00011979.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-333167/31.
XX PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

XX Disclosure; Page 330; 738pp; French.
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0
 US-09-966-880A-8 (1-198) x ACC65317 (1-17)
 QY 43 SerLeuAspPheGly 47
 DB 3 TCCTGGACTTGGT 17
 RESULT 102
 ACC67174
 ID ACC67174 standard; DNA; 17 BP.
 AC ACC67174;
 XX
 DT 01-JUL-2003 (first entry)
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4421.
 XX
 XX Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX WO2003025176-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004210.
 XX 17-SEP-2001; 2001FR-00011979.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-333167/31.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 547; 738pp; French.
 XX
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of

CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX Sequence 17 BP; 1 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0
 US-09-966-880A-8 (1-198) x ACC67174 (1-17)
 QY 179 IleLeuLeuProLeu 183
 DB 2 ATCTCTCTCTCTCTG 16
 RESULT 103
 ACC64429
 ID ACC64429 standard; DNA; 17 BP.
 AC ACC64429;
 XX
 DT 01-JUL-2003 (first entry)
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1676.
 XX
 XX Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX WO2003025176-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004210.
 XX 17-SEP-2001; 2001FR-00011979.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-333167/31.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 227; 738pp; French.
 XX
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC64429 (1-17)

QY 179 IleLeuLeuProLeu 183
DB 2 ATCCTTGGCACTG 16

RESULT 104

ACC68311
ID ACC68311 standard; DNA; 17 BP.

XX

AC ACC68311;

DT 01-JUL-2003 (first entry)

DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5558.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.

XX

OS Mus musculus.

XX WO2003025176-A2.

PN

PD 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004210.

PF

XX 17-SEP-2001; 2001PR-00011979.

PR (MOLE-) MOLECULAR ENGINES LAB.

XX

PI Teلمان A, Anson R, Tuijnder M;

XX WPI; 2003-333167/31.

DR New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.

PT

PS Disclosure; Page 680; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC6806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC Specifically cancer but also Alzheimer's disease and schizophrenia

XX Sequence 17 BP; 1 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC68311 (1-17)

QY 179 IleLeuLeuProLeu 183

Db 2 ATCCTTGGCCTTT 16

RESULT 105

ADA15891/c

ID ADA15891 standard; DNA; 17 BP.

XX

AC ADA15891;

DT 20-NOV-2003 (first entry)

DE Primer for amplification of GAPDH DNA #SEQ ID 70.

XX Human; beta-actin; GAPDH; loop-mediated isothermal amplification; LAMP;
KW glyceraldehyde-3-phosphate dehydrogenase; cancer; metastasis;
KW genetic engineering; PCR; primer; ss.

XX Homo sapiens.

OS

PN WO2003070935-A1.

XX

XX 28-AUG-2003.

XX 13-FEB-2003; 2003WO-JP001474.

PF

XX 20-FEB-2002; 2002JP-00043866.

PR

XX 20-FEB-2002; 2002JP-00043867.

XX (SYSM-) SYSMEX CORP.

XX

XX Tada S;

XX WPI; 2003-679880/64.

XX

DR Primers for nucleic acid amplification in detecting housekeeping gene
XX mRNAs to confirm amplification of beta-actin and glyceraldehyde-3-
PT phosphate dehydrogenase useful in diagnosis of cancer.

PT

PS Claim 5; Page 25; 90pp; Japanese.

XX The invention relates to primers for nucleic acid amplification for
CC detecting a housekeeping gene and/or a housekeeping gene-related mRNA by
CC the loop-mediated isothermal amplification (LAMP) method. Particularly
CC referred to are primers for the amplification of beta-actin or GAPDH. The
CC primers of the invention are for nucleic acid amplification in detecting
CC housekeeping gene mRNAs, e.g. to confirm amplification of beta-actin and
CC glyceraldehyde-3-phosphate dehydrogenase (GAPDH), which are useful in
CC diagnosis of cancer and metastasis. By applying such primers, the
CC amplification of beta-actin and GAPDH can be used to confirm the presence
CC or absence of a tumour marker, e.g. cytokeratin, which can be used in the
CC control of data correction in the LAMP method, particularly in genetic
CC engineering, molecular biology and clinical medicine including disease
CC diagnosis. Using this method, diagnosis is fast (within 15 minutes) and
CC highly reliable. The required primers were designed based upon the gene
CC domain of e.g. beta-actin. After reaction by the reverse transcriptase-
CC loop-mediated isothermal amplification (RT-LAMP) method, the
CC amplification product was detected to confirm amplification of beta-actin
CC in the samples. The current sequence represents a primer for the
CC amplification of human GAPDH.

XX Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x ADA15891 (1-17)

QY 82 ThrSerTrpSerPro 86

```

Db      15  ACCTCGTGGAGTCCA 1
RESULT 106
ADB42925
ID      ADB42925 standard; DNA; 17 BP.
XX
AC      ADB42925;
XX
DT      18-DEC-2003 (revised)
DT      04-DEC-2003 (first entry)
XX
DE      Tumour suppression/reversion associated nucleotide #3248.
XX
KW      cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW      primer; probe; tumour suppression; tumour reversion; apoptosis;
KW      virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW      diagnosis.
XX
OS      Homo sapiens.
XX
EN      WO2003040369-A2.
XX
PD      15-MAY-2003.
XX
PF      17-SEP-2002; 2002WO-IB004219.
XX
PR      17-SEP-2001; 2001PR-00011981.
XX
PA      (MOLE-) MOLECULAR ENGINES LAB.
XX
PI      Telerman A, Amson R, Tuijnder M;
XX
DR      WPI; 2003-441574/41.
XX
PT      New nucleic acid encoding human prostate membrane-specific antigen,
PT      useful e.g. for treatment of tumors and viral infection, also related
PT      polypeptide and antibodies.
XX
FS      Disclosure; Page 411; 771pp; French.
XX
CC      The invention relates to the isolation of 6327 nucleotide sequences,
CC      fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC      sequence having at least 80% identity, after optimal alignment with the
CC      nucleotides, a sequence that hybridizes under stringent conditions with
CC      the nucleotides, or the complement, or corresponding RNA, of the
CC      nucleotides. The nucleotides are used as probes or primers for detecting,
CC      identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC      sense and antisense sequences, of nucleotides involved in tumour
CC      suppression or reversion, apoptosis and or viral resistance, to produce
CC      recombinant polypeptides, and to prepare transgenic animals, as
CC      experimental models. The nucleotides (also vectors containing them and
CC      cells containing the vectors), the encoded polypeptides and antibodies
CC      (Ab) against the polypeptide are useful for prevention and/or treatment
CC      of viral infections or diseases characterized by development of tumours
CC      or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC      Analysis of the expression of the nucleotides can be used for diagnosis
CC      and/or prognosis of these diseases. The nucleotides and polypeptides can
CC      also be used to screen for their specific interactive molecules,
CC      potentially useful for treating diseases associated with abnormal
CC      expression of the nucleotides.
XX
SQ      Sequence 17 BP; 1 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      8.13e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%      Mismatches: 0
Best Local Similarity: 100.00%      Indels:      0
Query Match:    2.53%          Gaps:        0
DB:
US-09-966-880A-8 (1-198) x ADB42925 (1-17)

Oy      179 IleleulenProJen 183
Db      2 ATCTCTGCTCTG 16
RESULT 107
ADB43664
ID      ADB43664 standard; DNA; 17 BP.
XX
AC      ADB43664;
XX
DT      18-DEC-2003 (revised)
DT      04-DEC-2003 (first entry)
XX
DE      Tumour suppression/reversion associated nucleotide #3987.
XX
KW      cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW      primer; probe; tumour suppression; tumour reversion; apoptosis;
KW      virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW      diagnosis.
XX
OS      Homo sapiens.
XX
EN      WO2003040369-A2.
XX
PD      15-MAY-2003.
XX
PF      17-SEP-2002; 2002WO-IB004219.
XX
PR      17-SEP-2001; 2001PR-00011981.
XX
PA      (MOLE-) MOLECULAR ENGINES LAB.
XX
PI      Telerman A, Amson R, Tuijnder M;
XX
DR      WPI; 2003-441574/41.
XX
PT      New nucleic acid encoding human prostate membrane-specific antigen,
PT      useful e.g. for treatment of tumors and viral infection, also related
PT      polypeptide and antibodies.
XX
FS      Disclosure; Page 498; 771pp; French.
XX
CC      The invention relates to the isolation of 6327 nucleotide sequences,
CC      fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC      sequence having at least 80% identity, after optimal alignment with the
CC      nucleotides, a sequence that hybridizes under stringent conditions with
CC      the nucleotides, or the complement, or corresponding RNA, of the
CC      nucleotides. The nucleotides are used as probes or primers for detecting,
CC      identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC      sense and antisense sequences, of nucleotides involved in tumour
CC      suppression or reversion, apoptosis and or viral resistance, to produce
CC      recombinant polypeptides, and to prepare transgenic animals, as
CC      experimental models. The nucleotides (also vectors containing them and
CC      cells containing the vectors), the encoded polypeptides and antibodies
CC      (Ab) against the polypeptide are useful for prevention and/or treatment
CC      of viral infections or diseases characterized by development of tumours
CC      or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC      Analysis of the expression of the nucleotides can be used for diagnosis
CC      and/or prognosis of these diseases. The nucleotides and polypeptides can
CC      also be used to screen for their specific interactive molecules,
CC      potentially useful for treating diseases associated with abnormal
CC      expression of the nucleotides.
XX
SQ      Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      8.13e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%      Mismatches: 0
Best Local Similarity: 100.00%      Indels:      0
Query Match:    2.53%          Gaps:        0
DB:

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US-09-966-880A-8 (1-198) x ADB43664 (1-17)
QY 179 ILeLeuLeuProLeu 183
Db 2 ATCTTGTGCCATTG 16

RESULT 108
ADB39967/C
ID ADB39967 standard; DNA; 17 BP.
XX AC ADB39967;
XX AC
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #290.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX
XX Disclosure; Page 66; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX CC Analysis of the expression of the nucleotides can be used for diagnosis
XX CC and/or prognosis of these diseases. The nucleotides and polypeptides can
XX CC also be used to screen for their specific interactive molecules,
XX CC potentially useful for treating diseases associated with abnormal
XX CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 7 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0
US-09-966-880A-8 (1-198) x ADB39967 (1-17)
QY 46 PheGLYTYrLeuArg 50
Db 17 TTGGATATCTCAGA 3

RESULT 109
ADB43195
ID ADB43195 standard; DNA; 17 BP.
XX AC ADB43195;
XX AC
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #3518.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
XX
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX
XX Disclosure; Page 443; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX CC Analysis of the expression of the nucleotides can be used for diagnosis
XX CC and/or prognosis of these diseases. The nucleotides and polypeptides can
XX CC also be used to screen for their specific interactive molecules,
XX CC potentially useful for treating diseases associated with abnormal
XX CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00% Mismatches: 0

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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
DB: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x ADB43195 (1-17)

QY 118 AspArgLysAlaGlu 122
DB 1 GATCGCAAGGCTGAG 15

RESULT 110

ADB45489

ID ADB45489 standard; DNA; 17 BP.

XX AC ADB45489;

XX DT 18-DEC-2003 (first entry)

XX DE Tumour suppression/reversion associated nucleotide #5812.

XX KW cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.

XX OS Homo sapiens.

XX PN WO2003040369-A2.

XX PD 15-MAY-2003.

XX PF 17-SEP-2002; 2002WO-IB004219.

XX PR 17-SEP-2001; 2001FR-00011981.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-441574/41.

XX PT New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.

XX PS Disclosure; Page 711; 771pp; French.

XX CC The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.

SQ Sequence 17 BP; 3 A; 2 C; 5 G; 7 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
DB: 9
Matches: 5
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x ADB45489 (1-17)

QY 43 SerieuAspPheGly 47
DB 3 TCCTTAGATTGGG 17

RESULT 111

ADB45286

ID ADB45286 standard; DNA; 17 BP.

XX AC ADB45286;

XX DT 18-DEC-2003 (first entry)

XX DE Tumour suppression/reversion associated nucleotide #5609.

XX KW cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.

XX OS Homo sapiens.

XX PN WO2003040369-A2.

XX PD 15-MAY-2003.

XX PF 17-SEP-2002; 2002WO-IB004219.

XX PR 17-SEP-2001; 2001FR-00011981.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-441574/41.

XX PT New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.

XX PS Disclosure; Page 687; 771pp; French.

XX CC The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.

SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Alignment Scores:

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x AAN60649 (1-18)

QY 32 ValVallyeArgArg 36
 DB 2 GTTGTAAACGACGG 16

RESULT 114

AAQ58760
 ID AAQ58760 standard; DNA; 18 BP.

XX AC AAQ58760;

XX 25-MAR-2003 (revised)
 DT 03-OCT-1994 (first entry)

XX Glucagon receptor primer ZC976.

DE XX
 XX Rat; human; glucagon receptor; transgenic animal; metabolism; model;
 KW secretin; amplification; primer; polymerase chain reaction; PCR; ss.
 KW
 XX
 XX Synthetic.

OS WO9405789-A1.

XX 17-MAR-1994.

XX 30-AUG-1993; 93WO-US008174.

XX 28-AUG-1992; 92US-00938331.

PR 01-JUL-1993; 93US-00086631.

XX (ZYMO) ZYMOGENETICS INC.

XX Kindsvogle WR, Jelinek LJ, Sheppard PO, Grant FJ, Kuitjer JL;
 PI Foster DC, Lok S, Ohara PJ;
 XX WPI; 1994-101194/12.

XX New recombinant glucagon receptors and antibodies - useful to produce
 PT model transgenic animals for study and with therapeutic applications.

XX Example 4; Page 71; 112pp; English.

XX Rat and human glucagon receptor (GR) DNA was isolated. Primers for DNA
 CC amplification are ZC4715 and ZC4701 (rat and human; corresp. to regions
 CC of high conservation among the members of the secretin gene family); and
 CC ZC4758 and ZC4778 (human). To screen transformants for a human GR
 CC sequence, the insert DNA present in each transformant was amplified using
 CC oligonucleotides ZC447 and ZC976, which were designed as universal pUC
 CC sequencing primers and primed to pUC sequences flanking the PCR product
 CC insert. One clone, G30, was shown to hybridise with the full length rat
 CC cDNA probe. The nucleotide sequence of G30 is shown in AAQ67246. Host
 CC cells contg. GR DNA may be used for the prodn. of recombinant GR. GR DNA
 CC may also be expressed in non-human transgenic animals, pref. mice. Such
 CC animals may be readily used as models to study the role of the glucagon
 CC receptor in metabolism. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ58760 (1-18)

QY 32 ValVallyeArgArg 36
 DB 2 GTTGTAAACGACGG 16

RESULT 115

AAQ65771
 ID AAQ65771 standard; DNA; 18 BP.

XX AC AAQ65771;

XX 25-MAR-2003 (revised)
 DT 19-DEC-1994 (first entry)

XX Type II procollagen sequencing primer CW-5.

XX Type II procollagen; COL2A1; amplification; primer;
 KW polymerase chain reaction; PCR; osteoarthritis; cartilage; ss.
 KW
 XX Synthetic.

OS WO9411532-A1.

XX 26-MAY-1994.

XX 12-NOV-1993; 93WO-US010964.

XX 13-NOV-1992; 92US-00977284.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Prockop DJ, Ala-Kokko L, Williams CJ, Ritvaniemi P, Baldwin C;
 PI Hopkinson I, Ahmad NN;
 XX WPI; 1994-183530/22.

XX Detecting genetic pre-disposition to osteoarthritis - and other diseases
 PT involving mutation in cartilage protein genes, by amplification and
 PT analysis of DNA and comparison with standards.

XX Claim 18; Page 22; 112pp; English.

XX Claim 18 claims primers for use in detecting mutations in a mammalian
 CC gene for a structural protein of cartilage comprising a sequence
 CC identified in Table I (Page 18-31). Table I includes 179 primer sequences
 CC (see AAQ65728-Q65906). The following details are given for primer CW-5:
 CC Region/exon: 18 Direction: sense Primer position: 8351 (Updated on 25-MAR
 CC -2003 to correct PN field.)

XX Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ65771 (1-18)

QY 69 AspLeuAspProGly 73
 DB 3 GATCTGGATCTCGA 17

RESULT 116

AAQ72647/C
 ID AAQ72647 standard; DNA; 18 BP.

XX AC AAQ72647;

XX 25-MAR-2003 (revised)
DT 22-MAY-1995 (first entry)
XX
DE Probe 12, anneals to bases 189-206 of exon 2 of HLA-B*4601.
XX
XX Polymerase chain reaction; PCR; primer; amplify; detection; HLA-B;
KW human leukocyte antigen; B2P; allele; exon 2; B54(22); B52(5); B7801;
KW B2(15); B75(15); B71(70); B46; B79; B53; B5102; B5103; B58(17);
KW compatibility; donor; recipient; organ transplant; success-rate;
KW bone-marrow transplant; disease susceptibility study; probe;
KW forensic investigation; ss.
XX
XX Synthetic.
XX
XX WO9421818-A1.
PN
XX
XX 29-SEP-1994.
PD
XX
XX 07-MAR-1994; 94WO-EP000654.
XX
XX 18-MAR-1993; 93EP-00400700.
XX
XX (INNO-) INNOGENETICS NV SA.
PA
XX
XX Andrien M, Dupont E, Rossau R, De Canck I;
PI
XX
XX WPI; 1994-317037/39.
DR
XX
XX DNA typing using primers and probes enabling discrimination of HLA-B
PT alleles - esp. where difficult to discriminate by serological means.
PT
XX
XX Claim 7; Page 39; 66pp; English.
PS
XX
XX The sequences given in AAQ72636-55 are probes which were used to
CC discriminate HLA-B alleles which are characterised by having the sequence
CC 5'-GCCA-3' at position 30-33 of exon 2 of the HLA-B allele. Variants of
CC these sequences which may also be used are given in AAQ72656- 81. These
CC probes are used to identify the amplification products of the primers
CC given in AAQ72630-35. These primers may be used to distinguish between
CC HLA-B types which are serologically difficult to discriminate, eg.
CC B54(22), B52(5), B7801, B62(15), B75(15), B71(70), B46, B79, B53, B5102,
CC B5103 and B58(17). Using this method, HLA-B compatibility between donors
CC and recipients of organ transplants can be increased, thereby having a
CC beneficial impact on success-rate of organ and bone-marrow transplants.
CC HLA-B typing may be used to improve or facilitate disease susceptibility
CC studies and forensic investigations. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
XX Sequence 18 BP; 8 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Alignment Scores:
Pred. NO.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ72647 (1-18)

QY 112 ArgLeuTyrPheCys 116
DB 17 CGCTTGACTTCGT 3
RESULT 117
AAT36742
ID AAT36742 standard; DNA; 18 BP.
XX
AC AAT36742;
XX
DT 18-APR-1997 (first entry)
XX

DE Carnobacterium piscicola piscicolin 126 gene primer #1.
XX
XX Bacteriocin; Carnobacterium piscicola; Piscicolin 126; microorganism;
KW anti-microbial activity; PCR; polymerase chain reaction; amplification;
KW 16S rRNA gene; primer; probe; genomic library; phage lambda; nicin;
KW pediocin; food-borne pathogen; spoilage; starter culture; preservation;
KW beverage; ss.
XX
XX Synthetic.
XX
XX WO9626216-A1.
PN
XX
XX 29-AUG-1996.
PD
XX
XX 22-FEB-1996; 96WO-AU0000096.
XX
XX 22-FEB-1995; 95AU-00001310.
XX
XX (UYME) UNIV MELBOURNE.
PA
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (AUFO-) AUSTRALIAN FOOD IND SCI CENT.
XX
XX Wetenhall REH, Davidson BE, Hillier AJ, Harmark K, Jack RW;
PI Hickey MW, Coventry J, Wan J;
XX
XX WPI; 1996-402319/40.
DR
XX
XX Bacteriocin active against food-borne pathogens and spoilage organisms,
PT but not against beneficial bacteria - useful as preservative in foods and
PT beverages and in cheese starter cultures.
XX
XX Example 5; Page 6; 25pp; English.
PS
XX
XX The invention relates to the isolation of a novel bacteriocin designated
CC Piscicolin 126 from the microbe Carnobacterium piscicola strain JG126
CC (WO2211). The parent microorganism was isolated from a ham when a range
CC of microorganisms were assayed for anti-microbial activity. Primers
CC T36740-1 were used to identify the strain of microorganism by PCR
CC amplifying a region of the cell's 16S rRNA gene. The resultant sequence
CC was identical to a C. piscicola sequence (Genbank accession M5812). The
CC protein was isolated by conventional chromatography techniques and
CC subjected to amino acid sequencing. The degenerate primers (T36742-3)
CC were synthesised based on the amino acid sequence. These were used to
CC amplify a 107 bp fragment of the gene which was used as a probe to screen
CC a genomic library in phage lambda. From this screen, a positive clone
CC containing the piscicolin gene (T36876) was isolated. The new bacteriocin
CC has a more limited range of activity than nicin or pediocin Pa-1 and is
CC active against a range of food-borne pathogens or spoilage organisms but
CC not against beneficial organisms e.g. starter cultures. The bacteriocin
CC can thus be used to preserve food and beverages
XX
XX Sequence 18 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 6 Other;

Alignment Scores:
Pred. NO.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT36742 (1-18)

QY 51 AsnLysAsnGlyCys 55
DB 4 AAYAAARAYGGTGY 18
RESULT 118
AAX64476/c
ID AAX64476 standard; RNA; 18 BP.
XX
AC AAX64476;
XX

DT 20-JUL-1999 (first entry)
 XX Rabbit stromelysin hairpin target sequence SEQ ID NO:1108.
 DE
 XX
 KW Arthritic condition; graft tolerance; immune response; target; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
 KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
 KW diagnosis; ss.
 XX
 XX Oryctolagus cuniculus.
 OS
 XX
 XX WO9618736-A2.
 PN
 XX
 XX 20-JUN-1996.
 PD
 XX
 XX 22-NOV-1995; 95WO-US015516.
 PF
 XX
 XX 13-DEC-1994; 94US-00354920.
 PR
 XX 23-DEC-1994; 94US-00363253.
 PR
 XX 23-DEC-1994; 94US-00363254.
 PR
 XX 17-FEB-1995; 95US-00390850.
 PR
 XX 20-APR-1995; 95US-00426124.
 PR
 XX 02-MAY-1995; 95US-00432874.
 PR
 XX 04-MAY-1995; 95US-00434509.
 PR
 XX 07-JUL-1995; 95US-0000951P.
 PR
 XX 07-JUL-1995; 95US-0000974P.
 PR
 XX 07-AUG-1995; 95US-00512861.
 PR
 XX 05-OCT-1995; 95US-00541365.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
 PI McSwiggan J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
 PI Karpelsky A, Thompson JD, Modak A, Burgin A;
 XX
 XX WPI; 1996-300653/30.
 DR
 XX
 XX Enzymatic nucleic acid molecules having a hammer-head motif - used for
 PT the treatment of arthritis, induction of graft tolerance or treatment of
 PT auto-immune diseases.
 PT
 XX
 XX Example 1; Page 165; 307pp; English.
 PS
 XX
 CC The present invention describes a novel enzymatic nucleic acid (ENA)
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
 CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
 CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
 CC can inhibit collagenase and stromelysin production in the synovial
 CC membrane of joints for the treatment or prevention of arthritis,
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
 CC be used to treat antigen presenting cells of a donor to induce tolerance
 CC in a recipient to an alloantigen of a donor. They can also be used for
 CC enhancing graft tolerance or for treating autoimmune disease, and for
 CC treating allergies and other inflammatory conditions. The ENA's can also
 CC be used in diagnosis. Ribozyme therapy impacts on the expression of
 CC stromelysin without introducing the non-specific effects upon gene
 CC expression which accompany treatment with retinoids and dexamethasone.
 CC The concentration of ribozyme required to affect a therapeutic treatment
 CC is lower than that required of antisense molecules, and is highly
 CC specific. The present sequence is used in the exemplification of the
 CC present invention
 CC
 XX
 XX Sequence 18 BP; 2 A; 7 C; 3 G; 0 T; 6 U; 0 Other;

US-09-966-880A-8 (1-198) x AAY64476 (1-18)
 QY 119 ArgLysalaGluPro 123
 Db 15 AGAAAGCGGAGACCG 1
 RESULT 119
 AAT76355
 ID AAT76355 standard; DNA; 18 BP.
 XX
 XX AC AAT76355;
 XX
 XX 15-SEP-1997 (first entry)
 DT
 XX Human fibronectin antisense oligonucleotide HUMFNA/HSFIB1AS23.
 DE
 XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
 KW chronic obstructive pulmonary disease; bronchitis; ss.
 KW
 XX Synthetic.
 OS
 XX WO9640162-A1.
 PN
 XX 19-DEC-1996.
 PD
 XX 06-JUN-1996; 96WO-US009306.
 PF
 XX 07-JUN-1995; 95US-00474497.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX
 XX Nyce JW, Metzger WJ;
 PI
 XX WPI; 1997-051871/05.
 DR
 XX Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligo:nucleotide to airway epithelium of
 PT subject.
 PT
 XX
 XX Claim 5; Page 36; 71pp; English.
 PS
 CC A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide
 CC HUMFNA/HSFIB1AS23 specific for the human fibronectin. The method can be
 CC used to treat airway diseases such as cystic fibrosis, asthma, chronic
 CC obstructive pulmonary disease, bronchitis and other airway diseases
 CC characterised by an inflammatory response. By eliminating adenosine from
 CC the antisense ON, its liberation upon antisense degradation is prevented,
 CC thereby preventing adenosine-induced bronchoconstriction in patients
 CC with hyper-reactive airways
 CC
 XX Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAT76355 (1-18)
 QY 59 LeuLeuPheLeuArg 63
 Db 4 CTCCTGTTCCTCCGT 18
 RESULT 120
 AAV59406
 ID AAV59406 standard; DNA; 18 BP.
 XX

AC AAV59406;
XX DT 21-JAN-1999 (first entry)
XX DE
XX PCR primer ZC976 used to amplify a zsig32 DNA fragment.
XX
XX Secreted salivary polypeptide; zsig32; salivary gland; human;
KW mucous associated; digestive dysfunction; wound healing dysfunction;
KW salivary gland carcinoma; sarcoidosis; pneumocystic carinii; PCR primer;
KW emphysema; chronic bronchitis; cystic fibrosis; tumour; xerostomia;
KW adult respiratory distress syndrome; ARDS; dental caries; osteomyelitis;
KW sudden infant death syndrome; SIDS; oral candidiasis; prostate carcinoma;
KW migraine; buccal mucosa infection; Sjogren's syndrome; mumps; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9841628-A1.
FN
XX
XX 24-SEP-1998.
PD
XX
XX 18-MAR-1998; 98WO-US005255.
PF
XX
XX 19-MAR-1997; 97US-0041263P.
PR
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Sheppard PO;
PI
XX
XX WPI; 1998-531567/45.
DR
XX
XX New isolated mucous-associated polypeptide, zsig32 - used to develop
PT products for treating e.g. digestive or lung dysfunction, microbial
PT infections, cystic fibrosis, inflammation or tumour metastasis.
XX
XX Example 8; Page 100; 118pp; English.
PS
XX
XX PCR primers AAV59406-07 were used to amplify fragments of DNA encoding a
CC secreted salivary polypeptide designated zsig32. The protein is involved
CC in salivary gland and mucous associated functions. The products can be
CC used in the treatment of e.g. digestive dysfunction, wound healing
CC dysfunction, inadequate saliva production or composition, mucosal
CC integrity breakdown, failure or diminished anti-microbial function.
CC salivary gland carcinoma, sarcoidosis, pneumocystic carinii (particularly
CC as associated with AIDS patients), emphysema, chronic bronchitis, cystic
CC fibrosis, adult respiratory distress syndrome (ARDS), sudden infant death
CC syndrome (SIDS), lung diseases, tumour metastasis, xerostomia, dental
CC caries, osteomyelitis, oral candidiasis, buccal mucosa infections,
CC chronic inflammation (Sjogren's syndrome), mumps, prostate carcinoma or
CC migraine
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV59406 (1-18)

OY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 121
AAV59324
ID AAV59324 standard; cDNA; 18 BP.
XX
XX AAV59324;
XX
XX 02-FEB-1999 (first entry)
XX
XX Human chemokine ZSIG-35 PCR primer ZC976.
XX
XX ZSIG-35; beta-chemokine; human; ligand; lymphocyte migration;
KW inflammation; ischaemia; reperfusion injury; baculovirus; vector;
KW PFSGE35; PCR; primer; ss.
XX

DT 21-DEC-1998 (first entry)
XX
XX zsig10 primer ZC976.
XX
XX ss; human; mucous-mediated function; adhesion; tumour metastasis;
KW bacterial colonisation; microbial infection; AIDS; cystic fibrosis;
KW chronic obstructive pulmonary disease; asthma; Crohn's disease;
KW sinonasal inflammatory disease; inflammatory bowel disease; bronchitis;
KW PCR; primer; amplification.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9841627-A1.
FN
XX
XX 24-SEP-1998.
PD
XX
XX 18-MAR-1998; 98WO-US005251.
PF
XX
XX 19-MAR-1997; 97US-0039631P.
PR
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Sheppard PO;
PI
XX
XX WPI; 1998-531566/45.
DR
XX
XX New isolated mucous-associated polypeptide, zsig10 - used to develop
PT products for treating e.g. tumour metastasis, microbial infections,
PT cystic fibrosis, asthma, bronchitis or inflammatory bowel disease.
XX
XX Example 1; Page 85; 109pp; English.
PS
XX
XX The primer AAV59321-V59327 were used in the production of a human
CC polypeptide zsig10. zsig10 is involved in mucous-mediated functions such
CC as adhesion. The products of the invention can be used in the study and
CC treatment of e.g. tumour metastasis, bacterial colonisation,
CC susceptibility to and persistence of infection, microbial infections,
CC AIDS, cystic fibrosis, chronic obstructive pulmonary disease, asthma,
CC sinonasal inflammatory disease, inflammatory bowel disease, bronchitis,
CC or Crohn's disease. The products can also be used for detection,
CC diagnosis and drug screening
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV59324 (1-18)

OY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 122
AAV5453
ID AAV5453 standard; cDNA; 18 BP.
XX
XX AAV5453;
XX
XX 02-FEB-1999 (first entry)
XX
XX Human chemokine ZSIG-35 PCR primer ZC976.
XX
XX ZSIG-35; beta-chemokine; human; ligand; lymphocyte migration;
KW inflammation; ischaemia; reperfusion injury; baculovirus; vector;
KW PFSGE35; PCR; primer; ss.
XX

```

OS Synthetic.
XX Homo sapiens.
XX
XX WO9844117-A1.
XX
XX PD 08-OCT-1998.
XX
XX 27-MAR-1998; 98WO-US006115.
XX PF
XX 28-MAR-1997; 97US-0042862P.
XX PR
XX 09-MAY-1997; 97US-0046083P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Sheppard PO;
XX
XX WPI; 1998-557114/47.
XX
XX New human chemokine ZSIG-35 - used for, e.g. treating inflammatory
XX disease, lymphocyte migration and ischaemia/reperfusion injury.
XX
XX Example 7; Page 90; 105pp; English.
XX
XX Primer ZC976 and primer ZC447 (see AAV45454) were used in PCR
XX amplification of bacmid DNA isolated from DH5-alpha cells following
XX transformation with a baculovirus vector carrying human beta-chemokine
XX ZSIG-35 DNA (see also AAV45444). PCR was performed to screen for the
XX correct insert in positive colonies. Those having the correct insert were
XX used to transfect Spodoptera frugiperda Sf9 cells for production of
XX recombinant ZSIG35 polypeptides (see AAV30565). Novel ZSIG-35
XX polypeptides of the invention can be used in therapeutic compositions for
XX the regulation of acute and chronic inflammatory disease conditions,
XX lymphocyte migration and ischaemia/reperfusion injury
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0
US-09-966-880A-8 (1-198) x AAV45453 (1-18)
QY 32 ValVallysArgArg 36
DB 2 GTTGTAAACGACGG 16
RESULT 123
AAV32961
ID AAV32961 standard; cDNA; 18 BP.
XX
XX AAV32961;
XX
XX 26-OCT-1998 (first entry)
XX
XX Human ZPPAR6 nuclear hormone receptor cDNA primer ZC976.
XX
XX Human ZPPAR6 nuclear hormone receptor; ZPPAR6 NHR; transcription;
XX cell differentiation, cell proliferation; embryogenesis; cancer; PCR;
XX primer; amplification; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9831797-A1.
XX
XX 23-JUL-1998.
XX
XX 15-JAN-1998; 98WO-US000678.
XX

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PR 15-JAN-1997; 97US-0033762P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Holloway JL;
XX
XX WPI; 1998-414097/35.
XX
XX Nuclear hormone receptor, ZPPAR6 - useful for developing products for
XX modulating transcription of target genes, cellular differentiation and
XX proliferation.
XX
XX Example 1; Page 51; 58pp; English.
XX
XX Primers ZC976 and ZC447 (AAV32962) were used to amplify the human ZPPAR6
XX nuclear hormone receptor (ZPPAR6 NHR) cDNA fragment (AAV32960) from an
XX EST present within a human brain cDNA library clone. The invention claims
XX for the ZPPAR6 NHR protein (AAW49094) which can be used to identify
XX compounds that modulate its activity. These compounds may be useful as
XX therapeutic agents for modulating transcription of target genes, for e.g.
XX agonists for such receptors are claimed to be useful for influencing
XX transcription, cellular differentiation, and/or proliferation during
XX development, in particular during embryogenesis while antagonists are
XX claimed to be useful for out-competing endogenous human ZPPAR6 ligands
XX and exert control over the receptor. Antagonists are also claimed to be
XX useful as research reagents for characterising sites of ligand receptor
XX interaction. The ZPPAR6 cDNA and protein are also claimed to be useful in
XX detection and diagnosis, e.g. elevated or depressed levels of ligand or
XX receptor may be indicative of pathological conditions, including cancers
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0
US-09-966-880A-8 (1-198) x AAV32961 (1-18)
QY 32 ValVallysArgArg 36
DB 2 GTTGTAAACGACGG 16
RESULT 124
AAV32155
ID AAV32155 standard; DNA; 18 BP.
XX
XX AAV32155;
XX
XX 23-APR-1999 (first entry)
XX
XX Human IVS17 3'-acceptor splice site PCR primer #3.
XX
XX IVS17 acceptor splice site; PCR primer; detection; base-pair mutation;
XX heteroduplex; homoduplex; migration; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX US5874212-A.
XX
XX 23-FEB-1999.
XX
XX 06-JUN-1995; 95US-00468551.
XX
XX 13-MAY-1993; 93US-00061574.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Ganguly A, Rock MJ, Prockop DJ;
XX

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XX WPI; 1999-179967/15.
 XX Detection of nucleic acid mutations - by electrophoresis in
 PT polyacrylamide gel that distinguishes heteroduplexes from homoduplexes.
 XX Disclosure; Col 5; 16pp; English.
 XX
 CC AAX02153-X02161 are primers used in a method for detecting one or more
 CC base-pair mutations in a nucleic acid sequence by differentiating
 CC heteroduplexes from homoduplexes. The method involves generating
 CC heteroduplexes and heteroduplexes in a sample and performing gel
 CC electrophoresis on the sample using a polyacrylamide gel that causes
 CC heteroduplexes to migrate more slowly than homoduplexes. The gel
 CC comprises 3-20% polyacrylamide, 1-50% of at least one denaturing agent
 CC selected from aliphatic alcohols, cyclic alcohols, alicyclic compounds,
 CC amides, ureas and carbamates, 10-100 mM borate-free TE [Tris-HCl, EDTA]
 CC buffer, and 10-100 mM taurine. The method has a high reliability and can
 CC be improved by allowing for the presence of the mutations in domains with
 CC high melting temperatures. These primers can specifically detect a
 CC mutation in the human IVS17 3'-acceptor splice site
 XX
 SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAX02155 (1-18)
 QY 69 AspLeuAspProGly 73
 DB 3 GATCTGGATCTCGA 17
 RESULT 125
 AAZ41011
 ID AAZ41011 standard; DNA; 18 BP.
 XX AAZ41011;
 XX 26-JAN-2000 (first entry)
 DT Cellular inhibitor of apoptosis-2 phosphorothioate antisense oligo #3.
 DE
 XX Identification; genetic target; gene modulation; human; probe;
 KW antisense oligonucleotide; phosphorothioate; PCR primer;
 KW nucleotide sequence-based technology; antisense drug discovery;
 KW target validation; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9953101-A1.
 PN 21-OCT-1999.
 PD 13-APR-1999; 99WO-US008268.
 XX 13-APR-1998; 98US-0081483P.
 PR 28-APR-1998; 98US-00067638.
 XX (ISIS-) ISIS PHARM INC.
 PA Cowsert LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
 XX WPI; 1999-620446/53.
 XX Identifying compounds which modulate expression of nucleic acids, used to

PT provide compounds having defined physical, chemical or bioactive
 XX properties, e.g. antisense activity.
 XX Example 21; Page 100; 264pp; English.
 XX
 CC A method has been developed of defining a set of compounds that modulate
 CC the expression of a target nucleic acid (tNA) sequence via binding of the
 CC compounds with the tNA sequence. The method comprises generating a
 CC library of virtual compounds in silico according to defined criteria, and
 CC evaluating in silico the binding of the virtual compounds with the tNA
 CC according to defined criteria. Also described are: (1) a method of
 CC defining a set of oligonucleotides (ONs) that modulate the expression of
 CC a tNA sequence via binding of the ONs with the tNA sequence comprising
 CC generating a library of virtual compounds in silico according to defined
 CC criteria, and evaluating in silico the binding of the virtual ONs with
 CC the tNA according to defined criteria; and (2) a method of defining a set
 CC of compounds that modulate the expression of a tNA sequence via binding
 CC of the compounds with the tNA. The methods can be used for the generation
 CC and identification of synthetic compounds having defined physical,
 CC chemical or bioactive properties. Information gathered from assays of
 CC such compounds is used to identify nucleic acid sequences that are
 CC tractable to a variety of nucleotide sequence-based technologies, e.g.
 CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
 CC AAY52701 to AAY52706, represent sequences used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 18 BP; 4 A; 3 C; 2 G; 9 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAZ41011 (1-18)
 QY 59 LeuLeuPheLeuArg 63
 DB 4 CTTTATTCTTAGA 18
 RESULT 126
 AAZ41043
 ID AAZ41043 standard; DNA; 18 BP.
 XX AAZ41043;
 XX 26-JAN-2000 (first entry)
 DT Cellular inhibitor of apoptosis-2 phosphorothioate antisense oligo #35.
 DE
 XX Identification; genetic target; gene modulation; human; probe;
 KW antisense oligonucleotide; phosphorothioate; PCR primer;
 KW nucleotide sequence-based technology; antisense drug discovery;
 KW target validation; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9953101-A1.
 PN 21-OCT-1999.
 PD 13-APR-1999; 99WO-US008268.
 XX 13-APR-1998; 98US-0081483P.
 PR 28-APR-1998; 98US-00067638.
 XX (ISIS-) ISIS PHARM INC.
 PA Cowsert LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
 XX WPI; 1999-620446/53.
 XX Identifying compounds which modulate expression of nucleic acids, used to

XX WPI; 1999-620446/53.
 XX Identifying compounds which modulate expression of nucleic acids, used to
 XX provide compounds having defined physical, chemical or bioactive
 XX properties, e.g. antisense activity.
 XX Example 21; Page 101; 264pp; English.
 XX A method has been developed of defining a set of compounds that modulate
 XX the expression of a target nucleic acid (tNA) sequence via binding of the
 XX compounds with the tNA sequence. The method comprises generating a
 XX library of virtual compounds in silico according to defined criteria, and
 XX evaluating in silico the binding of the virtual compounds with the tNA
 XX according to defined criteria. Also described are: (1) a method of
 XX defining a set of oligonucleotides (ONs) that modulate the expression of
 XX a tNA sequence via binding of the ONs with the tNA sequence comprising
 XX generating a library of virtual compounds in silico according to defined
 XX criteria, and evaluating in silico the binding of the virtual ONs with
 XX the tNA according to defined criteria; and (2) a method of defining a set
 XX of compounds that modulate the expression of a tNA sequence via binding
 XX of the compounds with the tNA. The methods can be used for the generation
 XX and identification of synthetic compounds having defined physical,
 XX chemical or bioactive properties. Information gathered from assays of
 XX such compounds is used to identify nucleic acid sequences that are
 XX tractable to a variety of nucleotide sequence-based technologies, e.g.
 XX antisense drug discovery and target validation. AA240852 to AA241220, and
 XX AA152701 to AA152706, represent sequences used in the exemplification of
 XX the present invention
 XX SQ Sequence 18 BP; 2 A; 4 C; 3 G; 9 T; 0 U; 0 Other;
 Alignment Scores: Length: 18
 Pred. No.: 8.57e+03 Matches: 5
 Score: 5.00 Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 2
 US-09-966-880A-8 (1-198) x AA241043 (1-18)
 QY 38 SerAlaThrSerPhe 42
 DB 4 AGTGTACTCTCTTTT 18
 RESULT 127
 AA241092/C
 ID AA241092 standard; DNA; 18 BP.
 XX AC AA241092;
 XX DT 26-JAN-2000 (first entry)
 XX DE Human ELK-1 phosphorothioate antisense oligonucleotide SEQ ID NO:244.
 XX KW Identification; genetic target; gene modulation; human; probe;
 XX KW antisense oligonucleotide; phosphorothioate; PCR primer;
 XX KW nucleotide sequence-based technology; antisense drug discovery;
 XX KW target validation; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO9953101-A1.
 XX PD 21-OCT-1999.
 XX PF 13-APR-1999; 99WO-US008268.
 XX PR 13-APR-1998; 98US-0081483P.
 XX PR 28-APR-1998; 98US-00067638.

PA (ISIS-) ISIS PHARM INC.

XX Cowsett LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;
 XX Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
 XX WPI; 1999-620446/53.

XX Identifying compounds which modulate expression of nucleic acids, used to
 XX provide compounds having defined physical, chemical or bioactive
 XX properties, e.g. antisense activity.

XX Example 24; Page 105; 264pp; English.

XX A method has been developed of defining a set of compounds that modulate
 XX the expression of a target nucleic acid (tNA) sequence via binding of the
 XX compounds with the tNA sequence. The method comprises generating a
 XX library of virtual compounds in silico according to defined criteria, and
 XX evaluating in silico the binding of the virtual compounds with the tNA
 XX according to defined criteria. Also described are: (1) a method of
 XX defining a set of oligonucleotides (ONs) that modulate the expression of
 XX a tNA sequence via binding of the ONs with the tNA sequence comprising
 XX generating a library of virtual compounds in silico according to defined
 XX criteria, and evaluating in silico the binding of the virtual ONs with
 XX the tNA according to defined criteria; and (2) a method of defining a set
 XX of compounds that modulate the expression of a tNA sequence via binding
 XX of the compounds with the tNA. The methods can be used for the generation
 XX and identification of synthetic compounds having defined physical,
 XX chemical or bioactive properties. Information gathered from assays of
 XX such compounds is used to identify nucleic acid sequences that are
 XX tractable to a variety of nucleotide sequence-based technologies, e.g.
 XX antisense drug discovery and target validation. AA240852 to AA241220, and
 XX AA152701 to AA152706, represent sequences used in the exemplification of
 XX the present invention

XX SQ Sequence 18 BP; 5 A; 1 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores: Length: 18
 Pred. No.: 8.57e+03 Matches: 5
 Score: 5.00 Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 2

US-09-966-880A-8 (1-198) x AA241092 (1-18)

QY 103 AsnLeuSerLeuArg 107

DB 17 AACCTTCTCTCAGA 3

RESULT 128

AA202856

ID AA202856 standard; DNA; 18 BP.

XX AC AA202856;

XX DT 14-MAY-1999 (first entry)

XX DE Human zsig46 PCR primer ZC976.

XX KW Secreted protein; zsig46; human; chromosome 13; thyroid; disease;
 XX KW hypothyroidism; Graves' disease; thyrotoxicosis; thyroid cancer;
 XX KW Hirschsprung's disease; neuronal ceroid-lipofuscinosis; Wilson disease;
 XX KW Reiger syndrome; immunoassay; detection; anti-idiotypic antibody;
 XX KW therapy; diagnostic; PCR primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9905275-A1.

XX PD 04-FEB-1999.


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PN US958771-A.
XX
XX
PD 28-SEP-1999.
XX
XX PF 03-DEC-1998; 98US-00205144.
XX
XX PR 03-DEC-1998; 98US-00205144.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Bennett CF, Cowsett LM, Ackermann EJ;
XX
XX DR WPI; 1999-561046/47.
XX
XX PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2
XX useful for e.g. diagnostics, therapeutics, and as research reagents.
XX
XX SQ Claim 3; Col 39; 33pp; English.
XX
XX CC The invention provides antisense compounds of 8-30 nucleotides that
XX inhibit the expression of human Cellular Inhibitor of Apoptosis-2 (c-IAP-
XX 2). The antisense compounds may be used for diagnostics, therapeutics
XX (for modulating the expression of c-IAP-2), prophylaxis (e.g. to prevent
XX or delay infection, inflammation, or tumor formation), as research
XX reagents (e.g. to distinguish between members of a biological pathway)
XX and in kits. Sequences AA22103-142 represent phosphorothioate
XX oligonucleotides used for antisense inhibition of cellular inhibitor of
XX apoptosis-2
XX
XX SQ Sequence 18 BP; 2 A; 4 C; 3 G; 9 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AA222137 (1-18)
XX
XX QY 38 SerAlaThrSerPhe 42
XX
XX Db 4 AGTGCTACCTCTTT 18
XX
XX RESULT 131
XX AA222105
XX ID AA222105 standard; DNA; 18 BP.
XX
XX AC AA222105;
XX
XX DT 26-NOV-1999 (first entry)
XX
XX DE Human c-IAP-2 mRNA inhibiting antisense oligo ISIS #23414.
XX
XX KW Cellular inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;
XX c-IAP-2; prophylaxis; infection; inflammation; tumor formation; ss.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX PN US958771-A.
XX
XX XX 28-SEP-1999.
XX
XX PF 03-DEC-1998; 98US-00205144.
XX
XX PR 03-DEC-1998; 98US-00205144.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Bennett CF, Cowsett LM, Ackermann EJ;
XX
XX DR WPI; 1999-561046/47.
XX
XX PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2
XX useful for e.g. diagnostics, therapeutics, and as research reagents.
XX
XX SQ Claim 3; Col 39; 33pp; English.
XX
XX CC The invention provides antisense compounds of 8-30 nucleotides that
XX inhibit the expression of human Cellular Inhibitor of Apoptosis-2 (c-IAP-
XX 2). The antisense compounds may be used for diagnostics, therapeutics
XX (for modulating the expression of c-IAP-2), prophylaxis (e.g. to prevent
XX or delay infection, inflammation, or tumor formation), as research
XX reagents (e.g. to distinguish between members of a biological pathway)
XX and in kits. Sequences AA22103-142 represent phosphorothioate
XX oligonucleotides used for antisense inhibition of cellular inhibitor of
XX apoptosis-2
XX
XX SQ Sequence 18 BP; 2 A; 4 C; 3 G; 9 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AA222105 (1-18)
XX
XX QY 59 LeuLeuPheLeuArg 63
XX
XX Db 4 CTTTATTCTTAGA 18
XX
XX RESULT 132
XX AA223878
XX ID AA223878 standard; DNA; 18 BP.
XX
XX AC AA223878;
XX
XX DT 25-JUN-1999 (first entry)
XX
XX DE PCR primer ZC976.
XX
XX KW Chromosomal mutagenesis; chromosomal loci; genotype; enzyme production;
XX lipase; cellulase; protease; enzyme inhibitor; growth factor; cytokine;
XX platelet derived growth factor; fibroblast growth factor; hormone;
XX epidermal growth factor; erythropoietin; thrombopoietin; insulin; leptin;
XX glucagon; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX OS Pichia methanolica.
XX
XX PN WO9914320-A1.
XX
XX PD 25-MAR-1999.
XX
XX PF 11-SEP-1998; 98WO-US019448.
XX
XX PR 15-SEP-1997; 97US-00929748.
XX
XX PR 30-DEC-1997; 97US-00001141.
XX
XX PA (ZYMO) ZYMOGENETICS INC.
XX
XX PI Raymond CK;
XX
XX DR WPI; 1999-229528/19.
XX
XX PT Altering a selected chromosomal locus to produce strains with desired
XX genotypes.
XX
XX PS Example 4; Page 68; 72pp; English.
XX
XX This invention describes a novel method for introducing mutations into

```

CC chromosomal loci of Pichia methanolica to produce strains having desired
CC genotypes. P. methanolica strains having altered target loci are useful
CC as hosts for the expression of heterologous genes. Proteins that can be
CC produced in P. methanolica included proteins of industrial and
CC pharmaceutical interest, e.g. enzymes (lipases, cellulases, proteases),
CC enzyme inhibitors, growth factors such as a platelet derived growth
CC factor, fibroblast growth factor and epidermal growth factor, cytokines
CC such as erythropoietin and thrombopoietin, and hormones such as insulin,
CC leptin and glucagon. Directed mutagenesis allows the introduction of
CC mutations into predetermined genomic loci, permitting the selective
CC alteration of gene activity. However, some mutation methods are
CC unsuitable for Pichia methanolica cells, e.g. the pop-in/pop-out method
CC which requires selection against 5-fluoro orotic acid to which P.
CC methanolica cells are resistant. The methods can be used to easily and
CC readily mutate P. methanolica cells

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX23878 (1-18)

OY 32 ValVallysArgArg 36
DB 2 GTTGTAAACGACGG 16

RESULT 133

AAX32591

ID AAX32591 standard; DNA; 18 BP.

XX AC AAX32591;

XX DT 24-JUN-1999 (first entry)

XX DE PCR primer ZC976.

XX KW Pichia methanolica; vacuolar protease; genetic defect; proteinase; ss;

XX KW industrial; pharmaceutical; enzyme; enzyme inhibitor; growth factor;

XX KW cytokine; hormone; insulin; leptin; glucagon; proteolysis; PCR primer.

XX OS Synthetic.

XX PN WO9914347-A1.

XX PD 25-MAR-1999.

XX PF 11-SEP-1998; 98WO-US019449.

XX PR 15-SEP-1997; 97US-00929748.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Raymond CK, Vanaja E;

XX DR WPI; 1999-244037/20.

XX PT Pichia methanolica defective in vacuolar protease.

XX PS Example 3; Page 50; 54pp; English.

XX CC The invention relates to Pichia methanolica cell which are functionally
XX CC defective in a vacuolar protease. The functional deficiency is due to a
XX CC genetic defect in the parent gene, wherein said parent gene encodes
XX CC proteinase A or proteinase B. The new cells are hosts for production of
XX CC heterologous proteins of industrial or pharmaceutical value, e.g. a wide
XX CC range of enzymes, enzyme inhibitors, growth factors, cytokines and
XX CC hormones (such as insulin, leptin and glucagon). The protease-defective

CC cells should show reduced proteolysis of recombinant proteins. Sequences
CC AAX32582-595 represent PCR primers used during the course of the
CC invention

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX32591 (1-18)

OY 32 ValVallysArgArg 36

DB 2 GTTGTAAACGACGG 16

RESULT 134

AAX34800

ID AAX34800 standard; DNA; 18 BP.

XX AC AAX34800;

XX DT 06-JUL-1999 (first entry)

XX DE Human ZSIG-11 DNA amplifying primer ZC976.

XX KW Secretory protein; ZSIG-11; ligand polypeptide; testis; endoprotease;

XX KW prohormone convertase; fertility; therapeutic; human; PCR primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9916870-A1.

XX PD 08-APR-1999.

XX PF 23-SEP-1998; 98WO-US020449.

XX PR 29-SEP-1997; 97US-0060327P.

XX PR 29-SEP-1997; 97US-00939897.

XX PR 19-MAY-1998; 98US-00081310.

XX PR 19-MAY-1998; 98US-0085966P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Sheppard PO;

XX DR WPI; 1999-263692/22.

XX PT Polynucleotide encoding a human secretory protein, ZSIG-II.

XX PS Example 1; Page 105; 113pp; English.

XX CC The invention relates to a human secretory protein, ZSIG-11. Host cells
XX CC containing a vector comprising the ZSIG-11 nucleic acid are used for the
XX CC recombinant expression of the protein. ZSIG-11 is a novel ligand
XX CC polypeptide and specific antibodies can be used to detect its presence in
XX CC a biological sample. Probes derived from ZSIG-11 nucleotide sequences can
XX CC also be used in detection of ZSIG-11 RNA. ZSIG-11 is expressed at high
XX CC levels in testis, and could be used to identify/study prohormone
XX CC convertases or endoproteases that exhibit testis specificity.
XX CC Antagonists, including antibodies, are useful for inhibiting or
XX CC eliminating the function of ZSIG-11. It is possible that ZSIG-11 and its
XX CC antagonists will be useful as fertility inducing therapeutics. Sequences
XX CC AAX34800-21 represent PCR primers for amplifying the ZSIG-11 DNA
XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX34800 (1-18)

QY 32 ValVallyArgArg 36
AAZ24778
DB 2 GTTGTAAACGACGG 16

RESULT 135

ID AAZ24778 standard; DNA; 18 BP.

AC AAZ24778;

DT 31-JAN-2000 (first entry)

DE Human soluble protein ZTMPO-1 DNA sequencing primer ZC976.

KW Soluble protein; ZTMPO-1; thymopietin-emerin family; human; cancer;
KW nuclear membrane protein; cardiac disorder; autoimmune disorder; testis;
KW infectious disease; cellular proliferation; skeletal muscle; thyroid;
KW adrenal gland; tumor; spermatogenesis; sperm activation; PCR primer;
KW contraception; immune response; humoral response; vaccination; ss.

XX Synthetic.

OS Homo sapiens.

XX

XX WO9954468-A1.

XX 28-OCT-1999.

XX

PF 19-APR-1999; 99WO-US008601.

XX

PR 21-APR-1998; 98US-00063838.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Sheppard PO, Conklin DC, Farrah TM, Maurer MF, Grossmann A;

XX WPI; 1999-634003/54.

XX

XX New isolated ZTMPO-1 polypeptides used for diagnosis and treatment of
e.g. cancer, cardiac and autoimmune disorders and infectious diseases and
for developing contraceptives.

XX Example 1; Page 98; 110pp; English.

CC The invention provides a human soluble protein ZTMPO-1 which has homology
to the thymopietin-emerin family of nuclear membrane proteins. The ZTMPO
-1 protein can be expressed by standard recombinant methodology. Altered
levels of ZTMPO-1 receptor polypeptides may be indicative of pathological
conditions including cancer, cardiac and autoimmune disorders and
infectious diseases. The nucleic acid can be used as a source of
hybridization probes for detecting a genetic abnormality in a patient.
The ZTMPO-1 polypeptides can be used to modulate cellular proliferation
and differentiation in a diverse array of tissues such as testis,
skeletal muscle, thyroid and adrenal gland. Antagonists of ZTMPO-1 can be
used in modulating cellular proliferation and differentiation such as in
tumor growth and development. They can also be used for inhibiting
spermatogenesis and sperm activation. Such ZTMPO-1 antagonists can be used
for contraception in humans and animals, and in particular, domestic and
zoological animals and livestock, where they would act to prevent
fertilization of an egg. ZTMPO-1 antagonists could also be used to
mediate immune response, e.g. by boosting the humoral response in
individuals at risk for an infectious disease or as a supplement to
vaccination. Sequences AAZ24777-791 represent primers used for sequencing
the ZTMPO-1 DNA

XX

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ24778 (1-18)

QY 32 ValVallyArgArg 36

DB 2 GTTGTAAACGACGG 16

RESULT 136

AAZ06607/C

ID AAZ06607 standard; DNA; 18 BP.

XX

XX AAZ06607;

XX

DT 23-NOV-1999 (first entry)

XX

DE ELK-1 expression modulator #47.

XX

KW Human ELK-1; p62TCP; Ets domain transcription factor protein; apoptosis;
KW expression inhibition; infection; inflammation; tumour formation;
KW diagnosis; phosphorothioate; antisense compound; ss.

XX Synthetic.

OS

XX

XX Key

XX modified_base

XX /tag= a

XX /note= "Internucleoside phosphorothioate linkages"

XX modified_base

XX /tag= b

XX /note= "Optionally 2-methoxyethyl (2'-MOE) nucleosides

XX except cytosine residues which are 5-methylcytosine"

XX modified_base

XX /tag= c

XX /note= "Optionally 2-methoxyethyl (2'-MOE) nucleosides

XX except cytosine residues which are 5-methylcytosine"

XX

PN US5948680-A.

XX

PD 07-SEP-1999.

XX

PF 17-DEC-1998; 98US-00213767.

XX

PR 17-DEC-1998; 98US-00213767.

XX

PA (ISIS) ISIS PHARM INC.

XX

PI Baker BF, Cowsett LM;

XX

XX WPI; 1999-517959/43.

XX

XX Antisense compound useful for diagnosis, treatment and prevention of

XX disease associated with ELK-1 expression.

XX

PS Claim 3; Col 39; 31pp; English.

XX

CC Sequences AAZ06571-206607 are antisense polynucleotides targeted to a

CC nucleic acid molecule encoding human ELK-1 (also known as p62TCP). ELK-1

CC is a member of the ternary complex factor subfamily of Ets-domain

CC transcription factor proteins. The polynucleotides inhibit the expression

CC of human ELK-1, and this sequence targets the 3' untranslated region of

CC the ELK-1 RNA. Sequences AAZ06571-206607 all cause at least 30%

CC inhibition of ELK-1 expression. The antisense sequences can be used to

CC inhibit the expression of human ELK-1 in human cells or tissues in vitro.

CC ELK-1 uses a bipartite recognition mechanism mediated by both protein-DNA

CC

CC and protein-protein interactions to regulate genes by direct and indirect
CC DNA binding and has been shown to control various signal transduction
CC pathways and other cell functions including apoptosis. This means that
CC antisense compounds inhibiting expression of ELK-1 can be used to treat
CC diseases associated with its expression in animals, particularly humans
CC and to prevent or delay infection, inflammation or tumour formation. The
CC compounds can also be used for diagnosis, as research reagents and in
CC kits.
XX
SQ Sequence 18 BP; 5 A; 1 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAZ06607 (1-18)

OY 103 AsnLeuSerLeuArg 107
DB 17 AACCTTCTCTCAGA 3

RESULT 137
AAZ44028
ID AAZ44028 standard; DNA; 18 BP.

AC AAZ44028;

DT 20-MAR-2000 (first entry)

XX P. methanolica ADE2 PCR primer ZC976.

XX Alcohol oxidase; industrial enzyme; pharmaceutical protein; ADE2;
KW PCR primer; ss.

XX Pichia methanolica.

XX US6001597-A.

PD 14-DEC-1999.

XX 15-DEC-1998; 98US-00211631.

XX 09-NOV-1995; 95US-0006397P.

PR 17-JUL-1996; 96US-0042910P.

PR 26-AUG-1996; 96US-00703807.

PR 15-SEP-1997; 97US-0058822P.

PR 11-SEP-1998; 98US-00152180.

XX (ZYMO) ZYMOGENETICS INC.

XX Vanaaja E, Raymond CK;

XX WPI; 2000-071656/06.

XX Pichia cell with disrupted genes, useful for producing polypeptides of
XX economic importance, including industrial enzymes and pharmaceutical
XX proteins.

XX Example 9; Col 39-40; 27pp; English.

XX This invention describes a novel Pichia methanolica cell in which an
XX alcohol oxidase gene has been disrupted. The cell is useful for producing
XX polypeptides of economic importance, including industrial enzymes and
XX pharmaceutical proteins. This sequence represents a PCR primer used in
XX the amplification of the ADE2 gene described in the method of the
XX invention

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAZ44028 (1-18)

OY 32 ValVallyysargarg 36
DB 2 GTTGTAACGACGG 16

RESULT 138

AAA75596

ID AAA75596 standard; DNA; 18 BP.

XX AAA75596;

XX 22-JAN-2001 (first entry)

XX PCR primer for DNA encoding a human zalphall ligand fragment.

XX zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour; PCR primer; ss.

XX Homo sapiens.

OS WO200053761-A2.

PD 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US006067.

PR 09-MAR-1999; 99US-00264908.

PR 11-MAR-1999; 99US-00265992.

PR 01-JUL-1999; 99US-0142013P.

XX (ZYMO) ZYMOGENETICS INC.

XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;

PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX WPI; 2000-565600/52.

XX New human cytokine, designated zalphall ligand, useful for stimulating
XX the proliferation and/or development of hematopoietic cells in vitro and
XX in vivo, and for treating tumorigenesis.

XX Example 30; Page 228; 256pp; English.

XX PCR primers AAA75595-96 were used to amplify DNA encoding a fragment of
XX human zalphall ligand polypeptide. Zalphall ligand is a cytokine. The
XX zalphall ligand is useful for stimulating the proliferation and
XX development of haematopoietic cells in vitro and in vivo. Zalphall ligand
XX polynucleotides can be used as primers or probes for cloning the zalphall
XX gene. The zalphall ligand is useful for treating tumorigenesis. A
XX zalphall ligand-saporin fusion toxin may be used for treating leukaemias
XX and lymphomas. Antagonists against zalphall ligand are useful as research
XX reagents for characterizing ligand-receptor interaction. Antagonists are
XX also useful for inhibiting expansion, proliferation, activation and
XX differentiation of cells involved in regulating hematopoiesis. The
XX zalphall ligand may also be used to stimulate an immune response against
XX B cell tumour, a virus, a parasite or a bacterium. The zalphall
XX polypeptides, polynucleotides, antagonists, agonists and antibodies are
XX also useful for the detection, diagnosis, prevention, and treatment of
XX diseases associated with a zalphall ligand genetic defect

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA75596 (1-18)

QY 32 ValVallysArgArg 36
DB 2 GTTGTAAACGACGG 16

RESULT 139
AAZ44774/C
ID AAZ44774 standard; DNA; 18 BP.

XX AAZ44774;

XX 19-APR-2000 (first entry)

XX Human FADD primer ISIS #23874.

XX FADD; human; antisense; inhibitor; Fas-associated death domain; primer;
KW probe; ss.

XX Homo sapiens.

XX US6015712-A.

XX 18-JAN-2000.

XX 19-JUL-1999; 99US-00357072.

XX 19-JUL-1999; 99US-00357072.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Cowseert LM, Baker BP, Zhang H;

XX WPI; 2000-126316/11.

XX Antisense oligonucleotides, useful for inhibiting human Fas-associated
PT death domain (FADD) expression are targeted to the 3' untranslated region
PT of the FADD gene.

PS Example 16; Col 53-54; 37pp; English.

XX This invention describes novel antisense oligonucleotides (OCNs) (I) 8-20
CC nucleotides in length that specifically hybridize with and inhibit
CC nucleic acids encoding human Fas-associated death domain (FADD), targeted
CC to the 3' untranslated region (3'UTR). (I) can be used to treat animals,
CC especially humans, suspected of having or being prone to a disease or
CC condition associated with FADD expression. AAZ44746-244831 represent
CC primers and probes used in the method of the invention

SQ Sequence 18 BP; 6 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ44774 (1-18)

QY 43 SerLeuAspPheGly 47
DB 17 AGCCTGGACTTGGT 3

RESULT 140
AAA33601

ID AAA33601 standard; DNA; 18 BP.
XX AAA33601;
AC AAA33601;
XX 28-JUL-2000 (first entry)
DT Low adenosine antisense oligonucleotide SEQ ID NO:1290.
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX Homo sapiens.
OS WO200009525-A2.
XX 24-FEB-2000.
XX 03-AUG-1999; 99WO-US017712.
XX 03-AUG-1998; 98US-0095212P.
XX (UYEC-) UNIV EAST CAROLINA.
XX Nyce JW;
XX WPI; 2000-205971/18.
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX Claim 18; Page 426; 1343pp; English.
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytosstatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAZ32313 to AAZ3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AA332323 to
CC AAZ33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX SQ Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA33601 (1-18)

QY 59 IeuleuPheLeuArg 63
Db 4 CTCCTGTTCTCCGT 18

RESULT 141
AAZ35164
ID AAZ35164 standard; DNA; 18 BP.
XX
AC AAZ35164;
XX
DT 13-MAR-2000 (first entry)
XX
DE Human immunomodulator zsig57 primer ZC976.
XX
KW Immunomodulator; zsig57; human; transcytosis receptor; immunostimulant;
KW antiviral; virucide; wound healing; vulnery; gene therapy; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9966040-A1.
XX
PD 23-DEC-1999.
XX
PF 20-MAY-1999; 99WO-US011337.
XX
PR 18-JUN-1998; 98US-00099600.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO;
PI
XX
DR WPI; 2000-097745/08.
XX
PT Polynucleotides encoding the polypeptide zsig57 useful for regulating the
PT immune system.
XX
PS Example 1; Page 131; 144pp; English.
XX
CC This primer, termed ZC976, was used in the sequence analysis of an EST
CC clone that had been obtained by querying an EST database for sequences
CC homologous to proteins having a secretory signal sequence. Primers
CC designed from the isolated EST clone were used in the isolation of full-
CC length cDNA (see AAZ35141) coding for zsig57 (see AAY32397). Zsig57 is a
CC novel human immunomodulator that is a member of the immunoglobulin
CC superfamily of proteins and which may act as a transcytosis receptor. The
CC invention provides zsig57 polypeptides, polynucleotides and antibodies
CC that may be useful in the treatment of human disease states
XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ35164 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 142
AAZ44135
ID AAZ44135 standard; DNA; 18 BP.

XX AAZ44135;
AC
XX
DT 24-MAR-2000 (first entry)
XX
DE Human EGR-1 DNA antisense primer #24157.
XX
KW EGR-1; early growth response 1; antisense; inhibition; human; primer;
KW anti-inflammatory; cytostatic; antiviral; detection; diagnosis;
KW viral infection; inflammation; tumor; ss.
XX
OS Homo sapiens.
OS
XX
PN US6008048-A.
XX
PD 28-DEC-1999.
XX
PF 04-DEC-1998; 98US-00205921.
XX
PR 04-DEC-1998; 98US-00205921.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowseert LM;
PI
XX
DR WPI; 2000-096375/08.
XX
CC Antisense oligonucleotides that inhibit expression of human early growth
CC response-1, useful for diagnosis, treatment and prevention of tumors,
CC inflammation and infection.
XX
PS Claim 1; Col 37-38; 31pp; English.
XX
CC This invention describes novel antisense oligonucleotides (I) capable of
CC inhibiting expression of human EGR-1 (early growth response-1). The
CC products of the invention have anti-inflammatory, cytostatic and
CC antiviral activity. (I) was tested for its effects on EGR-1 mRNA levels
CC by real-time polymerase chain reaction (PCR), results indicated that 60%
CC inhibition was achieved. When (I) was modified by 2'-O-methoxyethyl
CC substitution of the first 4 and last 4 residues, and by replacing any C
CC in these flanking regions with 5-methyl-C, the degree of inhibition was
CC increased to 71%. (I) is used to inhibit expression of EGR-1 in cells and
CC tissues in vitro, for research or diagnosis, e.g. detecting EGR-1
CC encoding nucleic acid. (I) may also be used to treat or prevent EGR-1-
CC associated diseases, particularly viral infections, inflammation and
CC tumors. AAZ44134-244159 represent antisense primers used to inhibit the
CC human EGR-1 protein
XX
SQ Sequence 18 BP; 1 A; 13 C; 3 G; 1 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ44135 (1-18)

QY 127 ArgArgLeuHisArg 131
Db 4 CGCGCGCTCCACGC 18

RESULT 143
AAZ75987
ID AAZ75987 standard; DNA; 18 BP.
XX
AC AAZ75987;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:10343.

XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX

OS Homo sapiens.
 XX
 PN WO9954500-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 21-APR-1999; 99WO-IB000822.
 XX
 PR 21-APR-1998; 98US-0082614P.
 XX
 PR 23-NOV-1998; 98US-0109732P.
 XX

PA (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.

XX Claim 9; Page 2435; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

SQ Sequence 18 BP; 7 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ75987 (1-18)

QY 34 LysArgArgAspSer 38

DB 4 AAGAGACGAGACTCC 18

RESULT 144

AAZ72263

ID AAZ72263 standard; DNA; 18 BP.

XX AAZ72263;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker upstream amplification primer SEQ ID NO:6619.

XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.

XX Claim 9; Page 1642; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

SQ Sequence 18 BP; 5 A; 8 C; 0 G; 5 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ72263 (1-18)

QY 102 ProAsnLeuSerLeu 106

DB 4 CCAATCTATCTCCCTC 18

RESULT 145

AAZ52254

ID AAZ52254 standard; DNA; 18 BP.

XX AAZ52254;

XX 18-JUL-2000 (first entry)

XX Primer ZC976 for sequencing human stomach protein zsig28 cDNA.

XX Human; stomach; zsig28 protein; chromosome 3q22.1-3q22.2; gene therapy;
 KW claudin; oligodendrocyte-specific protein; OSP; apoptosis; RVP.1;
 KW rat androgen-withdrawal apoptosis protein; growth factor receptor;
 KW cell-cell signalling molecule; cytostatic; antibacterial; food poisoning;
 KW Botulism; diarrhoea; inflammation; cramping; cancer; gastric ulcer;

KW diagnosis; prevention; treatment; primer; ss.
 XX Homo sapiens.
 XX WC200015659-A2.
 XX 23-MAR-2000.

XX 14-SEP-1999; 99WO-US021023.
 XX 16-SEP-1998; 98US-00154444.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Foley KP;
 XX WPI; 2000-271379/23.

XX New isolated polynucleotide encoding a stomach zsig28 polypeptide used
 PT for diagnosis, prevention and treatment of stomach disorders caused by
 PT bacteria, gastric ulcers or cancer.
 XX

XX Example 1; Page 121; 121pp; English.
 PS The present sequence is a primer ZC976 used for sequencing a cDNA
 CC corresponding to an expressed sequence tag identified in a human lung
 CC library to obtain full length clone of polynucleotide encoding stomach
 CC protein zsig28. The zsig28 gene is located at 3q22.1-3q22.2 region of
 CC human chromosome 3. The zsig28 protein shows homology to a diverse family
 CC of receptor proteins containing e.g. human claudin 1 and 2, human and
 CC murine oligodendrocyte-specific protein (OSP) and rat androgen-withdrawal
 CC apoptosis protein RVP.1. It is thought to be a cell-cell signalling
 CC molecule, a growth factor receptor or extracellular matrix associated
 CC protein with growth factor hormone activity and may be involved in an
 CC apoptotic cellular pathway. The protein may act as an anti-microbial
 CC agent and may bind toxins produced by bacteria which cause food
 CC poisoning, Botulism, severe diarrhoea, inflammation and cramping. zsig28
 CC agonists are useful for promoting apoptosis in cells over-expressing
 CC zsig28 e.g. in cancer cells. They are also useful for stimulating cell
 CC growth or differentiation. Altered levels of zsig28 protein in a test
 CC sample such as saliva, serum, sweat or biopsy can be monitored as an
 CC indication of digestive function, gastric ulcer or cancer. zsig28
 CC expression can be used as a differentiation marker to determine the stage
 CC of tumour or cell maturity, particularly in epithelial cells.
 CC Polynucleotides encoding zsig28 can be used in gene therapy applications
 CC to increase or inhibit zsig28 activity
 XX

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ52254 (1-18)

QY 32 ValVallyeArgArg 36
 DB 2 GTTGTAACGACGG 16

RESULT 146

AAZ30211
 ID AAA30211 standard; DNA; 18 BP.
 XX
 AC AAA30211;
 XX

XX 16-AUG-2000 (first entry)

DE Human RING finger protein zapop3 gene sequencing primer ZC976.
 XX

KW Human; RING finger; leucine rich repeat; LRR; zapop3; chromosome 9q34.11;
 KW myocardial infarction; dilated myopathy;
 KW retinitis pigmentosa-deafness syndrome 1; apoptosis inhibition;
 KW angiogenesis; hyperplasia; pulmonary hypertension; gene therapy;
 KW sequencing primer; ss.
 XX

XX Homo sapiens.

XX WO200029430-A1.

XX 25-MAY-2000.

XX 04-NOV-1999; 99WO-US026104.

XX 12-NOV-1998; 98US-00191500.

XX (ZYMO) ZYMOGENETICS INC.

XX Venezia D, Grossmann A;

XX WPI; 2000-387737/33.

XX Polynucleotides encoding zapop3 polypeptides useful for detecting
 PT chromosomal abnormalities comprising a sequence identical to a specific
 PT amino acid sequence, identity being determined by a specific program.
 XX

XX Example 1; Page 99; 104pp; English.

XX The present sequence is a sequencing primer for the human zapop3 gene.
 CC The Zapop3 protein was isolated by searching an EST database for proteins
 CC similar to proteins with a RING finger sequence, with the full length
 CC clone being obtained from a peripheral blood granulocyte library. BRCA1
 CC is an example of a RING finger protein. The gene is found on chromosome
 CC 9q34.11, and its locus is associated with retinitis pigmentosa-deafness
 CC syndrome 1. In addition to gene therapy for this disease, the protein,
 CC nucleic acid and antibodies can be used to diagnose and treat myocardial
 CC infarction, congestive heart failure, hypertrophic cardiomyopathy,
 CC dilated myopathy, to limit infarct size following a heart attack, to aid
 CC recovery after heart transplantation, to promote angiogenesis and wound
 CC healing, to develop coronary collateral circulation, for
 CC revascularisation in the eye, for complications related to poor
 CC circulation, for stroke, induction of skeletal muscle neogenesis and/or
 CC hyperplasia, kidney regeneration and treatment of systemic and pulmonary
 CC hypertension. In addition to a RING finger domain, the protein also
 CC contains eight leucine rich repeat motifs
 XX

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA30211 (1-18)

QY 32 ValVallysArgArg 36
 DB 2 GTTGTAACGACGG 16

RESULT 147

AAF19723
 ID AAF19723 standard; DNA; 18 BP.
 XX
 AC AAF19723;
 XX

XX 14-MAR-2001 (first entry)

DE Human fibronectin polynucleotide fragment #1290.
 XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX Homo sapiens.
 OS
 XX WO200062736-A2.
 PN
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US008020.
 PE
 XX 06-APR-1999; 99US-0127958P.
 PF
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX (NYCE/) NYCE J W.
 PI
 XX Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 PT
 XX Claim 14; Page 221; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors and
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention

XX Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAF19723 (1-18)
 Qy 59 LeuLeuPheLeuArg 63
 Db 4 CTCCTGTTCTCGT 18
 RESULT 148
 AAA29424/c
 ID AAA29424 standard; DNA; 18 BP.
 XX
 AC AAA29424;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Primer extension product modulating module #1.
 XX
 KW Primer extension product; modular oligonucleotide; identification;
 KW hybridisation; probe; ss.
 XX
 OS Unidentified.
 XX
 PN WO200015842-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 15-SEP-1999; 99WO-GB003056.
 XX
 PR 15-SEP-1998; 98US-00153242.
 PR 16-SEP-1998; 98GB-00020185.
 XX
 PA (DYNA-) DYNAL AS,
 PA (JONE/) JONES E L.
 XX
 PI Lundeberg J, Uhlen M;
 XX WPI; 2000-271472/23.
 DR
 XX Isolating primer extension products using modular oligonucleotides.
 PT
 XX Claim 13; Page 15; 74pp; English.
 PS
 XX A method (I) has been developed of isolating primer extension products,
 CC produced from template vectors and containing sequences corresponding to
 CC or complementary to (i) to (iii) below, where the method comprises
 CC binding a modular oligonucleotide, comprising 2 parts (or modules), to
 CC adjacent stretches on the primer extension products (the modular
 CC oligonucleotide is complementary to and capable of binding to the vector
 CC derived sequences of the primer extension products and at least 1 module
 CC (the capture module) is immobilized or can be immobilized: (i) a primer
 CC binding region; (ii) an insert; and (iii) vector derived sequence(s).
 CC Also described is a method for determining the nucleotide sequence of a
 CC nucleic acid insert in a vector, in which sequencing products are
 CC generated by performing appropriate extension reaction on the vector, the
 CC sequencing products are isolated via (i) and the isolated products are
 CC separated by an appropriate technique and the labels carried on the
 CC sequencing products are visualised to allow determination of the sequence
 CC of the insert or a portion of it. (i) may be used for isolating primer
 CC extension products, particularly sequencing reaction products in which
 CC the products contain sequences corresponding or complementary to primer
 CC binding regions, inserts and vector derived sequences. The present
 CC sequence represents a specifically claimed modular oligonucleotide which
 CC is used in the exemplification of the present invention

SQ Sequence 18 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ29424 (1-18)

QY 32 ValVallysArgArg 36
 Db 17 GTTGTAAACGACGG 3

RESULT 149

AAZ58580

ID AAZ58580 standard; cDNA; 18 BP.

XX AC AAZ58580;

XX DT 05-JUN-2000 (first entry)

XX DE zsig58 cDNA PCR primer ZC976.

XX KW Human; zsig58; vulnery; gonadotropin activity enhancer; osteopathic;

XX KW antitumor; hormone dependent tumour growth inhibitor; gene therapy;

XX KW PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200008154-A1.

XX PD 17-FEB-2000.

XX PF 03-AUG-1999; 99WO-US017552.

XX PR 03-AUG-1998; 98US-00128372.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Sheppard PO, Chandrasekhar Y;

XX WPI; 2000-205709/18.

XX PT New polynucleotide encoding a member of trabecular meshwork-induced

XX PT glucocorticoid response protein for treating ovarian, pancreatic, ocular,

XX PT blood and bone disorders such as osteoporosis and Paget's disease.

XX PS Example 9; Page 119; 138pp; English.

XX CC The present sequence is that of primer ZC986, which was used with primer

XX CC ZC447 (see AAZ58581) to screen Escherichia coli DH5 alpha cells following

XX CC transformation with a baculovirus expression vector including zsig58

XX CC cDNA. Clones having the correct insert were used to transfect Sf9 insect

XX CC cells. zsig58 (see AAY79147) is a novel cell-cell signalling molecule,

XX CC growth factor, or secreted extracellular matrix associated protein with

XX CC growth factor/hormone activity, that is a novel member of the trabecular

XX CC meshwork-induced glucocorticoid response protein (TIGR) family of

XX CC proteins. It is strongly expressed in ovary, pancreas and small

XX CC intestine. zsig58 nucleic acids (see AAZ58586) can be used in gene

XX CC therapy to increase or inhibit zsig58 activity and to identify regions of

XX CC the genome associated with disease states

XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ58580 (1-18)

QY 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 150

AAZ93482/c

ID XX AAZ93482 standard; DNA; 18 BP.
 XX AC AAZ93482;
 XX DT 24-JUL-2000 (first entry)
 XX DE TRADD antisense oligonucleotide.
 XX KW TRADD; TNF; tumour necrosis factor; NF-kappa-B; apoptosis;
 KW KW programmed cell death; antisense; inhibition; treatment; therapy;
 KW KW septic shock; inflammation; cancer; antiinflammatory; human; ss.
 XX OS Synthetic.
 XX EH Key Location/Qualifiers
 FT misc_binding complement(1..18)
 FT FT /*tag= a
 FT FT /note= "Complementary to bases 702-685 of the human TRADD
 FT FT sequence described in GENESEQ record AAZ93431"
 XX PN WO200012527-A1.
 XX PD 09-MAR-2000.
 XX PF 25-AUG-1999; 99WO-US019614.
 XX PR 28-AUG-1998; 98US-00143212.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Monia BP, Cowsett LM;
 XX WPI; 2000-237846/20.
 XX PT New antisense compounds that limit the expression of human TRADD protein,
 PT useful in the treatment and diagnosis of cancer, inflammation and septic
 PT shock.
 XX PS Claim 3; Page 52; 85pp; English.

XX CC The intracellular protein TRADD has been identified as a critical link
 CC between tumour necrosis factor (TNF) receptor binding and downstream
 CC activation of NF-kappa-B. Overexpression of native TRADD activates NF-
 CC kappa-B in the absence of TNF and dominant negative mutants of TRADD
 CC block TNF-induced NF-kappa-B activation. A second effect of TNF in many
 CC cell types is the induction of apoptosis (programmed cell death). TRADD
 CC overexpression has been shown to mimic TNF induction of apoptosis as
 CC well. Data indicates that TRADD and other downstream effector proteins
 CC are the rate limiting step of TNF action and would therefore serve as the
 CC most efficient targets for inhibition of TNF-induced events. Antisense
 CC oligonucleotides capable of inhibiting TRADD function may therefore be
 CC useful in a number of therapeutic, diagnostic and research applications.
 CC Inhibiting expression of TRADD by contacting human cells or tissues with
 CC the antisense compound may be used to treat a disease or condition
 CC associated with TRADD expression, for example, septic shock,
 CC inflammation, or cancer. TRADD antisense oligonucleotides of varying
 CC inhibitory capabilities are listed in GENESEQ records AAZ93438-243517.
 CC The antisense oligonucleotides exhibit enhanced inhibitory capabilities
 CC when they have 2'-MOE wings and a deoxy gap

SQ Sequence 18 BP; 2 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ93482 (1-18)

QY 121 AlaGluProGluGly 125

Db 16 GCTGACCTGAAGGA 2

RESULT 151
AAC64070
ID AAC64070 standard; DNA; 18 BP.
XX AC AAC64070;
XX DT 19-FEB-2001 (first entry)
XX DE Baculovirus expression vector pZBV32L PCR primer, SEQ ID NO:19.
XX KW Human zacr3p; adipocyte complement related protein homologue; ACRP30;
KW Clq domain; collagen-like domain; energy balance modulation;
KW cellular metabolism; metabolic disorder; obesity; anorexia;
KW antimicrobial agent; infection; platelet aggregation inhibition;
KW adhesion; activation; vascular injury; antibacterial; antiviral;
KW PCR primer; ss.
XX OS Synthetic.
XX PN WO200063377-A1.
XX PD 26-OCT-2000.
XX PF 19-APR-2000; 2000WO-US010454.
XX PR 20-APR-1999; 99US-00294943.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Piddington CS, Bishop PD;
XX WPI; 2000-665243/64.
XX DR Novel zacr3p polypeptides used to treat or prevent bacterial or viral
XX PT infections, for wound healing, improving blood flow, and to analyze
XX PT energy efficiency in mammals.
XX PS Example 2; Page 120; 123pp; English.

XX CC The invention relates to the human zacr3p protein (AA29590) and to
XX CC nucleic acids which encode it (AAC64058, AAC64063). Zacr3p is a homologue
XX CC of adipocyte complement related protein (ACRP30) and contains a collagen-
XX CC like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a C-
XX CC terminal Clq domain comprising 10 beta-strands. The zacr3p gene is
XX CC located on chromosome 5p12. The invention also relates to zacr3p
XX CC fragments, fusion proteins containing zacr3p polypeptides, zacr3p-
XX CC specific antibodies, expression constructs and host cells comprising
XX CC zacr3p nucleic acids, and methods of recombinant production of zacr3p.
XX CC Human zacr3p, and its agonists and antagonists may be used in the study
XX CC and modulation of cellular metabolism and energy balance in mammals, and
XX CC may therefore be used to treat disorders such as obesity and anorexia,
XX CC and conditions associated with these disorders. Due to its Clq like
XX CC domain, zacr3p and zacr3p-containing fusion proteins may be useful as
XX CC antimicrobial agents, promoting lysis or phagocytosis of infectious
XX CC organisms such as bacteria or viruses. Zacr3p, its fragments, fusion
XX CC proteins, antibodies and activity modulators may also be used to inhibit
XX CC collagen-induced platelet aggregation, adhesion, or activation, and may
XX CC therefore have potential for promoting blood flow within the vasculature
XX CC of a mammal e.g., to treat injury to the vasculature or other collagenous
XX CC tissue. Human zacr3p and its antibodies may additionally be used to study
XX CC dimerisation and oligomerisation. The present sequence represents a PCR
XX CC primer used in an exemplification of the invention

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAC64070 (1-18)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 152
AAC65144
ID AAC65144 standard; DNA; 18 BP.
XX AC AAC65144;
XX DT 12-FEB-2001 (first entry)
XX DE Human adipocyte complement related protein homologue zacr2p primer #10.
XX KW Human; zacr2p; adipocyte complement related protein; acrp30;
KW energy balance; metabolism; haemostasis; anti-microbial; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200063376-A1.
XX PD 26-OCT-2000.
XX PF 19-APR-2000; 2000WO-US010452.
XX PR 20-APR-1999; 99US-00295072.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Piddington CS, Bishop PD;
XX WPI; 2000-647517/62.
XX DR Human DNA sequence encoding a zacr2p polypeptide which has homology to an
XX PT adipocyte complement related protein (Acirp30), useful in gene therapy
XX PT applications for inhibiting or increasing zacr2p activity.
XX PS Example 3; Page 122; 125pp; English.

XX CC The present invention is related to the isolation and uses of a homologue
XX CC to the adipocyte complement related protein Acirp30, known as zacr2p. The
XX CC zacr2p protein is involved in energy balance, and the protein, its
XX CC antibodies and coding sequence can be used to modulate energy balance,
XX CC haemostasis, calcium ion concentration, muscle contraction, hormone
XX CC secretion, DNA synthesis and cell growth, inositol phosphate turnover,
XX CC arachidonate release, phospholipase-C activation, gastric emptying, human
XX CC neutrophil activation or ADCC capability and superoxide anion production.
XX CC They may also have uses in antimicrobial applications

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAC65144 (1-18)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 153
AAC90239
ID AAC90239 standard; DNA; 18 BP.

AC AAC90239;
 DT 14-MAR-2001 (first entry)
 DE Primer ZC976.
 KW Vacuolar protease; proteinase A; proteinase B; protein production; ss.
 OS Pichia methanolica.
 PN US6153424-A.
 PD 28-NOV-2000.
 PF 09-MAR-1999; 99US-00265628.
 PR 09-NOV-1995; 95US-0006397P.
 PR 17-JUL-1996; 96US-0042510P.
 PR 26-AUG-1996; 96US-00703807.
 PR 15-SEP-1997; 97US-0058822P.
 PR 11-SEP-1998; 98US-00152180.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Vanaaja E, Raymond CK;
 DR WPI; 2001-040516/05.
 PT A new Pichia methanolica cell with functional deficiency in vacuolar
 PT protease, useful as hosts for production of proteins of interest.
 XX Example 4; Col 39; 27pp; English.
 CC The present invention relates to a Pichia methanolica cell with a
 CC functional deficiency in a vacuolar protease, resulting from a genetic
 CC defect, where the defect is an insertion, deletion, or substitution of at
 CC least 4 contiguous base pairs in a parent gene, which encodes proteinase
 CC A or proteinase B. The invention can be used for the production of a
 CC protein of industrial and pharmaceutical interest. These include enzymes,
 CC enzyme inhibitors, growth factors, cytokines and hormones
 XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0
 US-09-966-880A-8 (1-198) x AAC90239 (1-18)
 Qy 32 ValVallylsArgArg 36
 Db 2 GTTGTAAACGACGG 16
 RESULT 154
 AAD07920
 ID AAD07920 standard; DNA; 18 BP.
 AC AAD07920;
 DT 03-AUG-2001 (first entry)
 DE ZC976 primer related to human Zsig87 protein.
 KW Human; Zsig87 protein; cardiovascular disease; infertility; cytostatic;
 KW male reproductive dysfunction; ovarian disorder; testicular; pancreatic;
 KW lymphatic; bone; blood; uterine; stomach; cancer; inflammatory disorder;
 KW immunosuppressive; anti-fertility vaccine; spermatogenesis; arthritis;
 KW sperm capacitation; wound healing; diabetes; vulvar; ocular; asthma;

KW chromosomal abnormality; forensic DNA profiling; leukaemia; gene therapy;
 KW vasotropic; gynaecological; gastrointestinal-gen; primer; ss.
 OS Homo sapiens.
 PN WO200142292-A2.
 PD 14-JUN-2001.
 PF 08-DEC-2000; 2000WO-US033539.
 PR 08-DEC-1999; 99US-00456641.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Sheppard PO;
 DR WPI; 2001-381639/40.
 PT Novel secreted protein, zsig87 polypeptides and polynucleotides for
 PT detecting human chromosomal abnormalities, as immunosuppressives and
 PT for diagnosing, treating cancer, cardiovascular and inflammatory
 PT diseases.
 XX Disclosure; Page 107; 107pp; English.
 CC The present invention relates to polynucleotides and polypeptides for
 CC zsig87, a novel secreted protein. Zsig87 polypeptides are useful for
 CC producing antibodies, which are useful for detecting cancer. Zsig87
 CC modulators are useful for treating cardiovascular diseases, infertility,
 CC in vitro fertilisation, birth control, treating impotence or other male
 CC reproductive dysfunctions. Zsig87 polypeptides are useful for promoting
 CC wound healing for e.g. in the pancreas, for anti-microbial applications
 CC and for diagnosing, preventing and treating ovarian, ocular, testicular,
 CC pancreatic, immune, lymphatic, bone or blood disorders, uterine, stomach
 CC cancer and disorders associated with gastrointestinal mobility and
 CC dysfunction, as components in immunosuppressive or anti-fertility
 CC vaccines and for modulating spermatogenesis and sperm capacitation.
 CC Zsig87 sequence and its modulators are useful for treating diabetes,
 CC pancreatic cancer and inflammatory diseases, such as asthma and
 CC arthritis. Zsig87 polynucleotide sequences are useful for detecting human
 CC chromosomal abnormalities and as diagnostics in forensic DNA profiling.
 CC Zsig87-cytokine fusion proteins or antibody-cytokine fusion proteins are
 CC useful for enhancing in vivo killing of target tissue for e.g. leukaemia,
 CC blood and bone marrow cancers. Zsig87 DNA is used in gene therapy. The
 CC present sequence is a primer related to human Zsig87 protein
 XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0
 US-09-966-880A-8 (1-198) x AAD07920 (1-18)
 Qy 32 ValVallylsArgArg 36
 Db 2 GTTGTAAACGACGG 16
 RESULT 155
 AAF69050
 ID AAF69050 standard; DNA; 18 BP.
 AC AAF69050;
 DT 12-APR-2001 (first entry)
 DE COXI PCR primer #26.
 XX

KW Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;
 XX ss.
 XX Homo sapiens.
 OS
 XX
 PN US6171859-B1.
 XX
 PD 09-JAN-2001.
 XX
 XX 30-MAR-1995; 95US-00413740.
 PF
 XX 30-MAR-1994; 94US-00219842.
 PR
 XX (MITO-) MITOKOR.
 PA
 XX Herrstadt C, Parker WD;
 PI
 XX WPI; 2001-136875/14.
 DR
 XX
 XX Targeting conjugate molecule to mitochondria having defective cytochrome
 PT C oxidase activity for diagnosing Alzheimer's disease, involves
 PT contacting mitochondria with a conjugate of targeting molecule and toxin.
 PT
 XX
 XX Example 2; Col 41-42; 88pp; English.
 PS
 XX The present invention relates to a method for selectively accumulating a
 CC mitochondrial disabling or destructive amount of a conjugate molecule in
 CC mitochondria having defective cytochrome C oxidase (COX) activity or
 CC displaying increased membrane potential. The method involves contacting
 CC mitochondria with a conjugate molecule comprising a targeting molecule
 CC conjugated to a toxin, where the conjugate or targeting molecule selected
 CC accumulates in the mitochondria. The method is useful for diagnosis of
 CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is
 CC a PCR primer used in the method of the present invention
 CC
 XX Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-9 (1-198) x AAF69050 (1-18)

Qy 125 GlyLeuArgGln 129
 Db 2 GGCTACGGAGGCTC 16
 RESULT 156
 AAH45321
 ID AAH45321 standard; DNA; 18 BP.
 XX
 AC AAH45321;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Human MHC S DNA PCR primer S2_02a (R).
 XX
 KW Human; MHC S; major histocompatibility complex S; vulgar psoriasis;
 KW diagnosis; primer; SEEK1; HCR; a-helix coiled-coil rod homologue;
 KW polymorphism; PCR primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200142458-A1.
 FN
 XX 14-JUN-2001.
 PD
 XX 06-DEC-2000; 2000WO-JP008624.
 PF
 XX

PR 06-DEC-1999; 99JP-00346867.
 XX
 XX (INOK/) INOKO H.
 PA
 XX Inoko H, Tamiya G;
 PI
 XX WPI; 2001-381680/40.
 DR
 XX
 XX New primer DNA, useful for detecting vulgar psoriasis.
 PT
 XX
 XX Example 1; Page 13; 106pp; Japanese.
 PS
 XX The invention relates to a method of diagnosing vulgar psoriasis using
 CC primers based on the sequences of the human MHC S, SEEK1 and HCR genes.
 CC By analysing the sequences of these genes in Japanese patients with
 CC psoriasis and in normal subjects, it has been found that some of the
 CC examined polymorphisms correlate significantly to the group of patients
 CC with psoriasis. Vulgar psoriasis can therefore be diagnosed by analysing
 CC these gene polymorphisms. The present sequence is a primer designed to
 CC detect a genetic polymorphism in the human major histocompatibility
 CC complex (MHC) S gene
 CC
 XX Sequence 18 BP; 4 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH45321 (1-18)

Qy 128 ArgLeuHisArgAla 132
 Db 4 CGCCTCCACAGAGCT 18
 RESULT 157
 AAD02427
 ID AAD02427 standard; DNA; 18 BP.
 XX
 AC AAD02427;
 XX
 DT 24-APR-2001 (first entry)
 XX
 XX PCR primer, ZC976 used to generate Pichia methanolica PRB1 probe.
 DE
 XX Glyceraldehyde 3-phosphate dehydrogenase 1; GAP1; GAPDH-1; promoter;
 KW terminator; industrial enzyme; unglycosylated pharmaceutical protein;
 KW cellulase; enzyme inhibitor; protease inhibitor; growth factor;
 KW platelet derived growth factor; PGDF; glutamic acid decarboxylase; GAD;
 KW cytokine; interleukin; hormone; insulin; PRB1; PCR primer; ss.
 XX
 OS Pichia methanolica.
 XX
 XX WO200078978-A1.
 FN
 XX 28-DEC-2000.
 PD
 XX 16-JUN-2000; 2000WO-US016671.
 PF
 XX 24-JUN-1999; 99US-0140703P.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA (MILL/) MILLER B G.
 PA (SLOA/) SLOAN J S.
 XX
 XX Miller BG, Sloan JS, Raymond CK, Vanaja E;
 PI
 XX WPI; 2001-102728/11.
 DR
 XX New Pichia methanolica glyceraldehyde 3-phosphate dehydrogenase-1 (GAPDH-
 PT

1) promoter for producing industrial enzymes and (unglycosylated) pharmaceutical proteins.

Example 4; Page 36; 39pp; English.

The invention relates to transcription promoter and terminator sequences of Pichia methanolica glyceralddehyde 3-phosphate dehydro- Genase 1 (GAPDH -1) gene, designated as GAP1. These sequences are used within DNA constructs for the production of proteins of interest in cultured P. methanolica cells. The protein of interest includes industrial enzymes and (unglycosylated) pharmaceutical proteins e.g. enzymes such as cellulases, enzyme inhibitors such as protease inhibitors, growth factors such as platelet derived growth factor (PDGF), glutamic acid decarboxylase (GAD), cytokines such as interleukins, hormones such as insulin, and receptors expressed as truncated forms or as fusion proteins. The present sequence is PCR primer, ZC976 used to generate Pichia methanolica PRB1 probe. This primer is specifically used for amplifying the desired region of PRB1 gene in PCZR150 plasmid

Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.57e+03	Length:	18
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-138) x AAD02427 (1-18)

QY 32 ValVallylsArgArg 36
|||
Db 2 GTTGTAAACGCGG 16
|||
RESULT 158
AAD09752
ID AAD09752 standard; DNA; 18 BP.
XX AAD09752;
AC AAD09752;
XX
10-SEP-2001 (first entry)

ZC976 PCR primer, to construct zCytol8-CEE/pZBV32L expression vector.

XX KW Mouse; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
XX KW cancer; inflammation; gene therapy; PCR primer; ss.
XX
XX Unidentified.
XX OS
XX WO200146422-A1.
XX PN
XX PD 28-JUN-2001.
XX PF 22-DEC-2000; 2000WO-US035308.
XX PR 23-DEC-1999; 99US-00471767.
XX PR 01-DEC-2000; 2000US-0250841P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX
XX Presnell SR, Kindsvogel W;
XX WPI; 2001-408648/43.
XX
XX Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer.
XX Example 18A; Page 163; 167pp; English.

The patent discloses novel human cytokine, ZCYTO18 protein and its corresponding DNA. ZCYTO18 protein induces proliferation of cells expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity in K562 cells. ZCYTO18 DNA is useful for detecting a genetic abnormality in

CC a patient. ZCYT018 DNA and its antibodies are useful for detecting cancer
CC and inflammation. ZCYT018 protein is useful for killing cancer cells. It
CC is useful for increasing platelets in a patient or injured tissue. It is
CC also used in gene therapy. The present sequence is PCR primer, ZC976
CC which is used in the construction of C-terminal Glu-Glu (CEE) tagged
CC zCyt018/pZBV32L expression vector
XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.57e+03	Length:	18
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-860A-8 (1-198) x AAD09752 (1-18)

QY 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 159

AAFS7008

1D AAFS7008 standard; DNA; 18 BP.

AC AAFS7008;

XX

DT 14-MAY-2001 (first entry)

XX

DE P. methanolic PRB1 DNA amplifying primer ZC976.

XX

KW Pichia methanolic; auxotrophic; chromosomal locus; protease; PRB1;

KW proteinase A; proteinase B; alcohol oxidase; fermentation; PCR primer;

XX nutritional marker; ss.

XX

OS Pichia methanolic.

XX

US6183953-B1.

PN

XX

PD 06-FEB-2001.

XX

PF 30-DEC-1997; 97US-00001141.

XX

XX

PR 15-SEP-1997; 97US-0058822P.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Raymond CK;

XX

DR WPI; 2001-201998/20.

XX

PT

PT Altering chromosomal locus in Pichia methanolic cells for large-scale

PT protein production, by transforming the cells with DNA construct

PT comprising target locus having altered nucleotide pair and selectable

PT marker.

XX

XX

PS Example 3; Col 39-40; 27pp; English.

XX

CC The invention relates to altering a chromosomal locus in Pichia

CC methanolic cells (C) auxotrophic for adenine that comprises introducing

CC a DNA construct containing a segment with a portion of target locus

CC having an altered nucleotide pair and a selectable marker that

CC complements adenine auxotrophy, into (C) and identifying a subset of (C)

CC in which the DNA construct has been chromosomally integrated, thereby

CC altering the locus. The method is useful for altering a selected

CC chromosomal locus, especially a nutritional marker or a locus that

CC encodes a protease, such as proteinase A or B and/or an alcohol oxidase

CC of P. methanolic cells. The method is thus useful for designing strains

CC of P. methanolic for use in large-scale fermentation for protein

CC production. Sequences AAFS7007-57008 represents PCR primers for

CC amplifying the P. methanolic PRB1 DNA

XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAP57008 (1-18)
 QY 32 ValVallysArgArg 36
 DB 2 GTTGTAAACGCGG 16

RESULT 160
 AAH47591/C
 ID AAH47591 standard; DNA; 18 BP.
 XX AC AAH47591;
 XX 30-NOV-2001 (first entry)
 XX Human Her-3 mRNA inhibiting antisense oligo ISIS # 19606.
 XX Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;
 XX antiinflammatory; cytostatic; antibacterial; antisense; ss.
 XX Synthetic.
 XX Homo sapiens.
 XX US6277640-B1.
 XX 21-AUG-2001.
 XX 31-JUL-2000; 2000US-00630706.
 XX 31-JUL-2000; 2000US-00630706.
 XX (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Cowser LM;
 XX WPI; 2001-535134/59.
 XX Antisense compounds capable of modulating expression of human Her-3.
 XX member of epidermal growth factor family of receptor/tyrosine kinases,
 XX useful for preventing or delaying infection, inflammation or tumor
 XX formation.
 XX Claim 1; Col 43-44; 49pp; English.

XX CC The invention provides antisense compounds capable of inhibiting the
 XX expression of human Her-3, a member of epidermal growth factor (EGF)
 XX family of receptor/tyrosine kinases. The antisense oligonucleotides are
 XX useful for inhibiting the expression of Her-3 in cells or tissues. They
 XX are commonly used as research reagents and in diagnostics for example, to
 XX elucidate the function of particular genes. The antisense compounds are
 XX also useful for distinguishing between functions of various members of a
 XX biological pathway and for research use. They are also utilized for
 XX diagnostics, therapeutics, prophylaxis and in kits. They are useful
 XX prophylactically, e.g. to prevent or delay infection, inflammation or
 XX tumor formation. Sequences AAH4752-47615 represent chimeric antisense
 XX phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap,
 XX used for the inhibition of Her-3 mRNA expression

XX SQ Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH47591 (1-18)
 QY 186 ValAspAspleuArg 190
 DB 17 GTTGATGACCTCGG 3

RESULT 161
 AAC91084
 ID AAC91084 standard; DNA; 18 BP.
 XX AC AAC91084;
 XX 19-MAR-2001 (first entry)
 XX Primer ZC976.
 XX Cytokine; zsig 81; wound healing; proliferation; differentiation;
 XX migration; metabolism; ss.
 XX Unidentified.
 XX OS
 XX WO200073459-A1.
 XX 07-DEC-2000.
 XX 01-JUN-2000; 2000WO-US015002.
 XX 01-JUN-1999; 99US-00323582.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Piddington CS, West JR, Holly RD, Burkhead SK;
 XX WPI; 2001-061540/07.
 XX New zsig81 polypeptides and polynucleotides useful for e.g. promoting
 XX wound healing, or in diagnosing or treating disorders associated with
 XX cell loss or abnormal cell proliferation, such as cancer.
 XX Example 5; Page 105; 109pp; English.

XX CC The present invention relates to zsig81 and fragments thereof. The
 XX invention is useful for promoting wound healing, for modulating the
 XX proliferation, differentiation, migration or metabolism of responsive
 XX cell types that includes both primary and cultured cell lines, and for
 XX stimulating the proliferation of cells expressing markers associated with
 XX dendritic lineage cells

XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x AAC91084 (1-18)
 QY 32 ValVallysArgArg 36
 DB 2 GTTGTAAACGCGG 16

RESULT 162
 AAP55422
 ID AAP55422 standard; DNA; 18 BP.
 XX

AC AAF55422;
DT 29-MAY-2001 (first entry)
XX PCR primer for a probe for the PRB1 gene.
DE
XX
XX Glyceraldehyde-3-phosphate dehydrogenase; GAPDH; GAP2; GAP1; PRB1;
KW GAPDH promoter; GAPDH terminator; methylotrophic yeast; PCR primer; ss.
XX
XX Saccharomyces cerevisiae.
OS
XX
XX WO200118182-A1.
PN
XX
XX 15-MAR-2001.
PD
XX
XX 01-SEP-2000; 2000WO-US024110.
PF
XX
XX 08-SEP-1999; 99US-00391951.
PR
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Raymond CK;
PI
XX
XX WPI; 2001-235197/24.
DR
XX
XX New transcription promoter and terminator sequences from Pichia
PT methanolica, useful within DNA constructs for producing proteins of
PT economic importance, e.g. industrial enzymes, proteins for research or
PT pharmaceutical proteins.
XX
XX Example 4; Page 40; 43pp; English.
XX
XX PCR primers AAF55421-22 were used to amplify a probe for the PRB1 gene.
CC The amplified sequence was used to construct a Pichia methanolica strain
CC deficient for vacuolar proteases. The specification describes GAP1 and
CC GAP2 gene fragments. GAP gene encode glyceraldehyde-3-phosphate
CC dehydrogenase (GAPDH). GAPDH transcription promoter and terminator
CC sequences are useful, within DNA constructs, in methylotrophic yeast for
CC producing polypeptides of economic importance, including industrial
CC enzymes, proteins for research or pharmaceutical proteins. In particular,
CC these proteins include lipases, cellulases or proteases, enzyme
CC inhibitors (e.g. protease inhibitors), growth factors (e.g. platelet
CC derived growth factor, fibroblast growth factors, epidermal growth
CC factor, or vascular endothelial growth factors), glutamic acid
CC decarboxylase (GAD); cytokines (e.g. erythropoietin, colony stimulating
CC factors, interleukins or interleukin antagonists); hormones (e.g.
CC insulin, proinsulin, leptin or glucagon), or receptors (e.g. growth
CC factor receptors)
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0
US-09-966-880A-8 (1-198) x AAF55422 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGCG 16
RESULT 163
AAH26911
ID AAH26911 standard; DNA; 18 BP.
XX
XX AAH26911;
AC
XX 21-DEC-2001 (first entry)
DT
XX

DE Fluorescent oligonucleotide target for electronic hybridisation.
XX
XX Capture probe; hybridisation; electronics; photonics; nanotechnology; ss.
KW
XX Synthetic.
OS
XX Key Location/Qualifiers
FT modified_base 1/*tag= a
FT /mod_base= OTHER
FT /note= "fluorescent dye with 493 nm absorption and 503 nm
FT emission"
XX
XX WO200153799-A1.
PN
XX
XX 26-JUL-2001.
PD
XX
XX 12-JAN-2001; 2001WO-US000926.
PF
XX
XX 24-JAN-2000; 2000US-00489855.
PR
XX
XX (NANO-) NANOGEN INC.
PA
XX
XX Edman CF, Heller MJ, Gurtner C, Formosa R;
PI
XX
XX WPI; 2001-607116/69.
DR
XX
XX Device for photoelectric transport of charged materials in liquid
PT environment for micro- and opto- electronic devices, has a substrate
PT generating light induced current, conductor, permeation layer and light
PT source to illuminate substrate.
XX
XX Disclosure; Page 60; 119pp; English.
XX
XX The present sequence is that of fluorescent target oligonucleotide T2,
CC which was used to demonstrate an electron hybridisation method of the
CC invention. Mn203 stabilised n-type silicon photoelectrodes coated with a
CC streptavidin-agarose permeation layer were shown to constitute a simple
CC platform for rapid manipulation of DNA oligonucleotides by electron
CC hybridisation. In this process, a set of unlabelled oligonucleotides
CC (capture strands) are first targeted to specific locations and anchored.
CC A second set of fluorescent labeled oligonucleotides (target strands) is
CC then targeted to the same locations and actively hybridised to the
CC capture strands. In the example provided, 2 sets of biotinylated capture
CC probes, C1 (see AAH26908) and C2 (see AAH26909), were successively
CC transported and anchored to 4 different locations on a streptavidin-
CC agarose and Mn203 coated amorphous silicon substrate. 2 Fluorescence
CC labeled target sequences, T1 (see AAH26910) and T2 (present sequence),
CC were then transported to a location with complementary capture probes and
CC a location with non-complementary capture probes. This step produced 2
CC clearly detectable fluorescence signals at the 2 locations with matching
CC sequences. The ratio between signal and non-specific background was
CC better than 4. The method allows for detection of DNA oligonucleotides in
CC an extremely short time. The invention generally provides systems and
CC devices for photoelectroretro transport and hybridisation of
CC oligonucleotides. The techniques of the invention have wide use in
CC manufacture of micro electronic and opto electronic devices. Self-
CC assembly fabrication techniques based on DNA polymers enables micron, sub
CC -micron or nanoscale devices to be fabricated
XX
XX Sequence 18 BP; 5 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0
US-09-966-880A-8 (1-198) x AAH26911 (1-18)
QY 56 HisValGluteuLeu 60
XX

Db

RESULT 164

AAS43573

ID AAS43573 standard; DNA; 18 BP.

XX AC AAS43573;

XX AC AAS43573;

DT 18-DEC-2001 (first entry)

DE Corneodesmosin PCR primer #43.

XX Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;

KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.

KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.

XX Homo sapiens.

OS

XX WO200162788-A2.

FN

XX 30-AUG-2001.

XX

PD

XX

PF 23-FEB-2001; 2001WO-GB000795.

XX

PR 23-FEB-2000; 2000GB-00004312.

XX

XX (OXAG-) OXAGEN LTD.

PA

XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;

PI

XX WPI; 2001-570627/64.

DR

XX

XX Corneodesmosin protein and polynucleotide encoding it, having one or more

PT polymorphisms useful in treating, diagnosing or determining

PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory

PT diseases.

XX

XX Disclosure; Page 36; 60pp; English.

PS

XX The invention relates to corneodesmosin protein (I) and nucleic acid (II)

CC encoding the corneodesmosin gene, where the gene comprises a base

CC substitution, deletion or insertion at one or more positions. (I) and

CC (II) are useful for screening for agents for use in prognosis, diagnosis

CC and treatment of individuals having or being susceptible to

CC corneodesmosin-mediated disease, by monitoring the reaction between the

CC molecules and the agents. The nucleotide and amino acid polymorphisms are

CC useful for diagnosing or determining subsequent treatment of the disease

CC mediated disease, which facilitates subsequent treatment of the disease

CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)

CC are useful in diagnostic, prognostic or therapeutic methods and as

CC research tools for e.g. in drug screening. (II) is useful as probes or

CC primers for detecting an allele of the polymorphism or in the regulation

CC of corneodesmosin gene. Antibodies which binds to (I) are useful for

CC screening DNA clone libraries for cells secreting the antigen. (II) is

CC useful as a model to investigate the role of corneodesmosin in normal

CC skin function. AAS43492-AAS43749 represent corneodesmosin coding

CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the

CC invention

XX

SQ Sequence 18 BP; 4 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.57e+03	Length:	18
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	5	Gaps:	0

US-09-966-880A-8 (1-198) x AAS43573 (1-18)

QY 129 LeuHisArgAlaGly 133

Db 3 CTCCACAGAGCTGGA 17

Db

RESULT 165

AAS43571

ID AAS43571 standard; DNA; 18 BP.

XX AC AAS43571;

XX AC AAS43571;

DT 18-DEC-2001 (first entry)

DE Corneodesmosin PCR primer #41.

XX Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;

KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.

KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.

XX Homo sapiens.

OS

XX WO200162788-A2.

FN

XX 30-AUG-2001.

XX

PD

XX

PF 23-FEB-2001; 2001WO-GB000795.

XX

PR 23-FEB-2000; 2000GB-00004312.

XX

XX (OXAG-) OXAGEN LTD.

PA

XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;

PI

XX WPI; 2001-570627/64.

DR

XX

XX Corneodesmosin protein and polynucleotide encoding it, having one or more

PT polymorphisms useful in treating, diagnosing or determining

PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory

PT diseases.

XX

XX Disclosure; Page 36; 60pp; English.

PS

XX The invention relates to corneodesmosin protein (I) and nucleic acid (II)

CC encoding the corneodesmosin gene, where the gene comprises a base

CC substitution, deletion or insertion at one or more positions. (I) and

CC (II) are useful for screening for agents for use in prognosis, diagnosis

CC and treatment of individuals having or being susceptible to

CC corneodesmosin-mediated disease, by monitoring the reaction between the

CC molecules and the agents. The nucleotide and amino acid polymorphisms are

CC useful for diagnosing or determining subsequent treatment of the disease

CC mediated disease, which facilitates subsequent treatment of the disease

CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)

CC are useful in diagnostic, prognostic or therapeutic methods and as

CC research tools for e.g. in drug screening. (II) is useful as probes or

CC primers for detecting an allele of the polymorphism or in the regulation

CC of corneodesmosin gene. Antibodies which binds to (I) are useful for

CC screening DNA clone libraries for cells secreting the antigen. (II) is

CC useful as a model to investigate the role of corneodesmosin in normal

CC skin function. AAS43492-AAS43749 represent corneodesmosin coding

CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the

CC invention

XX

SQ Sequence 18 BP; 4 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.57e+03	Length:	18
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	5	Gaps:	0

US-09-966-880A-8 (1-198) x AAS43571 (1-18)

QY 129 LeuHisArgAlaGly 133

Db 3 CTCCACAGAGCTGGA 17

RESULT 166

AA543567
 ID AAS43567 standard; DNA; 18 BP.
 XX
 AC AAS43567;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Corneodesmosin PCR primer #37.
 XX
 KW Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
 KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162788-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-GB000795.
 XX
 PR 23-FEB-2000; 2000GB-00004312.
 XX
 PA (OXAG-) OXAGEN LTD.
 XX
 PI Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
 XX
 DR WPI; 2001-570627/64.
 XX
 CC Corneodesmosin protein and polynucleotide encoding it, having one or more
 PT polymorphisms useful in treating, diagnosing or determining
 PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
 PT diseases.
 XX
 PS Disclosure; Page 36; 60pp; English.

XX
 CC The invention relates to corneodesmosin protein (I) and nucleic acid (II)
 CC encoding the corneodesmosin gene, where the gene comprises a base
 CC substitution, deletion or insertion at one or more positions. (I) and
 CC (II) are useful for screening for agents for use in prognosis, diagnosis
 CC and treatment of individuals having or being susceptible to
 CC corneodesmosin-mediated disease, by monitoring the reaction between the
 CC molecules and the agents. The nucleotide and amino acid polymorphisms are
 CC useful for diagnosing or determining susceptibility to corneodesmosin-
 CC mediated disease, which facilitates subsequent treatment of the disease
 CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
 CC are useful in diagnostic, prognostic or therapeutic methods and as
 CC research tools for e.g. in drug screening. (II) is useful as probes or
 CC primers for detecting an allele of the polymorphism or in the regulation
 CC of corneodesmosin gene. Antibodies which binds to (I) are useful for
 CC screening DNA clone libraries for cells secreting the antigen. (II) is
 CC useful as a model to investigate the role of corneodesmosin in normal
 CC skin function. AAS43492-AAS43749 represent corneodesmosin coding
 CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
 CC invention

XX
 SQ Sequence 18 BP; 4 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x AAS43567 (1-18)

QY 129 LeuHisArgAlaGly 133

DB 3 CTCACAGAGCTGGA 17

RESULT 167

AAK98893
 ID AAK98893 standard; DNA; 18 BP.
 XX
 AC AAK98893;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE PCR primer ZC976 for amplification of Pichia methanolica gene PRB1.
 XX
 KW Glyceralddehyde-3-phosphate dehydrogenase 2; GAP2; industrial; cytokine;
 KW pharmaceutical; unglycosylated; enzyme; hormone; growth factor; PCR;
 KW primer; ss.
 XX
 OS Unidentified.
 XX
 PN US6348331-B1.
 XX
 PD 19-FEB-2002.
 XX
 PF 01-SEP-2000; 2000US-00653403.
 XX
 PR 08-SEP-1999; 99US-0152744P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Raymond CK;
 XX
 DR WPI; 2002-266520/31.
 XX
 CC New Pichia methanolica glyceralddehyde-3-phosphate dehydrogenase 2 gene
 PT promoter, useful for producing desired protein in cultured yeast cell
 PT which is functionally deficient in vacuolar proteases proteinase A and
 PT proteinase B.
 XX
 PS Example 4; Col 35; 20pp; English.

XX
 CC The invention relates to an isolated polynucleotide comprising Pichia
 CC methanolica glyceralddehyde-3-phosphate dehydrogenase 2 gene (GAP2)
 CC promoter, of up to 5000 nucleotides comprising nucleotide 93-1080 of a
 CC fully defined nucleotide sequence of 3333 base pairs as given in the
 CC specification. A Pichia methanolica cell containing a DNA construct is
 CC useful for producing a desired protein by culturing the cell, where a DNA
 CC segment (other than GAP2) is expressed and desired protein is produced,
 CC and recovering the desired protein from the cultured cell, where the
 CC proteins are preferably of research, industrial, or pharmaceutical
 CC interest e.g. unglycosylated pharmaceutical proteins. Proteins include
 CC enzymes, cytokines, hormones and growth factors. This polynucleotide
 CC sequence represents a PCR primer for amplification of the Pichia
 CC methanolica gene PRB1

XX
 SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AAK98893 (1-18)

QY 32 ValVallyysArgArg 36

DB 2 GTTGTAAACGACGG 16

RESULT 168

ABK91359
 ID ABK91359 standard; DNA; 18 BP.
 XX
 AC ABK91359;
 XX

```

RESULT 169
ABK4997
ID ABK4997 standard; DNA; 18 BP.
XX
XX ABK4997;
AC
XX
XX 15-JUL-2002 (first entry)
XX
XX Human ZTMPO-1 sequencing primer ZC976.
XX
XX ZTMPO; human; immunosuppressive; inotropic; cardiac; leukaemia; cardiac;
XX KW cytostatic; antidiabetic; hypotensive; immunological; ss; reproductive;
XX KW muscle pathology; diabetes; muscular dystrophy; haematopoietic disorder;
XX KW hypertension; chromosome 12q24.33; sequencing; primer; ZC976.
XX
XX Homo sapiens.
OS
XX US6372889-B1.
XX
XX 16-APR-2002.
XX
XX 19-APR-1999; 99US-00294531.
XX
XX 21-APR-1998; 98US-0082513P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Sheppard PO, Conklin DC, Farrah TM, Maurer MF, Grossmann A;
XX
XX WPI; 2002-350566/38.
XX
XX Novel isolated ZTMPO-1 polypeptide, useful for modulating cell
XX proliferation, and for treating disorders such as diabetes, muscular
XX dystrophy and hypertension.
XX
XX Example 1; Col 59; 40pp; English.
XX
XX This invention relates to the cDNA and protein sequences of a novel
XX isolated ZTMPO-1 polypeptide. ZTMPO-1 is a soluble protein with homology
XX to the nuclear membrane proteins emerin and thymoposins. The protein of
XX the invention may have immunosuppressive, inotropic, cardiac,
XX cytosolic, antidiabetic and hypotensive activities. The invention also
XX comprises antibodies to ZTMPO-1 proteins which can be used to detect
XX ZTMPO proteins and may be used to regulate the function of the protein.
XX The sequences of the invention may be used for modulating cellular
XX proliferation and differentiation, and for diagnostic purposes. The
XX polypeptides can be used to treat immunological, reproductive, cardiac,
XX and muscle pathologies, such as diabetes, muscular dystrophy,
XX haematopoietic disorders, leukaemias, and hypertension. The present
XX sequence represents a human ZTMPO-1 gene sequencing primer used to
XX sequence the ZTMPO gene of the invention
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
SQ

```

```

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK4997 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 170
AAS20707
ID AAS20707 standard; DNA; 18 BP.
XX
XX AAS20707;
AC

```

```

15-NOV-2002 (first entry)
XX
XX Pichia methanolica PRB1 gene, PCR primer ZC976.
XX
XX Glyceraldehyde-3 phosphate dehydrogenase; GAPDH; PRB1; yeast; primer; ss;
XX KW enzyme production; enzyme inhibitor production; growth factor; PCR;
XX KW cytokine; interleukin; hormone; unglycosylated pharmaceutical protein.
XX
XX Pichia methanolica.
OS
XX US2002086366-A1.
XX
XX 04-JUL-2002.
XX
XX 07-DEC-2001; 2001US-00013784.
XX
XX 08-SEP-1999; 99US-0152744P.
XX
XX 01-SEP-2000; 2000US-00653403.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Raymond CK;
XX
XX WPI; 2002-635677/68.
XX
XX Novel isolated DNA molecule useful within DNA constructs for producing
XX polypeptides of economical importance including industrial enzymes and
XX pharmaceutical proteins, in cultured Pichia methanolica cells.
XX
XX Example 4; Page 19; 21pp; English.
XX
XX The invention relates to an isolated DNA molecule comprising a DNA
XX construct comprising operably linked elements of a first DNA segment with
XX a functional transcription promoter or Pichia methanolica gene
XX transcription promoter, a second DNA segment encoding a protein of
XX interest other than P. methanolica glyceraldehyde-3-phosphate
XX dehydrogenase or P. methanolica protein, and a third DNA segment
XX comprising a transcription terminator. A P. methanolica cell containing
XX the DNA construct is useful for producing protein of interest, where the
XX second DNA segment is expressed and the protein of interest is produced
XX and recovered from the cultured cell. The transformed cell is useful for
XX producing polypeptides of economical importance including industrial
XX enzymes and pharmaceutical proteins, for producing proteins of research,
XX industrial, or pharmaceutical interest. The proteins include enzymes such
XX as lipase, cellulase, and protease, enzyme inhibitor including protease
XX inhibitors, growth factors such as platelet derived growth factor (PDGF),
XX fibroblast growth factors (FGF), epidermal growth factor (EGF), vascular
XX endothelial growth factors (VEGFs), glutamic acid decarboxylase (GAD),
XX cytokines, such as erythropoietin, thrombopoietin, colony stimulating
XX factors, interleukins, and interleukin antagonist, hormones such as
XX insulin, prolinsulin, leptin, and glucagon, and receptors, including
XX growth factor receptors, which are expressed in truncated form or as
XX fusion proteins with, e.g., immunoglobulin constant region sequences. The
XX transformed cell is also useful for producing unglycosylated
XX pharmaceutical proteins. The present sequence represents a P. methanolica
XX PRB1 gene, PCR primer
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
SQ

```

```

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK91359 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

```

```

XX 09-APR-2002 (first entry)
XX Human zalphall Ligand bacmid DNA, transposable element PCR primer ZC976.
XX
XX Cytokine: zalphall Ligand; zalphall receptor; NK cell progenitor;
XX natural killer cell proliferation; T-cell proliferation;
XX B-cell proliferation; anti-tumour response; immune system;
XX immunostimulant; cytostatic; human; PCR primer; ss.
XX
XX Synthetic.
XX
XX US6307024-B1.
XX
XX 23-OCT-2001.
XX
XX 09-MAR-2000; 2000US-00522217.
XX
XX 09-MAR-1999; 99US-0123547P.
XX
XX 11-MAR-1999; 99US-0123904P.
XX
XX 01-JUL-1999; 99US-0142013P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI; 2002-040208/05.
XX
XX New zalphall ligand polypeptides and polynucleotides, useful for
XX stimulating proliferation, activation, differentiation and/or induction
XX of inhibition of specialized cell function, or for stimulating an
XX antigenic response.
XX
XX Example 30; Col 155; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
XX zalphall Ligand and the polynucleotide encoding it. The invention also
XX gives the sequence for the zalphall receptor and the polynucleotide
XX encoding it. The zalphall Ligand polypeptide stimulates proliferation of
XX natural killer (NK) cells or NK cell progenitors, the activation of NK
XX cells, proliferation of T-cells, proliferation of B-cells stimulated with
XX anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
XX reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
XX zalphall Ligand polypeptide is also useful in preparing antibodies that
XX bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can
XX be used as probes or primers to clone regions of a zalphall Ligand gene,
XX and in gene therapy. Zalphall Ligand may also be used to identify
XX inhibitors of its activity, to enhance the generation of anti-tumour
XX responses with or without the infusion of donor lymphocytes, and to
XX activate or stimulate the immune system. The present sequence represents
XX a PCR primer used in the methods of the present invention
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAS20707 (1-18)
XX
XX Qy 32 ValVallysArgArg 36
XX
XX Db 2 GTTGTAAACGACGC 16
XX
XX RESULT 171
XX ABK91070
XX ID ABK91070 standard; DNA; 18 BP.
XX
XX
XX 09-APR-2002 (first entry)
XX Human zalphall Ligand bacmid DNA, transposable element PCR primer ZC976.
XX
XX Cytokine: zalphall Ligand; zalphall receptor; NK cell progenitor;
XX natural killer cell proliferation; T-cell proliferation;
XX B-cell proliferation; anti-tumour response; immune system;
XX immunostimulant; cytostatic; human; PCR primer; ss.
XX
XX Synthetic.
XX
XX US6307024-B1.
XX
XX 23-OCT-2001.
XX
XX 09-MAR-2000; 2000US-00522217.
XX
XX 09-MAR-1999; 99US-0123547P.
XX
XX 11-MAR-1999; 99US-0123904P.
XX
XX 01-JUL-1999; 99US-0142013P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI; 2002-040208/05.
XX
XX New zalphall ligand polypeptides and polynucleotides, useful for
XX stimulating proliferation, activation, differentiation and/or induction
XX of inhibition of specialized cell function, or for stimulating an
XX antigenic response.
XX
XX Example 30; Col 155; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
XX zalphall Ligand and the polynucleotide encoding it. The invention also
XX gives the sequence for the zalphall receptor and the polynucleotide
XX encoding it. The zalphall Ligand polypeptide stimulates proliferation of
XX natural killer (NK) cells or NK cell progenitors, the activation of NK
XX cells, proliferation of T-cells, proliferation of B-cells stimulated with
XX anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
XX reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
XX zalphall Ligand polypeptide is also useful in preparing antibodies that
XX bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can
XX be used as probes or primers to clone regions of a zalphall Ligand gene,
XX and in gene therapy. Zalphall Ligand may also be used to identify
XX inhibitors of its activity, to enhance the generation of anti-tumour
XX responses with or without the infusion of donor lymphocytes, and to
XX activate or stimulate the immune system. The present sequence represents
XX a PCR primer used in the methods of the present invention
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x ABK91070 (1-18)
XX
XX Qy 38 SerAlaThrSerPhe 42
XX
XX Db 4 TCAGCAACGAGTTTC 18
XX
XX RESULT 172
XX AAD38796
XX ID AAD38796 standard; DNA; 18 BP.
XX
XX XX XX XX XX
XX AC AAD38796;
XX
XX XX
XX 23-SEP-2002 (first entry)
XX
XX Zlmda24 amplifying PCR primer, ZC976.
XX
XX Zlmda24; alpha-helical protein; cytokine-like polypeptide; gene therapy;
XX educational tool; molecular biology; immunocontraceptive;
XX protein chemistry; sperm capacitation; proliferation; differentiation;
XX antifertility vaccine; induction; haematopoiesis; immune function; PCR;
XX primer; ss.

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XX Unidentified.
OS
XX WO200234917-A2.
XX
XX 02-MAY-2002.
XX
XX 19-OCT-2001; 2001WO-US045508.
XX
XX 20-OCT-2000; 2000US-0242023P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Conklin DC, Gao Z, Lofton-Day CE, Whitmore TB;
XX
XX WPI; 2002-471440/50.
XX
XX Novel Zlmda24 polypeptide, a cytokine-like polypeptide with antiparallel
XX alpha helical structure, useful as a diagnostic to detect the presence of
XX disease in testis tissue.
XX
XX Example 5; Page 131; 133pp; English.
XX
XX The invention relates to secreted alpha-helical protein, zlmda24 which is
XX a cytokine-like polypeptide, and its corresponding nucleic acid. Zlmda24
XX is useful for identifying and isolating Zlmda24 ligands, and as antigen
XX to produce anti-Zlmda24 antibodies. Zlmda24 DNA is used gene therapy.
XX Zlmda24 DNA is also useful as educational tool in laboratory practical
XX kits for courses related to genetics, molecular biology, protein
XX chemistry, and antibody production and analysis. It is also useful as an
XX aid to prepare expression constructs for bacterial, viral or mammalian
XX expression, including fusion constructs, for determining the restriction
XX endonuclease cleavage sites of the polynucleotides, determining mRNA and
XX DNA localisation of zlmda24 polynucleotides in tissues, and for
XX identifying related polynucleotides and polypeptides by nucleic acid
XX hybridisation. Zlmda24 is also useful as an aid to teach preparation of
XX antibodies, identifying proteins by Western blotting, protein
XX purification, determining the weight of expressed zlmda24 polypeptides as
XX a ratio of total protein expressed, identifying peptide cleavage sites,
XX coupling amino and carboxyl terminal tags, amino acid sequence analysis,
XX useful for modulating sperm capacitation, and as germ-cell specific
XX of both the native and tagged protein in vitro and in vivo. Zlmda24 is
XX useful for teaching analytical skills, and for monitoring biological activities
XX antigens for used as immunoreceptor or antiferility vaccines to
XX induce formation of Ab and/or cell mediated immunity to selectively
XX inhibit reproduction in humans or animals. Zlmda24 is also useful for
XX stimulating proliferation activation, differentiation and/or induction
XX or inhibition of specialised cell function of cells involved in
XX haematopoiesis and immune function. The present sequence is a PCR primer
XX used for amplifying zlmda24 cDNA. This sequence is used for viral
XX generation of zlmda24-CEE/pZBV32L
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservatives: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAD38796 (1-18)
XX
XX QY 32 ValVallysArgArg 36
XX
XX Db 2 GTTGTAAACGACGG 16
XX
XX RESULT 173
XX ABS54171
XX ID ABS54171 standard; DNA; 18 BP.
XX
XX XX ABS54171;
XX AC

```

```

XX 26-NOV-2002 (first entry)
XX
XX Human RING finger protein zapop3, sequencing primer #2.
XX
XX Human; ss; zapop3; RING finger; chromosome 9q34.11; gene therapy;
XX myeloid leukaemia; chronic myelogenous leukaemia; myelocytic leukaemia;
XX lymphoblastic leukaemia; retinitis pigmentosa-deafness syndrome 1;
XX myocardial infarction; congestive heart failure; heart attack;
XX heart transplantation; angiogenesis; wound healing; angioplasty;
XX endarterectomy; coronary collateral circulation; revascularisation;
XX diabetic foot ulcer; stroke; cancer; coronary reperfusion; primer;
XX cardiac function; skeletal muscle neogenesis; hyperplasia;
XX kidney regeneration; systemic hypertension; pulmonary hypertension.
XX
XX Homo sapiens.
XX
XX US6440697-B1.
XX
XX 27-AUG-2002.
XX
XX 04-NOV-1999; 99US-00434408.
XX
XX 12-NOV-1998; 98US-0108258P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Venezia D, Grossmann A;
XX
XX WPI; 2002-705357/76.
XX
XX Novel expression vector comprising DNA segment encoding zapop3
XX polypeptide, useful for producing transformed cells expressing zapop3
XX polypeptide (a RING finger protein).
XX
XX Example 1; Col 55; 48pp; English.
XX
XX The invention relates to an expression vector comprising the following
XX operably linked elements: a transcription promoter; a DNA segment
XX encoding a polypeptide having a zapop3 (a RING finger protein) sequence;
XX and a transcription terminator, where the promoter is operably linked to
XX the DNA segment which is in turn operably linked to the transcription
XX terminator. The vector introduced into a cell and the protein expressed.
XX The cell is useful for producing the zapop3 polypeptide. The vector is
XX useful in gene therapy techniques to increase or inhibit zapop3 activity.
XX zapop3 polypeptide is useful for treating disorders associated with
XX myocardial infarction, congestive heart failure, hypertrophic
XX cardiomyopathy and dilated cardiomyopathy, for limiting infarct size
XX following a heart attack, aiding in recovery after heart transplantation,
XX promoting angiogenesis, and wound healing following angioplasty or
XX endarterectomy, to develop coronary collateral circulation, for
XX revascularisation in the eye, for complications related poor circulation
XX such as diabetic foot ulcer, for stroke, cancer, following coronary
XX reperfusion, and other indications, where angiogenesis is desired. The
XX polypeptide is also useful for improving cardiac function, inducing
XX skeletal muscle neogenesis and/or hyperplasia, kidney regeneration and/or
XX for treating systemic and pulmonary hypertension. The polypeptide is also
XX useful for identifying modulators of zapop3 activity, and for producing
XX antibodies. The gene for zapop3 is located on chromosome 9q34.11 an area
XX associated with myeloid leukaemia, chronic myelogenous leukaemia,
XX myelocytic leukaemia, lymphoblastic leukaemia and retinitis pigmentosa-
XX deafness syndrome 1. The present sequence is a sequencing primer for the
XX cDNA encoding zapop3
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservatives: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 6 Gaps: 0
XX

```

US-09-966-880A-8 (1-198) x ABS54171 (1-18)

QY 32 ValVallysArgArg 36
 DB 2 GTTGTAACGACGG 16

RESULT 174
 ABZ95417
 ID ABZ95417 standard; DNA; 18 BP.
 XX
 AC ABZ95417;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human fibronectin antisense fragment no.1281.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 DN WC200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 10659; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
 XX

Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABZ95417 (1-18)

QY 59 LeuLeuPheLeuArg 63
 DB 4 CTCCTGTTCTCCGT 18

RESULT 175
 ABX93718
 ID ABX93718 standard; DNA; 18 BP.
 XX
 AC ABX93718;
 XX
 DT 04-JUN-2003 (first entry)
 XX
 DE Human zsig58 cDNA sequencing primer #1.
 XX
 KW Human; zsig58; ss; gonadal development; pregnancy; pubertal change;
 KW menopause; ovarian cancer; fertility; ovarian function; pancreas; primer;
 KW polycystic ovarian syndrome; diabetes; eye disease; pituitary function;
 KW osteoporosis; bone disease; wound healing; bacterial infection;
 KW viral infection; fungal infection; analgesic; antidiabetic; vulnary;
 KW gynaecological; osteopathic; cytostatic; ophthalmological; sequencing.
 XX
 OS Homo sapiens.
 XX
 PN US2002182677-A1.
 XX
 PD 05-DEC-2002.
 XX
 XX 26-FEB-2002; 2002US-00086135.
 XX
 PR 03-AUG-1998; 98US-0095199P.
 PR 03-AUG-1999; 99US-00366448.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 XX Sheppard PO, Chandrasekher YA;
 PI WPI; 2003-328618/31.
 DR
 XX
 PT New pancreatic and ovarian zsig58 polypeptides useful for diagnosing or
 PT treating disorders associated with gonadal development, pregnancy, or
 PT pubertal changes, menopause, ovarian cancer, fertility, and ovarian or
 PT pancreatic function.
 XX
 CC Example 1; Page 35; 49pp; English.
 CC
 CC The invention relates to an isolated pancreatic and ovarian zsig58
 CC polypeptide and the polynucleotide encoding it. The polypeptide, zsig58
 CC polynucleotide and an antibody to the polypeptide are useful in
 CC diagnosing or treating disorders associated with gonadal development,
 CC pregnancy, pubertal changes, menopause, ovarian cancer, fertility,
 CC ovarian function, polycystic ovarian syndrome, pancreas, diabetes, eye
 CC disease, pituitary function, osteoporosis and other bone diseases. The
 CC zsig58 polypeptide may also be used in promoting wound healing, in anti-
 CC microbial applications, as a cell culture reagent in in vitro studies of
 CC exogenous microorganism infections (e.g. bacterial, viral or fungal
 CC infection), as an analgesic (e.g. bone pain), in identifying cells,
 CC tissues or cell lines that respond to a zsig58-stimulated pathway, in
 CC identifying agonists and antagonists of its activity and in preparing
 CC antibodies. The antibody may be used for tagging cells that express
 CC zsig58, for isolating zsig58 and for other diagnostic and therapeutic
 CC applications. The polynucleotide is also useful in identifying a region
 CC of the genome associated with human disease states. This sequence
 CC represents a sequencing primer used to sequence cDNA encoding the human
 CC zsig58 polypeptide
 XX

Alignment Scores: 8.57e-03 Length: 18
 Pred. No.:

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABX93718 (1-18)

QY 32 ValVallysArgArg 36
DB 2 GTTGTAACGACGG 16

RESULT 176

ABX10645/c
ID ABX10645 standard; DNA; 18 BP.

XX AC ABX10645;

XX DT 22-APR-2003 (first entry)

XX DE DNA encoding the mouse PDGF-A proteolytic cleavage site.

XX KW Mouse; trans-dominant suppressor gene; growth factor; oligomeric state;
XX KW suppressor gene; cell proliferation; autocrine loop; paracrine loop;
XX KW cancer; tumour; atherosclerosis; coronary artery disease;
XX KW rheumatoid arthritis; gene therapy; platelet derived growth factor; PDGF;
XX KW PDGF-A; PDGF-B; transforming growth factor beta; TGF-beta; TGF-beta1;
XX KW TGF-beta2; proteolytic cleavage site; mitogenic activity;
XX KW propeptide processing; cytoskeletal; cardiac; ds.

XX OS Mus musculus.

XX XX US6475781-B1.

XX PN 05-NOV-2002.

XX PD 21-DEC-1993; 93US-00171384.

XX PF 17-MAY-1990; 90US-00525245.

XX PR 06-MAR-1992; 92US-00846972.

XX PA (DAND) DANA FARBEN CANCER INST INC.

XX XX Mercola MK, Deininger PL, Stiles CD;

XX XX WPI; 2003-208835/20.

XX DR P-PSDB; ABG75586.

XX PT New eukaryotic trans-dominant suppressor gene encoding a protein
PT translation product which suppresses the activity of a growth factor,
PT useful for inhibiting unwanted cell proliferation e.g., cancer.

XX PS Disclosure; Fig 1; 23pp; English.

XX CC The invention discloses a eukaryotic trans-dominant suppressor gene
CC encoding a protein translation product which suppresses the activity of a
CC growth factor that requires an oligomeric state for function, by forming
CC an inactive oligomer with a wildtype subunit of the growth factor, the
CC protein translation product being a mutant form of a wildtype subunit of
CC the growth factor. The suppressor gene is useful for inhibiting unwanted
CC cell proliferation in a mammalian patient, where the proliferation is
CC stimulated in part by the presence of an autocrine or paracrine loop, and
CC the unwanted cell is cancer, and is also useful for treating patient
CC having atherosclerosis, coronary artery disease or rheumatoid arthritis
CC (e.g. gene therapy). The suppressor gene is further useful for creating a
CC transgenic laboratory animal which will serve as a disease model for
CC medical research. A vector comprising the suppressor gene is useful for
CC the production of dominant suppressor protein and also to transfect the
CC suppressor gene into mammalian cells such as COS (simian fibroblasts)

CC cells. Examples of growth factors to target are the dimeric protein,
CC platelet derived growth factor (PDGF), comprising the sub-units PDGF-A
CC and PDGF-B, and the transforming growth factor beta (TGF-beta) subfamily
CC (e.g. TGF-beta1 or TGF-beta2). Target regions of the growth factors to
CC mutate are the proteolytic cleavage sites and cysteine residues essential
CC for mitogenic activity. The sequence presented is the DNA encoding the
CC wild-type mouse PDGF-A proteolytic cleavage site
XX
SQ Sequence 18 BP; 7 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABX10645 (1-18)

QY 59 LeuLeuPheLeuArg 63

DB 17 CTTCTCTTCTGCGA 3

RESULT 177

ACC47946

ID ACC47946 standard; DNA; 18 BP.

XX AC ACC47946;

XX DT 11-AUG-2003 (first entry)

XX DE Nucleotide sequence of PCR primer ZC976.

XX KW Platelet-derived growth factor-D; PDGF-D; osteopathic; vulnery; bone;
XX KW connective tissue; PCR; primer; ss.

XX OS Synthetic.

XX PN WO2003033677-A2.

XX PD 24-APR-2003.

XX PF 18-OCT-2002; 2002WO-US033563.

XX PR 19-OCT-2001; 2001US-0346117P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX XX Moore MD, Fox BA;

XX DR WPI; 2003-421322/39.

XX PT New protein consisting of two platelet-derived growth factor-D
PT polypeptide chains, useful for stimulating the production of bone and/or
PT connective tissue in both humans and animals, e.g. in treating fractures
PT or osteoporosis.

XX PS Example 1; Page 47; 47pp; English.

XX CC The invention relates to a protein consisting of two platelet-derived
CC growth factor-D (PDGF-D) polypeptide chains. The protein is useful in
CC enhanced production of PDGF-D growth factor domain dimers. It may be used
CC to stimulate production of bone and/or connective tissue in both humans
CC and animals, such as in cases of fractures, bone grafts, implants, repair
CC of bony defects arising from surgery, surgical reconstruction following
CC traumatic injury, repair of hereditary or other physical abnormalities,
CC or in treatment of osteoporosis. The present sequence represents a PCR
CC primer used in the course of the invention

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 18
Score: 8.57e+03
Length: 18
Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x ACC47946 (1-18)

Qy 32 ValVallyysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 178

AD50482
ID AAD50482 standard; DNA; 18 BP.

XX AC AAD50482;
XX XX

DT 24-MAR-2003 (first entry)

DE ZC976 PCR primer used to amplify human zcyto20 DNA.

XX Human; leukaemia; carcinoma; acquired immune deficiency syndrome; AIDS;
KW melanoma; Kaposi's sarcoma; multiple myeloma; non-Hodgkin's lymphoma;
KW hepatitis; infection; myocarditis; blood vessel formation; gene therapy;
KW growth regulation; developmental process; immunotherapy; zcyto20; PCR;
KW primer; ss.
XX OS Homo sapiens.
XX XX

XX PN W0200286087-A2.

XX PD 31-OCT-2002.

XX PF 19-APR-2002; 2002WO-US012887.
XX PR 20-APR-2001; 2001US-0285408P.
XX PR 20-APR-2001; 2001US-0285424P.
XX PR 25-APR-2001; 2001US-0286482P.
XX PR 29-JUN-2001; 2001US-00895834.
XX PR 22-OCT-2001; 2001US-0341050P.
XX PR 22-OCT-2001; 2001US-0341105P.

XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Sheppard PO, Fox BA, Klucher KM, Taft DW, Kindsvogel WR;
XX DR WPI; 2003-093122/08.

XX New zcyto20, zcyto21, zcyto22, zcyto24 and zcyto25 polypeptides and
PT polynucleotides useful for treating leukemia, carcinoma, malignant
PT melanoma, AIDS-related Kaposi's sarcoma, myeloma, non-Hodgkin's lymphoma,
PT hepatitis and infections.
XX Example 6; Page 135; 160pp; English.

XX The invention relates to zcyto20, zcyto21, zcyto22, zcyto24 and zcyto25
CC polypeptides and polynucleotides. Sequences of the invention are useful
CC for treating hairy cell leukaemia, renal cell or basal cell carcinoma,
CC malignant melanoma, AIDS-related Kaposi's sarcoma, multiple myeloma, non-
CC Hodgkin's lymphoma, hepatitis B, C or D, infections (e.g. bacterial,
CC fungal or protozoal) or myocarditis. The invention is useful for growth
CC regulation in the liver, blood vessel formation and other developmental
CC processes. The invention is also useful in immunotherapy and gene
CC therapy. The present sequence is a PCR primer used to amplify human
CC zcyto20 DNA
XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x AAD50482 (1-18)

Qy 32 ValVallyysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 179

ADA4993
ID ADA4993 standard; DNA; 18 BP.

XX AC ADA4993;
XX XX

DT 20-NOV-2003 (first entry)

DE Human mitochondrial COX gene primer #41.

XX Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;
KW segregation; nontropic; neuroprotective; primer; ss.
XX OS Homo sapiens.
XX PN US2003087858-A1.
XX PD 08-MAY-2003.
XX PF 15-OCT-2001; 2001US-00978600.
XX PR 30-MAR-1994; 94US-00219842.
XX PR 30-MAR-1995; 95US-00413740.
XX PR 23-NOV-1999; 99US-00448312.
XX PA (MITO-) MITOKOR.

XX PI Herrnstadt C, Ghosh SS;
XX DR WPI; 2003-597110/56.

XX Compositions and methods for the treatment and diagnosis of Alzheimer's
PT disease using nucleic acids related in sequence to (mutants of) the
PT cytochrome c oxidase gene.
XX Example 2; Page 25; 93pp; English.
XX The present invention relates to compositions and method for the
CC treatment and diagnosis of Alzheimer's disease (AD). The method comprises
CC the use of genetic mutations in the human mitochondrial cytochrome c
CC oxidase (COX) gene and their segregation with AD. Also disclosed are
CC antisense sequences specific to mutant human cytochrome c oxidase genes
CC that are designed to bind and inhibit transcription or translation of the
CC target mutant COX genes without inhibiting transcription or translation
CC of wild-type cytochrome c oxidase genes. Also disclosed are probes for
CC detecting a disease state associated with one or more mutations in the
CC mitochondrial COX genes, and a kit comprising a probe for detection of an
CC Alzheimer's disease genotype which is complementary to the sense or
CC antisense strands of a mitochondrial COX gene. Definitive diagnosis of
CC Alzheimer's disease can currently only be accomplished by pathological
CC examination at autopsy, the new method provides a non-invasive diagnostic
CC that is reliable at or before the earliest manifestations of AD symptoms.
CC There is at present no effective therapy for AD other than certain
CC palliative treatments. The new therapeutic compositions and methods
CC provide an effective therapy that addresses the primary cause of AD. The
CC present sequence represents a primer for the human mitochondrial COX
CC gene.
XX SQ Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x ADA49993 (1-18)

QY 125 GlyLeuArgArgLeu 129
DB 2 GGTCTACGAGGCTC 16

RESULT 180

ACAG2736
ID ACAG2736 standard; cDNA; 18 BP.

XX AC AGA2736;

DT 21-AUG-2003 (first entry)

DE DE Bacmid transposable element primer ZC976.

XX KW Primer; ss; PCR; VCAM-1 inhibition; bacmid; inflammation; wound;
KW vascular cell adhesion molecule 1; energy balance; cellular metabolism;
KW adipogenesis; glucogenesis; glycogenolysis; glucose uptake; blood flow;
KW protein synthesis; thermogenesis; oxygen use; neurotransmitter; trauma;
KW acute vascular injury; angioplasty; coronary artery bypass graft; stroke;
KW aneurysm; obesity; diabetes; lipogenesis; transposable element.

XX OS Unidentified.

XX PN US6521233-B1.

XX PD 18-FEB-2003.

XX PF 19-APR-2000; 2000US-00552225.

XX PR 20-APR-1999; 99US-0130199P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Piddington CS, Bishop PD;

XX DR WPI; 2003-478795/45.

XX PT New adipocyte complement related protein (zacr3) bearing a collagen-like
PT domain and a C1q domain, useful for modulating energy, modulating fat
PT formation and storage, particularly for treating e.g. obesity, diabetes
PT or wounds.

XX PS Example 2; Col 65-66; 37pp; English.

XX CC The invention relates to an isolated polypeptide (designated zacrp3)
CC which inhibits the expression of vascular cell adhesion molecule 1 (VCAM-
CC 1). The zacrp3 polypeptide or the fusion protein is useful for modulating
CC energy balance in mammals by modulating cellular metabolic reaction, e.g.
CC adipogenesis, glucogenesis, glycogenolysis, lipogenesis, glucose uptake,
CC protein synthesis, thermogenesis, or oxygen use. The polypeptide is
CC particularly useful for modulating the formation and storage of fat in
CC mammals. The zacrp3 polypeptide is also useful for protecting endothelial
CC cells from injury, as neurotransmitters, or as modulators of
CC neurotransmission. The zacrp3 polypeptide is also useful for promoting
CC blood flow within the vasculature of a mammal, or for treating acute
CC vascular injury due to e.g. angioplasty, coronary artery bypass graft,
CC trauma, stroke or aneurysm. In particular, the zacrp3 polypeptide is
CC useful for treating or preventing obesity, diabetes, wounds,
CC inflammations, etc. The present sequence represents the bacmid
CC transposable element primer ZC976

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores: Pred. No.: 8.57e+03 Length: 18

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x ACA62736 (1-18)

QY 32 ValVallyeArgArg 36
DB 2 GTTGTAAACGACGG 16

RESULT 181

AA47867
ID AAD47867 standard; DNA; 18 BP.

XX AC AAD47867;

DT 27-AUG-2003 (first entry)

DE DE Human interleukin-21 DNA amplifying primer ZC976.

XX KW Interleukin-21; antagonist; cancer; inflammatory; autoimmune disorder;
KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KW myasthenia gravis; diabetes; human; IL-21; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO2003040313-A2.

XX PD 15-MAY-2003.

XX PF 28-OCT-2002; 2002WO-US034502.

XX PR 05-NOV-2001; 2001US-0337586P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Presnell SR, West JW, Novak JE;

XX DR WPI; 2003-441547/41.

XX PT New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
PT and treating disorders with aberrant expression or activity of the IL-21
PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
PT diabetes.

XX PS Example 5; Page 69; 71pp; English.

XX CC The invention relates to polynucleotides and polypeptides of interleukin-
CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
CC that is not detectable in receptor binding studies. The antagonists of
CC the invention have mutations in the D helix of the IL-21 molecule, and
CC can be used to inhibit the activity of IL-21 with its cognate receptor.
CC The IL-21 antagonists are useful for diagnosing and treating disorders
CC involving the aberrant expression or activity of the IL-21 polypeptide,
CC such as cancer, inflammatory and autoimmune disorders, including
CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
CC myasthenia gravis and diabetes. The polypeptides can also be used to
CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
CC and for enhancing in vivo killing of target tissues. The present sequence
CC is a PCR primer used in an exemplification of the invention to screen
CC baculovirus clones with the correct insert of human IL-21 DNA

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores: Pred. No.: 8.57e+03 Length: 18

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x AAD47867 (1-18)

QY 32 ValVallysArgArg 36
 Db 2 GTTGTAAACGACGG 16

RESULT 182

AD58385
 ID AAD58385 standard; DNA; 18 BP.

AC AAD58385;

DT 20-NOV-2003 (first entry)

XX PCR primer zc976 used in the exemplification of the invention.

XX Platelet-derived growth factor-D; PDGF-D; bone graft; osteopathic;
 KW radiation-induced osteonecrosis; periodontal disease; protein therapy;
 KW joint injury; osteoporosis; bone loss; fracture; bone healing; PCR;
 KW primer; ss.

XX Unidentified.

OS WO2003068802-A2.

PN 21-AUG-2003.

PD 11-FEB-2003; 2003WO-US004213.

PF 11-FEB-2002; 2002US-035882P.

PR (ZYMO) ZYMOGENETICS INC.

XX Fox BA, Moore MD, Swiderek KM, Birks CW;

PI WPI; 2003-646473/61.

PT New fusion protein comprising a first platelet-derived growth factor-D
 (PDGF-D) domain, a linker, and a second PDGF-D domain polypeptides,
 useful for stimulating the production of bone and/or connective tissue.

XX Example 1; Page 44; 50pp; English.

XX The invention relates to a fusion protein comprising, from amino to
 CC carboxyl terminus, a first platelet-derived growth factor-D (PDGF-D)
 CC domain polypeptide, a linker polypeptide, and a second PDGF-D domain
 CC polypeptide. The fusion proteins are useful for stimulating the
 CC production of bone and/or connective tissue in both human and non-human
 CC animals. The fusion proteins are specifically useful in non-union
 CC fractures and fractures in patients with compromised healing, bone
 CC grafts, bone healing following radiation-induced osteonecrosis, implants,
 CC or treatment of periodontal disease, joint injuries, osteoporosis or
 CC other conditions characterised by increased bone loss or decreased bone
 CC formation. The invention is useful in protein therapy. The present
 CC sequence is a PCR primer used in the exemplification of the invention.
 CC PDGF-D is known as zvegfa

XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x AAD58385 (1-18)

QY 32 ValVallysArgArg 36
 Db 2 GTTGTAAACGACGG 16

RESULT 183

ADB80425
 ID ADB80425 standard; DNA; 18 BP.

XX ADB80425;

DT 04-DEC-2003 (first entry)

DE Rat CLCAL gene PCR primer #11.

XX ss; primer; antiinflammatory; antiasthmatic; antiallergic; CLCAL;
 KW calcium activated chloride channel protein; chest disorder;
 KW airway disorder; chronic obstructive lung disease; chronic bronchitis;
 KW bronchial asthma; rhinitis; hay fever; pneumonia.

XX Rattus sp.

XX WO2003037927-A1.

XX 08-MAY-2003.

XX 01-NOV-2002; 2002WO-JP011417.

XX 02-NOV-2001; 2001JP-00337864.

PR 13-DEC-2001; 2001JP-00380099.

PR 18-JAN-2002; 2002JP-00010035.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Nakanishi A, Morita S;

XX WPI; 2003-430500/40.

PT Rat CLCAL gene and protein encoded by it useful for screening inhibitors
 of its activity and expression and as chronic obstructive lung disease

XX Example 3; Page 98; 115pp; Japanese.

XX The invention relates to proteins and their salts and partial peptides
 CC which are the expression product of the rat CLCAL gene or are related
 CC proteins with similar activity. CLCAL is a calcium activated chloride
 CC channel protein. The proteins are useful for the treatment, prevention
 CC and diagnosis of chest and airway disorders including chronic obstructive
 CC lung disease, chronic bronchitis, bronchial asthma, chronic rhinitis,
 CC acute rhinitis, allergic rhinitis, hay fever and pneumonia. This sequence
 CC corresponds to a PCR primer used to isolate and clone the rat CLCAL gene
 CC (ADB80434).

XX Sequence 18 BP; 3 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADB80425 (1-18)

QY 126 LeuArgArgLeuHis 130

Db 4 CTTCCGAGATTGCAT 18

RESULT 184

ADB80414/c
 ID ADB80414 standard; DNA; 18 BP.

XX ADB80414;

DT 04-DEC-2003 (first entry)

```

XX DE Rat CLCA1 gene PCR primer #1.
XX ss; primer; antiinflammatory; antiasthmatic; antiallergic; CLCA1;
KW calcium activated chloride channel protein; chest disorder;
KW airway disorder; chronic obstructive lung disease; chronic bronchitis;
KW bronchial asthma; rhinitis; hay fever; pneumonia.
XX Rattus sp.
XX WO2003037927-A1.
XX 08-MAY-2003.
XX 01-NOV-2002; 2002WO-JF011417.
XX 02-NOV-2001; 2001JP-00337864.
XX 13-DEC-2001; 2001JP-00380099.
XX 18-JAN-2002; 2002JP-00010035.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Nakanishi A, Morita S;
XX WPI; 2003-430500/40.
XX Rat CLCA1 gene and protein encoded by it useful for screening inhibitors
XX of its activity and expression and as chronic obstructive lung disease
XX and bronchial asthma remedies.
XX Example 1; Page 94; 115pp; Japanese.
XX The invention relates to proteins and their salts and partial peptides
XX which are the expression product of the rat CLCA1 gene or are related
XX proteins with similar activity. CLCA1 is a calcium activated chloride
XX channel protein. The proteins are useful for the treatment, prevention
XX and diagnosis of chest and airway disorders including chronic obstructive
XX lung disease, chronic bronchitis, bronchial asthma, chronic rhinitis,
XX acute rhinitis, allergic rhinitis, hay fever and pneumonia. This sequence
XX corresponds to a PCR primer used to isolate and clone the rat CLCA1 gene
XX (ADB80434).
XX Sequence 18 BP; 6 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 9 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x ADB80414 (1-18)
XX
XX QY 126 LeuArgArgLeuHis 130
XX DB 15 CTTCGGAGATTGCAT 1
XX
XX RESULT 185
XX AAD60481
XX ID AAD60481 standard; DNA; 18 BP.
XX AC AAD60481;
XX 18-DEC-2003 (first entry)
XX Human c-IAP-2 antisense oligonucleotide #ISIS #23454.
XX Human; antisense; cellular inhibitor of apoptosis-2; c-IAP-2; cancer;
KW hyperproliferative condition; apoptosis inhibitor 2; autoimmune disease;
KW API-1; hIAP-1; MIRC; gene therapy; phosphorothioate; ss.
XX Homo sapiens.
OS

```

```

OS Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..18
XX /tag= a
XX /mcd_base= OTHER
XX /note= "Phosphorothioate backbone; All cytidine residues
XX are 5-methylcytidines"
XX modified_base 1..4
XX /tag= b
XX /mcd_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX modified_base 15..18
XX /tag= c
XX /mcd_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX US2003083300-A1.
XX 01-MAY-2003.
XX 16-JUL-2002; 2002US-00197290.
XX 23-SEP-1999; 99WO-US022083.
XX 04-OCT-2001; 2001US-00857299.
XX (BENN/) BENNETT C F.
XX (ACKE/) ACKERMANN E J.
XX (COWS/) COWSERT L M.
XX Bennett CF, Ackermann EJ, Cowsert LM;
XX WPI; 2003-755119/71.
XX New antisense compound, preferably an oligonucleotide, for inhibiting
XX expression of human Cellular Inhibitor of Apoptosis-2 in human cells or
XX tissues, and for treating diseases, such as cancer or an autoimmune
XX disease.
XX Claim 3; Page 22; 34pp; English.
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding human cellular inhibitor of apoptosis-2 (also known as c-IAP-2,
XX apoptosis inhibitor 2, API-1, hIAP-1 and MIRC) to inhibit its expression.
XX Antisense compounds of the invention are used to induce apoptosis in
XX human cells or tissues to treat diseases or conditions associated with
XX insufficient apoptosis. They are used to treat diseases or conditions
XX associated with c-IAP-2 such as hyperproliferative conditions especially
XX cancer or autoimmune diseases. The invention is also useful in antisense
XX gene therapy. The present sequence is an antisense oligonucleotide
XX targetted to human c-IAP-2 DNA
XX Sequence 18 BP; 4 A; 3 C; 2 G; 9 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 9 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAD60481 (1-18)
XX
XX QY 59 LeuLeuPheLeuArg 63
XX DB 4 CTTTATTCTTAGA 18
XX
XX RESULT 186
XX AAD60513
XX ID AAD60513 standard; DNA; 18 BP.
XX AC AAD60513;

```

XX 18-DEC-2003 (first entry)
 XX Human c-IAP-2 antisense oligonucleotide #ISIS #23486.
 DE Human; antisense; cellular inhibitor of apoptosis-2; c-IAP-2; cancer;
 XX hyperproliferative condition; apoptosis inhibitor 2; autoimmune disease;
 KW API-1; HIAP-1; MHC; gene therapy; phosphorothioate; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT modified_base 1..18
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..4
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 15..18
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 XX US2003083300-A1.
 XX 01-MAY-2003.
 XX 16-JUL-2002; 2002US-00197290.
 XX 23-SEP-1999; 99WO-US022083.
 XX 04-OCT-2001; 2001US-00857299.
 XX (BENNETT) BENNETT C F.
 XX (ACKER) ACKERMANN E J.
 XX (COWS) COWSERT L M.
 XX Bennett CF, Ackermann EJ, Cowsert LM;
 XX WPI; 2003-755119/71.
 XX New antisense compound, preferably an oligonucleotide, for inhibiting
 FT expression of human Cellular Inhibitor of Apoptosis-2 in human cells or
 FT tissues, and for treating diseases, such as cancer or an autoimmune
 FT disease.
 XX Claim 3; Page 22; 34pp; English.
 XX The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding human cellular inhibitor of apoptosis-2 (also known as c-IAP-2,
 CC apoptosis inhibitor 2, API-1, HIAP-1 and MHC) to inhibit its expression.
 CC Antisense compounds of the invention are used to induce apoptosis in
 CC human cells or tissues to treat diseases or conditions associated with
 CC insufficient apoptosis. They are used to treat diseases or conditions
 CC associated with c-IAP-2 such as hyperproliferative conditions especially
 CC cancer or autoimmune diseases. The invention is also useful in antisense
 CC gene therapy. The present sequence is an antisense oligonucleotide
 CC targetted to human c-IAP-2 DNA
 XX Sequence 18 BP; 2 A; 4 C; 3 G; 9 T; 0 U; 0 Other;
 SQ Sequence 18 BP; 2 A; 4 C; 3 G; 9 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 Gaps: 0
 DB: 0

US-09-966-880A-8 (1-198) x AAD60513 (1-18)

QY 38 SerAlaThrSerPhe 42
 Db |||||
 4 AGTGTACCTCTTTT 18
 RESULT 187
 ADD24810/C
 ID ADD24810 standard; DNA; 18 BP.
 XX
 AC ADD24810;
 XX
 DT 15-JAN-2004 (first entry)
 XX Human CYP3A4 mutant A392G probe H193.
 DE
 DE diagnostic; pharmaceutical tolerance; side effect; drug; human;
 XX allelic variability; polymorphism; phase I; phase II;
 KW detoxification mechanism; PCR; primer; probe; NAT2; CYP2D6; CYP1A2;
 KW CYP3A4; MEH; TPMT; MTHFR; paraoxonase; CYP2C9; CYP2C19; CYP2E1; DPD; ss.
 XX Homo sapiens.
 OS
 XX WO2003018837-A2.
 PN
 XX 06-MAR-2003.
 PD
 XX 22-AUG-2002; 2002WO-EP009386.
 PF
 XX 24-AUG-2001; 2001DB-01040651.
 PR
 XX 30-APR-2002; 2002DE-01019373.
 PR
 XX (ADNA-) ADNAGEN AG.
 FA
 XX Waschuetza S, Schnakenberg E, Lustig M;
 XX WPI; 2003-290079/28.
 XX Diagnostic kit, useful for assessing a subject's tolerance of drugs,
 FT comprises reagents for determining alleles of genes encoding
 FT detoxification enzymes.
 FT
 XX Claim 6; Page 39; 156pp; German.
 PS
 XX This invention describes a novel diagnostic kit for determining tolerance
 CC of pharmaceuticals in humans by determining allelic variability of at
 CC least two polymorphisms of a human enzyme involved in phase I and/or II
 CC of the detoxification mechanism in a blood, tissue or other human sample,
 CC where tolerance is determined from presence or absence of alleles. The
 CC kit comprises two pairs of oligonucleotide primers, in which each pair
 CC amplifies by PCR, part of a gene for a human detoxification mechanism-
 CC associated enzyme. The kit may also contain two further pairs of
 CC oligonucleotides, serving as probes for detection of amplified DNA
 CC segments, especially where the probes are complementary to a single
 CC strand of one allele of the target gene. The probes are labelled with
 CC fluorophores (LC-Red640 or LC-Red705 for 5'-labelling or fluorescein for
 CC 3'-labelling) which generate a different signal in the hybridized and non
 CC hybridized condition. The enzymes detected include NAT2, CYP2D6, CYP1A2,
 CC CYP3A4, MEH, TPMT, MTHFR, paraoxonase, CYP2C9, CYP2C19, CYP2E1 or DPD.
 CC The kit is used to determine an individual's tolerance of a particular
 CC drug, to establish a suitable dose and/or to predict if a subject will
 CC show side-effects to a drug. The kit provides minimally invasive, safe
 CC and reliable determination of the metabolic capacity of phase I and/or II
 CC enzymes at the molecular level. This sequence represents a probe used in
 CC the kit of the invention.
 XX Sequence 18 BP; 0 A; 9 C; 2 G; 7 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 0

```

DB:          9          Gaps:          0
US-09-966-880A-8 (1-198) x ADD24810 (1-18)
QY          22 LysGlyArgArgGlu 26
           |||||
DB          16 AAGGCGAGGAGAG 2

RESULT 188
AAD61885
ID AAD61885 standard; DNA; 18 BP.
XX
AC AAD61885;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human Zalphall cDNA clone sequencing primer, ZC 976.
XX
KW Cytokine receptor; Zalphall; cell proliferation; cell development;
KW splenic disorder; blood disorder; bone disorder; immune disorder;
KW haematopoietic; lymphoid; inflammatory; therapy; human; primer; ss.
XX
OS Homo sapiens.
XX
PN US6576744-B1.
XX
PD 10-JUN-2003.
XX
PF 23-SEP-1999; 99US-00404641.
XX
PR 23-SEP-1998; 98US-0100896P.
PR 09-MAR-1999; 99US-0123546P.
PR 06-JUL-1999; 99US-0142574P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Presnell SR, Conklin DC, Novak JE, Hammond AK;
XX
DR WPI; 2003-799829/75.
XX
PT Novel cytokine receptor Zalphall useful for treating lymphoid, immune,
PT inflammatory, splenic, blood or bone disorders.
XX
PS Example 1; Col 85; Opp; English.
XX
CC The invention relates to a cytokine receptor designated Zalphall and its
CC nucleic acid sequence. Zalphall protein is useful for detecting ligands
CC that stimulate the proliferation and/or development of haematopoietic,
CC lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful
CC in identifying a region of the genome associated with human disease
CC states. Zalphall protein is useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. The present sequence is
CC a primer used for sequencing human Zalphall cDNA clone
XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:          Length:          18
Pred. No.:          8.57e+03          Matches:          5
Score:          5.00          Conservative:          0
Percent Similarity:          100.00%          Mismatches:          0
Best Local Similarity:          100.00%          Indels:          0
Query Match:          2.53%          Gaps:          0
DB:          9

US-09-966-880A-8 (1-198) x AAD61885 (1-18)
QY          32 valvallysArgArg 36
           |||||
DB          2 GTTGTAAACGACGG 16

RESULT 189
ADD36973/C
ID ADD36973 standard; DNA; 18 BP.

```

```

XX
AC ADD36973;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human papillomavirus E6 gene-specific PCR primer/probe Seq ID86.
XX
KW cervical carcinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervical cancer;
KW cervical cell; cervix; PCR; primer; probe; ss.
XX
OS Human papillomavirus.
XX
PN WO2003057914-A2.
XX
PD 17-JUL-2003.
XX
PF 07-JAN-2003; 2003WO-GE000034.
XX
PR 07-JAN-2002; 2002GB-00000239.
PR 19-JUN-2002; 2002GB-00014124.
XX
PA (NORC-) NORCHIP AS.
PA (ALLA/) ALLARD S J.
XX
PI Karlsen F;
XX
DR WPI; 2003-587136/55.
XX
PT An in vitro method of screening human subjects to assess their risk of
PT developing cervical carcinoma, comprises screening the subject for
PT expression of mRNA transcripts from the L1 gene and the E6 gene of human
PT papillomavirus.
XX
PS Disclosure; SEQ ID NO 86; 102pp; English.
XX
CC This invention relates to a novel method for the detection of human
CC papillomavirus mRNA for use in the screening of human female subjects to
CC assess their risk of developing cervical carcinoma. The invention
CC comprises screening the subject for expression of mRNA transcripts from
CC the L1 gene and the E6 gene of human papillomavirus, where subjects
CC positive for expression of L1 and/or E6 mRNA are scored as being at risk
CC of developing cervical carcinoma. The presence of the human
CC papillomavirus (in particular HPV16 and HPV18) has been associated with
CC cervical cancer in numerous epidemiological studies. The methods of the
CC invention are useful for screening human subjects to assess their risk of
CC developing cervical carcinoma, or for identifying human subjects having
CC abnormal cell changes in the cervix. The present sequence is that of a
CC PCR primer (which may also be suitable as a probe) which may be used to
CC amplify the E6 gene of human papillomavirus in the method of the
CC invention.
XX
SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Alignment Scores:          Length:          18
Pred. No.:          8.57e+03          Matches:          5
Score:          5.00          Conservative:          0
Percent Similarity:          100.00%          Mismatches:          0
Best Local Similarity:          100.00%          Indels:          0
Query Match:          2.53%          Gaps:          0
DB:          9

US-09-966-880A-8 (1-198) x ADD36973 (1-18)
QY          174 ArgGlnLeuArgArg 178
           |||||
DB          18 AGACAGCTCAGAGA 4

RESULT 190
ADD36831/C
ID ADD36831 standard; DNA; 18 BP.
XX
AC ADD36831;
XX

```

DT 15-JAN-2004 (first entry)
XX Human papillomavirus PCR primer 14.
DE
XX
XX cervical carcinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervical cancer;
KW cervical cell; cervix; PCR; primer; ss.
XX
XX Human papillomavirus.
OS
XX
XX WO2003057914-A2.
PN
XX
XX 17-JUL-2003.
PD
XX
XX 07-JAN-2003; 2003WO-GB0000034.
PF
XX
XX 07-JAN-2002; 2002GB-00000239.
PR
XX
XX 19-JUN-2002; 2002GB-00014124.
PR
XX
XX (NORC-) NORCHIP AS.
PA (ALLA/) ALLARD S J.
PA
XX
XX Karlisen F;
PI
XX
XX WPI; 2003-587136/55.
DR
XX
XX An in vitro method of screening human subjects to assess their risk of
PT developing cervical carcinoma, comprises screening the subject for
PT expression of mRNA transcripts from the L1 gene and the E6 gene of human
PT papillomavirus.
PT
XX
XX Example 1; Page 63; 102pp; English.
PS
XX
XX This invention relates to a novel method for the detection of human
CC papillomavirus mRNA for use in the screening of human female subjects to
CC assess their risk of developing cervical carcinoma. The invention
CC comprises screening the subject for expression of mRNA transcripts from
CC the L1 gene and the E6 gene of human papillomavirus, where subjects
CC positive for expression of L1 and/or E6 mRNA are scored as being at risk
CC of developing cervical carcinoma. The presence of the human
CC papillomavirus (in particular HPV16 and HPV18) has been associated with
CC cervical cancer in numerous epidemiological studies. The methods of the
CC invention are useful for screening human subjects to assess their risk of
CC developing cervical carcinoma, or for identifying human subjects having
CC abnormal cell changes in the cervix. The present sequence is that of a
CC PCR primer which was used to amplify sequence of the human papillomavirus
CC in the exemplification of the invention.
XX
SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD36831 (1-18)

QY 174 ArgGlnLeuArgArg 178
DB 18 AGACAGCTCAGAAGA 4

RESULT 191
ADD36741/c
ID ADD36741 standard; DNA; 18 BP.
XX
XX ADD36741;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX Human papillomavirus E6 gene-specific PCR primer 221.
DE
XX

KW cervical carcinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervical cancer;
XX cervical cell; cervix; PCR; primer; ss.
XX
XX Human papillomavirus.
OS
XX
XX WO2003057914-A2.
PN
XX
XX 17-JUL-2003.
PD
XX
XX 07-JAN-2003; 2003WO-GB0000034.
PF
XX
XX 07-JAN-2002; 2002GB-00000239.
PR
XX
XX 19-JUN-2002; 2002GB-00014124.
PR
XX
XX (NORC-) NORCHIP AS.
PA (ALLA/) ALLARD S J.
PA
XX
XX Karlisen F;
PI
XX
XX WPI; 2003-587136/55.
DR
XX
XX An in vitro method of screening human subjects to assess their risk of
PT developing cervical carcinoma, comprises screening the subject for
PT expression of mRNA transcripts from the L1 gene and the E6 gene of human
PT papillomavirus.
PT
XX
XX Disclosure; Page 54; 102pp; English.
PS
XX
XX This invention relates to a novel method for the detection of human
CC papillomavirus mRNA for use in the screening of human female subjects to
CC assess their risk of developing cervical carcinoma. The invention
CC comprises screening the subject for expression of mRNA transcripts from
CC the L1 gene and the E6 gene of human papillomavirus, where subjects
CC positive for expression of L1 and/or E6 mRNA are scored as being at risk
CC of developing cervical carcinoma. The presence of the human
CC papillomavirus (in particular HPV16 and HPV18) has been associated with
CC cervical cancer in numerous epidemiological studies. The methods of the
CC invention are useful for screening human subjects to assess their risk of
CC developing cervical carcinoma, or for identifying human subjects having
CC abnormal cell changes in the cervix. The present sequence is that of a
CC preferred PCR primer which may be used to amplify the E6 gene of human
CC papillomavirus in the method of the invention.
XX
SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD36741 (1-18)

QY 174 ArgGlnLeuArgArg 178
DB 18 AGACAGCTCAGAAGA 4

RESULT 192
ADD22030/c
ID ADD22030 standard; DNA; 18 BP.
XX
XX ADD22030;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX HPV E6 gene transcribed mRNA detecting oligonucleotide, SEQ ID No 69.
DE
XX
XX E6; human papillomavirus; HPV; NASBA; primer; PCR; ss.
KW
XX
XX Human papillomavirus.
OS
XX

PN WO2003057927-A2.
 XX 17-JUL-2003.
 PD
 XX
 PF 07-JAN-2003; 2003WO-GB000030.
 XX
 PR 07-JAN-2002; 2002GB-00000258.
 XX
 XX (NORC-) NORCHIP AS.
 PA (ALLA/) ALLARD S J.
 XX
 XX Karlseen F;
 PI
 XX WPI; 2003-587141/55.
 DR
 XX
 XX New oligonucleotide primer and probe for detecting the presence of mRNA
 PT transcripts from the E6 gene of a human papillomavirus in clinical
 PT samples.
 XX
 XX Claim 1; SEQ ID NO 69; 28pp; English.
 PS
 XX
 XX The invention relates to a novel oligonucleotide molecule used for
 CC detecting mRNA transcribed from the E6 gene of a human papillomavirus
 CC (HPV). The oligonucleotide comprises any of the 133 fully defined
 CC sequences having 17-26 bp given in the specification. The invention
 CC further provides the detection of HPV mRNA in a test sample suspected of
 CC containing HPV, comprising performing an amplification reaction on a
 CC preparation of a nucleic acid isolated from the test sample to amplify a
 CC portion of the mRNA transcribed from the E6 gene of HPV, where the
 CC amplification reaction is performed using the primer-pair of
 CC oligonucleotide cited above. The invention also provides: a reagent kit
 CC for use in the detection of HPV by NASBA, comprising an oligonucleotide
 CC primer-pair and, optionally, an enzyme mixture comprising an RNA directed
 CC DNA polymerase, a ribonuclease that hydrolyzes the RNA strand of an RNA-
 CC DNA hybrid without hydrolyzing single or double stranded RNA or DNA, and
 CC an RNA polymerase that recognises the promoter sequence present in at
 CC least one NASBA P1 primer oligonucleotide included in the reagent kit.
 CC The oligonucleotide of the invention is useful in detecting mRNA
 CC transcripts from the E6 gene of HPV in clinical samples. This
 CC polynucleotide sequence represents one of the 133 oligonucleotides used
 CC for detecting mRNA transcribed from the E6 gene of a human papillomavirus
 CC (HPV) of the invention.
 XX
 XX SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD22030 (1-18)

QY 174 AtgGlnLeuArgArg 178
 Db 18 AGACAGCTCAGAGA 4

RESULT 193
 ADD22316/c
 ID ADD22316 standard; DNA; 18 BP.
 XX
 XX
 XX ADD22316;

XX 15-JAN-2004 (first entry)
 DT
 XX
 XX HPV E6 gene transcribed mRNA detecting RT-PCR primer #48.

DE E6; human papillomavirus; HPV; NASBA; primer; RT-PCR; ss.
 XX
 XX Human papillomavirus.
 OS

PN WO2003057927-A2.
 XX 17-JUL-2003.
 PD
 XX
 PF 07-JAN-2003; 2003WO-GB000030.
 XX
 PR 07-JAN-2002; 2002GB-00000258.
 XX
 XX (NORC-) NORCHIP AS.
 PA (ALLA/) ALLARD S J.
 XX
 XX Karlseen F;
 PI
 XX WPI; 2003-587141/55.
 DR
 XX
 XX New oligonucleotide primer and probe for detecting the presence of mRNA
 PT transcripts from the E6 gene of a human papillomavirus in clinical
 PT samples.
 XX
 XX Disclosure; Page 25; 28pp; English.
 PS
 XX
 XX The invention relates to a novel oligonucleotide molecule used for
 CC detecting mRNA transcribed from the E6 gene of a human papillomavirus
 CC (HPV). The oligonucleotide comprises any of the 133 fully defined
 CC sequences having 17-26 bp given in the specification. The invention
 CC further provides the detection of HPV mRNA in a test sample suspected of
 CC containing HPV, comprising performing an amplification reaction on a
 CC preparation of a nucleic acid isolated from the test sample to amplify a
 CC portion of the mRNA transcribed from the E6 gene of HPV, where the
 CC amplification reaction is performed using the primer-pair of
 CC oligonucleotide cited above. The invention also provides: a reagent kit
 CC for use in the detection of HPV by NASBA, comprising an oligonucleotide
 CC primer-pair and, optionally, an enzyme mixture comprising an RNA directed
 CC DNA polymerase, a ribonuclease that hydrolyzes the RNA strand of an RNA-
 CC DNA hybrid without hydrolyzing single or double stranded RNA or DNA, and
 CC an RNA polymerase that recognises the promoter sequence present in at
 CC least one NASBA P1 primer oligonucleotide included in the reagent kit.
 CC The oligonucleotide of the invention is useful in detecting mRNA
 CC transcripts from the E6 gene of HPV in clinical samples. This
 CC polynucleotide sequence represents an oligonucleotide used for detecting
 CC mRNA transcribed from the E6 gene of a human papillomavirus (HPV) of the
 CC invention.
 XX
 XX SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8.57e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD22316 (1-18)

QY 174 AtgGlnLeuArgArg 178
 Db 18 AGACAGCTCAGAGA 4

RESULT 194
 AAN92708/c
 ID AAN92708 standard; DNA; 19 BP.
 XX
 XX
 XX AAN92708;

XX 31-OCT-2002 (revised)
 DT
 DT 14-MAY-1990 (first entry)
 XX
 XX Probe GH89 for DQalpha A1.2, A1.3 and A1.4 alleles.

DE DQalpha; GH89; ss.
 XX
 XX Synthetic.
 OS


```

XX PN WO8911548-A.
XX PD 30-NOV-1989.
XX PF 18-MAY-1989; 89WO-US000170.
XX PR 20-MAY-1988; 88US-00197000.
XX PS 04-MAY-1989; 89US-00347495.
XX PA (CETU ) CETUS CORP.
XX PI Saiki RK, Brlich HA;
XX DR WPI; 1989-370739/50.
XX
XX Assay reagent contg. oligo-nucleotide probe attached via spacer - each
XX probe having hybridisation region complementary to specific analyte
XX sequence, e.g. for diagnosis of genetic disease.
XX
XX Example; Page 29; 47pp; English.
XX
XX Probe fixed to a filter allows simultaneous non radioactive detection of
XX 50 or more specific nucleotide sequences in a single test sample.
XX (Updated on 31-OCT-2002 to add missing OS field.)
XX
XX Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x AAN92708 (1-19)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGACTGCTC 4

RESULT 195
AAQ38565/C
ID AAQ38565 standard; DNA; 19 BP.
XX
XX AC AAQ38565;
XX
XX 25-MAR-2003 (revised)
DT 15-APR-1993 (first entry)
XX
XX Negative control site.
XX
XX Probe; binding site; Giardia; genome; giardin; Hexamitidae; conserved;
XX region; hypervariable; detection assay; primer; PCR;
XX nucleic acid hybridisation; genus; subgroup; species; water; faecal;
XX human; pathogenic; internal positive control sequence; heat-induced;
XX mRNA; ss.
XX
XX Synthetic.
XX
XX EP517154-A1.
XX
XX 09-DEC-1992.
XX
XX 02-JUN-1992; 92EP-00109271.
XX
XX 06-JUN-1991; 91US-00712904.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Atlas RM, Bej AK, Mahbubani MH;
XX

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DR WPI; 1992-408636/50.
XX
XX Detection of Giardia species in water and faecal samples - by detecting
XX hybridisation of a probe to a complementary portion of giardin gene.
XX
XX Disclosure; Page 9; 34pp; English.
XX
XX The sequences given in AAQ31855, AAQ31856 and AAQ38565 are used as
XX internal control regions in a method to identify the giardin gene within
XX the Giardia genome. Giardia species are members of the Hexamitidae, and
XX all contain within their genomes the giardin gene. The giardin gene has
XX several conserved regions, esp. between 78-190 bp, 267-385 bp and 639-809
XX bp. The gene also has hypervariable regions, esp. between 405-62 bp. The
XX conserved and hypervariable regions can be used as targets for detection
XX assays based upon nucleic acid hybridisation. Probes which bind
XX substantially to the conserved regions will permit detection of all
XX members of the genus. Probes which bind substantially to the
XX hypervariable regions will permit detection of subgroups within the genus
XX or to specific species. This internal negative control sequence can be
XX used in detection of Giardia in water samples or in faecal samples from a
XX patient suspected of being infected with Giardia. Identification of the
XX hypervariable regions of the giardin gene allows differentiation between
XX human pathogenic Giardia and harmless species. By detecting the presence
XX or absence of heat-induced mRNA, living organisms can be distinguished
XX from dead organisms. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ38565 (1-19)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGACTGCTC 4

RESULT 196
AAQ25996/C
ID AAQ25996 standard; DNA; 19 BP.
XX
XX AC AAQ25996;
XX
XX 25-MAR-2003 (revised)
DT 15-JAN-1993 (first entry)
XX
XX Negative control-DQ alpha1.2, 1.3, 4.
XX
XX Internal positive control sequence; PCR; amplification; Legionella.
XX
XX Synthetic.
XX
XX WO9211273-A1.
XX
XX 09-JUL-1992.
XX
XX 19-DEC-1991; 91WO-US009688.
XX
XX 20-DEC-1990; 90US-00630899.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Picone TKH, McCallum T, Zoccoli MA;
XX
XX WPI; 1992-250019/30.
XX
XX Nucleic acid primers for the amplification of Legionella DNA - amplify
XX select target regions and enable detection of pathogenic and non-
XX

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```

PT pathogenic forms with shorter, simpler testing.
PS Disclosure; Page 31; 73pp; English.
XX
XX The sequence DQalpha1.2, 1.3, 4 is a negative control sequence for
XX Legionella. The positive control sequence is used in the co-
XX amplification of DNA from Legionella species using polymerase primers.
CC These primers allow for amplification of select target regions of the
CC genome of the genus Legionella. Detection of pathogenic and non-
CC pathogenic species and discrimination within the genus are possible using
CC less test sample and less time. See also AAQ25981-26000, 26376-26379.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ25996 (1-19)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGAACTGCTC 4

RESULT 197
AAQ48922/c
ID AAQ48922 standard; DNA; 19 BP.
XX
AC AAQ48922;
XX
DT 25-MAR-2003 (revised)
DT 16-MAR-1994 (first entry)
XX
DE Cross-linking oligonucleotide 18.
XX
KW Crosslink; ON; oligonucleotide; hairpin loop; stem loop; interior loop;
KW bulge; fixation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 9
FT /*tag= c
FT /note= "crosslinked to base 9 of (AAQ48910) via an oxime
FT linkage as in example 13b; The ONs also bind by
FT hybridisation"
FT modified_base 9
FT /*tag= a
FT /mod_base= 2'-O-[propion-3-yl-bis(o-nitrobenzyl)]
FT acetal] uridine
FT /note= "ref: example 4-A"
FT modified_base 17
FT /*tag= b
FT /mod_base= 2'-O-[propion-3-yl-bis(o-nitrobenzyl)]
FT acetal] uridine
FT /note= "ref: example 4-A"
FT misc_binding 18
FT /*tag= d
FT /note= "crosslinked to base 18 of (AAQ48910) via an oxime
FT linkage as in example 13b; The ONs also bind by
FT hybridisation"
XX
XX WO9318052-A1.
XX
XX 16-SEP-1993.
XX
XX 05-MAR-1993; 93WO-US002059.
XX

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PR 05-MAR-1992; 92US-00846376.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cook PD, Manoharan M, Bruce T;
XX
XX WPI; 1993-303395/38.
XX
XX New covalently crosslinked oligo-nucleotide(s) - used to fix duplex
XX structures or hairpin loop, stem loop, interior loop, bulge or other
XX structures.
XX
XX Disclosure; Page 71; 145pp; English.
XX
XX Sequences (AAQ48905-28) consist of novel crosslinked oligo-nucleotides. A
XX number of crosslinking methods are claimed, which are used to fix
XX separate ON strands in duplex structures or to fix a single ON strand in
XX a hairpin loop, stem loop, interior loop, bulge or other similar higher-
XX order structures. Fixing a strand or strands in a duplex structure also
XX can disrupt the normal function of a single stranded nucleic acid-binding
XX protein by forming nuclease resistant mimics of the protein binding
XX receptors. The ONs have diagnostic, therapeutic and prophylactic
XX applications as well as being used as research agents. (Updated on 25-MAR
XX -2003 to correct PN field.)
XX
SQ Sequence 19 BP; 8 A; 1 C; 8 G; 0 T; 2 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ48922 (1-19)
QY 179 IleLeuLeuProLeu 183
DB 17 ATTCTCTACCTCTG 3

RESULT 198
AAQ34454/c
ID AAQ34454 standard; DNA; 19 BP.
XX
XX AAQ34454;
XX
DT 17-DEC-2001 (revised)
DT 12-MAY-1993 (first entry)
XX
DE DQAl probe AG9.2, for alleles 0102, 0103 and 0501.
XX
KW Amplification; conformation polymorphism; SSCP; DQ-alpha; DQ-beta;
KW cystic fibrosis; neurofibromatosis; ss.
XX
OS Synthetic.
XX
XX USN7751892-N.
XX
XX 01-DEC-1992.
XX
XX 29-AUG-1991; 91US-00751892.
XX
XX 29-AUG-1991; 91US-00751892.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
XX Mann D, Dean M, Carrington M, White MB;
XX WPI; 1993-017809/02.
XX
XX Distinguishing multiple alleles and identifying new alleles - by single-
XX strand conformation polymorphism technique using specific gel
XX

```

PT electrophoresis conditions.
 XX Disclosure; Page 19; 36pp; English.
 XX
 CC The oligomer AG9.2 represents a probe for DQA1 alleles 0501, 0102 and 0103 and is used to distinguish multiple alleles of a gene of the immunoglobulin supergene family. The DNA encoding the gene of interest in a sample is amplified and then denatured. The amplified DNA is then separated on a non-denaturing polyacrylamide gel consisting of 5 percent bis-acrylamide with 0-10 percent glycerol, and the presence or absence of DNA bands showing hybridisation is detected. Before amplification of the gene, the alleles may be divided into subsets by oligonucleotide hybridisation. Using single stranded conformation polymorphism (SSCP) multiple alleles in complex genetic systems can be distinguished e.g. DQ-alpha and DQ-beta and new alleles identified. The method may be used in studying genetic associations with disease, in forensic analyses and typing tissues for transplantation. The SSCP method has been used for detection of mutant alleles which correlate with the presence of disorders such as cystic fibrosis and neurofibromatosis. See also AAQ34443-73. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
 XX
 SQ Sequence 19 BP; 5 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAQ34454 (1-19)
 QY 56 Hisvalgluleu 60
 Db 19 CACGTAAGACTGTC 5
 RESULT 199
 AAQ52889
 ID AAQ52889 standard; RNA; 19 BP.
 AC AAQ52889;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-MAY-1994 (first entry)
 XX
 DE Cytomegalovirus target sequence 66.
 XX
 KW RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HbRNA; picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV; papilloma virus; HPV; Epstein-Barr virus; EBV; TGLV;
 KW T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
 KW influenza virus; HSV; herpes simplex virus; vector; immune response; antibody; ribozyme; viral RNA; treatment; ss.
 XX
 OS Synthetic.
 XX
 FN WO9323569-A1.
 XX
 PD 25-NOV-1993.
 XX
 XX 29-APR-1993; 93WO-US004020.
 XX
 PR 11-MAY-1992; 92US-00882689.
 PR 14-MAY-1992; 92US-00882712.
 PR 14-MAY-1992; 92US-00882713.
 PR 14-MAY-1992; 92US-00882714.
 PR 14-MAY-1992; 92US-00882823.
 PR 14-MAY-1992; 92US-00882824.
 PR 14-MAY-1992; 92US-00882886.

PR 14-MAY-1992; 92US-00882888.
 PR 14-MAY-1992; 92US-00882889.
 PR 14-MAY-1992; 92US-00882921.
 PR 14-MAY-1992; 92US-00882922.
 PR 14-MAY-1992; 92US-00883823.
 PR 14-MAY-1992; 92US-00883849.
 PR 14-MAY-1992; 92US-00884073.
 PR 14-MAY-1992; 92US-00884074.
 PR 14-MAY-1992; 92US-00884333.
 PR 14-MAY-1992; 92US-00884422.
 PR 14-MAY-1992; 92US-00884431.
 PR 14-MAY-1992; 92US-00884436.
 PR 14-MAY-1992; 92US-00884521.
 PR 31-JUL-1992; 92US-00923738.
 PR 26-AUG-1992; 92US-00935854.
 PR 26-AUG-1992; 92US-00936086.
 PR 18-SEP-1992; 92US-00948359.
 PR 15-OCT-1992; 92US-00963322.
 PR 07-DEC-1992; 92US-00987129.
 PR 07-DEC-1992; 92US-00987130.
 PR 07-DEC-1992; 92US-00987133.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Draper KG, Dudycz LW, Mcswiggen JA, Macejak DG, Holecsek JU;
 PI Mamone JA;
 XX
 DR WPI; 1993-386599/48.
 XX
 PT Enzymatic RNA molecules - used to inhibit viral replication, infection and gene expression.
 PT
 PS Claim 5; Fig 13; 287pp; English.
 XX
 CC The sequences (AAQ52824-Q52890) are pref. Cytomegalovirus target sequences for enzymatic RNA molecules. The RNA molecules are complementary to a substrate binding region in the specified gene target. They also have enzymatic activity, in that they specifically cleave RNA in the target. The ERMs interfere with viral replication and therefore have anti-viral properties. They can be used to attenuate viruses to be used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 19 BP; 3 A; 5 C; 9 G; 0 T; 2 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAQ52889 (1-19)
 QY 124 GluclyLeuArg 128
 Db 1 GAGGCCUACGCCGU 15
 RESULT 200
 AAQ90410
 ID AAQ90410 standard; DNA; 19 BP.
 XX
 AC AAQ90410;
 XX
 DT 08-JAN-1996 (first entry)
 XX
 DE RC-A5 (synthetic DNA probe with 5' amino terminal #9).
 XX
 KW RC-A5; HLA; dQa; self-addressable electronic device; SAED; hybridisation; ss.
 KW

```

OS Synthetic.
XX FH Key
XX misc_feature 1
XX Location/Qualifiers
FT FT /*tag= a
FT FT /note= "3' aminolink2 Thymine; allows binding to any
FT FT amine"
XX
XX W09512808-A1.
XX
XX 11-MAY-1995.
XX
XX 26-OCT-1994; 94WO-US012270.
XX
XX 01-NOV-1993; 93US-00146504.
XX
XX (NANO-) NANOGEN INC.
XX
XX Heller MJ, Tu E;
XX
XX WPI; 1995-185870/24.
XX
XX New self-addressable electronic devices - used for multi-step and
XX multiplex reactions such as DNA hybridisation(s), clinical diagnostics
XX and bio:polymer synthesis.
XX
XX Example 1; Page 41; 86pp; English.
XX
XX The sequences represented by, AAQ90402-15 are synthetic DNA probes
XX containing 5' amino termini. The sequences shown in AAQ90390-401 are
XX synthetic DNA probes with 3' ribonucleoside termini. These sequences were
XX specific for the polymorphisms of HLA gene d0a. The sequences were used
XX in the device of the invention. This is a self-addressable electronic
XX device (SAED) that can be used to carry out multi-step and multiplex
XX reactions, such as nucleic acid hybridisations. The advantages of this
XX method are that these reactions can be carried out with complete and
XX precise electronic control, and that the rate, specificity and
XX sensitivity of these reactions are greatly improved at micro-locations
XX
XX SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ90410 (1-19)

QY 56 HisValGluLeuLeu 60
Db |||||
2 CACGTAGAACTGCTC 16

RESULT 201
AAT10762
ID AAT10762 standard; RNA; 19 BP.
XX
XX AAT10762;
XX
XX 09-SEP-1996 (first entry)
XX
XX Oligonucleotide probe, RC-A5.
XX
XX Electronically self-addressable device; ED: electrode; current source;
XX attachment layer; permeable; counterion; genetic typing; probe;
XX detection; ss.
XX
XX Synthetic.
XX
XX Key modified_base 1
XX Location/Qualifiers
FT FT

```

```

FT FT /*tag= a
FT FT /note= "5'-amino terminus"
XX
XX W09601836-A1.
XX
XX 25-JAN-1996.
XX
XX 05-JUL-1995; 95WO-US008570.
XX
XX 07-JUL-1994; 94US-00271882.
XX
XX (NANO-) NANOGEN INC.
XX
XX Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX
XX WPI; 1996-097582/10.
XX
XX Electronically self-addressable device - used for electronic control of,
XX e.g. nucleic acid hybridisation.
XX
XX Example 1; Page 61; 155pp; English.
XX
XX The sequences given in AAT10742-67 are synthetic oligonucleotides which
XX are used in the construction of the electronically self-addressable
XX device (ED) of the invention. The ED comprises a substrate, an electrode
XX or opt. a number of electrodes supported by the substrate, a current
XX source operatively connected to the electrode and an attachment layer
XX adjacent to the electrode which is permeable to a counterion but not
XX permeable to a molecule capable of insulating or binding to the
XX electrode. The attachment layer is capable of attaching a macromolecule.
XX The ED is used for genetic typing and comprises a number of
XX electronically addressable locations each comprising an electrode, and a
XX binding entity, such as one of these probes, attached to each of the
XX locations capable of detecting the presence of a genetic sequence
XX
XX SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT10762 (1-19)

QY 56 HisValGluLeuLeu 60
Db |||||
2 CACGTAGAACTGCTC 16

RESULT 202
AAT7746
ID AAT7746 standard; DNA; 19 BP.
XX
XX AAT7746;
XX
XX 25-MAR-2003 (revised)
XX
XX 26-SEP-1997 (first entry)
XX
XX Primer GP125 used in production of protein C transgene.
XX
XX Human; lactoferrin; transgenic bovine; ovum; bovine; ovary; zygote;
XX transgene; pre-implantation stage embryo; milk; milk protein;
XX serum protein; industrial enzyme; alpha-S1 casein; protein C; ss.
XX
XX Synthetic.
XX
XX US5633076-A.
XX
XX 27-MAY-1997.
XX
XX 16-NOV-1993; 93US-00154019.
XX
XX PF

```

XX 01-DEC-1989; 89US-00444745.
 PR 27-NOV-1990; 90US-00619131.
 PR 15-JUN-1992; 92US-00898956.
 PR 15-JUN-1993; 93US-00077788.
 PA (PHAR-) PHARMING BV.
 XX
 XX Heyneker HL, Deboer HA, Krimpenfort PJA, Lee SH, Platenburg G;
 PI Pieper F, Strijker R;
 XX WPI; 1997-297339/27.
 XX
 XX Production of transgenic bovine embryo - by introducing trans:gene into
 PT fertilised ovum in vitro.
 XX
 XX Example 17; Col 46; 91pp; English.
 XX
 XX The sequences given in AAT77746-47 are primers which were used in the
 CC production of a protein C transgene which was used in the method of the
 CC invention to produce a transgenic bovine. The method of the invention
 CC comprises obtaining an ovum from bovine ovaries, maturing it in vitro,
 CC fertilising the mature ovum in vitro to form a zygote, introducing a
 CC transgene into the zygote in vitro where the transgene integrates into
 CC the genome of the zygote to form a transgenic embryo, maturing the zygote
 CC to a preimplantation stage embryo in vitro, and transplanting the embryo
 CC into a recipient female bovine, who gestates the embryo to produce a
 CC transgenic bovine. The method may also be used to generate transgenic
 CC bovine embryo's. The transgenic cows produced by the method of the
 CC invention secrete recombinant proteins in their milk, especially human
 CC milk proteins, human serum proteins and industrial enzymes. The milk from
 CC the transgenic cows containing the recombinant polypeptides may be used
 CC in food formulations in liquid or dried form. The food formulations will
 CC be supplemented with one or more recombinant polypeptides from the
 CC transgenic milk. The production of transgenic bovine milk containing one
 CC or more recombinant polypeptides is desirable since it provides a matrix
 CC wherein little or no purification is necessary for human consumption.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT77746 (1-19)
 Qy 32 ValVallylsArgArg 36
 Db 5 GTTGTAACGACGG 19
 |||||
 RESULT 203
 AAT46986
 ID AAT46986 standard; DNA; 19 BP.
 XX
 AC AAT46986;
 XX
 DT 01-DEC-1997 (first entry)
 XX
 DE 19-mer probe for use with APX chip.
 XX
 XX apparatus; enhanced detection; biological reaction; biochip;
 KW fluid system; diagnosis; analysis; multistep; multiplex reaction;
 KW synthesis; biopolymer; automated DNA analysis system; self-addressable;
 KW self-assembling; electronic; target probe; denaturation; APX chip; ss.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH modified_base 9

FT modified_base 1
 FT /*tag= a
 FT /note= "5'-Bodipy Texas Red labelled C"
 XX
 XX W09712030-A1.
 XX
 XX 03-APR-1997.
 XX
 XX 06-SEP-1996; 96WO-US014353.
 XX
 XX 27-SEP-1995; 95US-00534454.
 XX
 XX (NANO-) NANOGEN INC.
 XX
 XX Heller MJ, Oconnell JP, Juncosa RD, Sosnowski RG, Jackson TR;
 PI WPI; 1997-212892/19.
 XX
 XX Self-addressable and self-assembling system for biological reactions -
 PT comprises array of specific binding regions on biochip, also new
 PT fluorescence detection system and stringency control device.
 XX
 XX Disclosure; Page 39; 69pp; English.
 XX
 XX The invention concerns an apparatus for enhanced detection of a
 CC biological reaction between a sample and an active area of a biochip,
 CC comprises the biochip and a fluidic system designed to pass the sample
 CC over the active area. The apparatus can be used for diagnosis, analysis
 CC and multistep/multiplex reactions (including synthesis of biopolymers),
 CC especially those involving nucleic acid hybridisation (but also antigen-
 CC antibody reactions). Use of a flow system improves diagnostic efficiency,
 CC allows more complete sampling and the detection device provides imaging
 CC of very small volumes. Together these elements provide a highly automated
 CC DNA analysis system from self-addressable and self-assembling electronic
 CC components. AAT46985-86 are 5'-labelled bodipy Texas Red target probes
 CC used to determine the results of electronic denaturation experiments
 CC run on an APX chip having 25 test microlocations with 80 micron diameter
 CC utilising platinum electrodes
 XX
 SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT46985 (1-19)
 Qy 56 HisValGluLeuLeu 60
 Db 2 CACGTAGAACTGCTC 16
 |||||
 RESULT 204
 AAV06677/C
 ID AAV06677 standard; RNA; 19 BP.
 XX
 AC AAV06677;
 XX
 DT 25-MAR-2003 (revised)
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Modified oligonucleotide in covalently cross-linked nucleic acid.
 XX
 XX Covalent cross-link; modified oligonucleotide; abasic site;
 KW space spanning group; ss.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH modified_base 9

FT FT /*tag= a
FT FT /note= "nucleotide is a 2'-O- [propion-3-yl bis(o-
FT FT nitrobenzyl)acetal] group"
FT FT 17
FT modified_base
FT FT /*tag= b
FT FT /note= "nucleotide is a 2'-O- [propion-3-yl bis(o-
FT FT nitrobenzyl)acetal] group"
XX XX
XX US5719271-A.
XX
XX 17-FEB-1998.
XX
XX 30-AUG-1994; 94US-00295743.
XX
XX 05-MAR-1992; 92US-00846376.
XX 05-MAR-1993; 93WO-US002059.
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Manoharan M, Bruice T, Cook PD;
XX WPI; 1998-158831/14.
XX
XX Covalently cross-linked nucleic acids - in which 2'- or 3'-hydroxy groups
PT on sugar moieties of nucleotide(s), on one or more oligonucleotide
PT strands, are linked by a non-phosphorus linkage.
XX Example 12; Col 42; 36pp; English.
XX
XX This sequence represents an oligonucleotide shown in the patent. The
CC invention relates to a cross-linked nucleic acid, which comprises: (a) a
CC first nucleotide located on a first oligonucleotide strand having a first
CC bond site located on either a 2'- or 3'-OH of the sugar moiety; (b) a
CC second nucleotide located on a second oligonucleotide strand having a
CC second bond site located on either a 2'- or 3'-OH of the sugar moiety.
CC The first strand is linked to the second strand via a non-phosphorus
CC covalent cross-linkage between the first and second bond sites, where not
CC both sites may be on a 3'-OH or a terminal nucleotide. The cross-linked
CC nucleic acids include materials in which oligonucleotide strands are
CC covalently cross-linked to themselves or to other strands. Such materials
CC can be used, e.g., as RNA mimics which are fixed in specific spatial
CC conformations. These materials may be used as therapeutic agents,
CC research reagents and diagnostic agents. (Updated on 25-MAR-2003 to
XX correct PR field.)
XX
SQ Sequence 19 BP; 8 A; 1 C; 8 G; 0 T; 2 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV06677 (1-19)
QY 179 IleLeuLeuProLeu 183
DB 17 ATTCTCTACTCTCTG 3
RESULT 205
AAV06469/C
ID AAV06469 standard; DNA; 19 BP.
XX AC
XX AAV06469;
XX
XX 06-MAY-1998 (first entry)
XX
XX Avian sex determination using Tsex sequence based primer Tsex JH-2.
XX Avian; sex determination; Tsex; probe; Z chromosome; W chromosome;
KW hybridisation; bird; PCR primer; ss.

XX Synthetic.
OS Meleagris gallopavo.
XX
PN US5707809-A.
XX
PD 13-JAN-1998.
XX
XX 12-APR-1996; 96US-00634331.
XX
XX 21-SEP-1990; 90US-00585915.
PR 17-SEP-1992; 92US-00947100.
PR 09-FEB-1994; 94US-00194131.
XX
XX (PEKE) PERKIN-ELMER CORP.
XX
XX Halverson J, Dvorak J;
PI WPI; 1998-109344/10.
XX
XX Avian nucleic acid amplification primers and probes - hybridise to Z
PT and/or W chromosomes; used for sex determination.
XX
XX Claim 6; Col 35-36; 20pp; English.
XX
XX This primer is based on a Tsex sequence obtained from a turkey cDNA
CC library. The Tsex sequence or its complementary sequence or a sequence of
CC at least eighteen contiguous nucleotides of one of these sequences can be
CC used for the identification of sex in avian species. These sequences can
CC be used for the production of a variety of nucleic acid hybridisation
CC probes and amplification primers. The primers and probes can hybridise to
CC both Z and W sex chromosomes allowing for differentiation between the two
CC chromosomes based on length polymorphisms. Alternatively, they may
CC hybridise to one of the chromosomes, permitting gender identification on
CC the basis of sex-specific hybridisation intensity. The combinations of
CC primers from different sequences allows amplification of fragments from a
CC specific chromosome. The primers/probes are used to determine the sex of
CC birds (e.g. poultry or emus) before development of obvious external
CC sexual differences
XX
SQ Sequence 19 BP; 1 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV06469 (1-19)
QY 82 ThrSerTirpSerPro 86
DB 17 ACAGCTGGAGCCCA 3
RESULT 206
AAV23570
ID AAV23570 standard; DNA; 19 BP.
XX AC
XX AAV23570;
XX
XX 14-JUL-1998 (first entry)
XX
XX Primer for alphaS1-casein transgene.
XX Transgenic bovine; mammary gland specific promoter; milk protein; human;
KW mammary secretory cell; lactoferrin; serum protein lysozyme; cow;
KW PCR primer; alphaS1-casein; ss.
XX Synthetic.
OS Bos sp.
XX

PN US5741957-A.
 XX 21-APR-1998.
 XX 05-JUN-1995; 95US-00461333.
 XX 01-DEC-1989; 89US-00444745.
 XX 27-NOV-1990; 90US-00619131.
 XX 15-JUN-1992; 92US-00898956.
 XX 15-JUN-1993; 93US-00077788.
 XX 16-NOV-1993; 93US-00154019.
 XX (PHAR-) PHARMING BV.
 XX Heyneker HL, Krimpenfort PJA, Deboer HA, Platenburg G, Lee SH;
 XX Pieper F, Strijker R;
 XX WPI; 1998-260573/23.
 XX Transgenic bovine useful for the production of heterologous proteins in
 PT its milk - contains a transgene linked to bovine secretory signal and is
 PT under the control of a mammary gland specific promoter and enhancer.
 XX
 XX Example 16; Col 45; 92pp; English.
 PS
 CC This sequence represents a primer for the bovine alphaS1-casein gene. The
 CC amplified sequence can be used in the transgenic bovine of the invention.
 CC The bovine contains in its somatic and germ cells contain a transgene
 CC comprising: (a) a mammary gland specific promoter and enhancer; (b) a DNA
 CC sequence encoding a signal sequence functional in bovine mammary gland
 CC secretory cells; and (c) a DNA sequence comprising a heterologous
 CC polypeptide of interest. Where the transgenic bovine or a female
 CC descendant of it expresses the transgene in mammary secretory cells so
 CC that the polypeptide is detectable in milk produced by the transgenic
 CC bovine or its descendant. The transgenic bovine is useful for the
 CC recombinant production of the human milk protein lactoferrin and the
 CC human serum protein lysozyme in its milk for use in pharmaceuticals and
 CC in infant formulae. The levels of transgenic protein secreted by the
 CC transgenic bovine in its milk are higher than that produced by transgenic
 CC sheep and mice. As the proteins are produced in the milk of the cow, they
 CC require little or no purification for human consumption
 XX
 SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAV23570 (1-19)
 QY 32 Valvallysargarg 36
 DB 5 GTTGTAAACGACGG 19
 RESULT 207
 AAX81321
 ID AAX81321 standard; DNA; 19 BP.
 AC AAX81321;
 XX 20-AUG-1999 (first entry)
 XX 5' amino oligonucleotide probe RC-A5.
 XX Microelectronic device; multi-step reaction; microscopic format;
 KW ion-permeable permeation layer; electrode; electrical control; transport;
 KW attachment; binding; DNA/RNA hybrid; probe; ss.
 XX Synthetic.
 OS

XX Key Location/Qualifiers
 misc_feature 1
 /*tag= a
 /note= "amino group attached at 5' terminal"
 WO9929711-A1.
 17-JUN-1999.
 01-DEC-1998; 98WO-US025475.
 05-DEC-1997; 97US-00986065.
 (NANO-) NANOGEN INC.
 Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;
 WPI; 1999-385567/32.
 New microelectronic device designed to carry out and control multi-step
 and multiplex molecular biological reactions in microscopic format.
 Example 1; Page 90; 179pp; English.
 The specification describes a self-addressable, self-assembling
 microelectronic device which is designed to actively carry out and
 control multi-step and multiplex molecular biological reactions in
 microscopic formats. A key aspect of this invention is played by the ion
 -permeable permeation layer which overlies the electrode. This permeation
 layer allows attachment of nucleic acids to permit immobilization but
 also separates the attached oligonucleotides and hybridized target DNA
 sequences from the highly reactive electrochemical environment generated
 immediately at the electrode surface. The microelectronic device is
 designed and fabricated to actively carry out and control reactions such
 as nucleic acid hybridizations, antibody/antigen reactions, sample
 preparation, diagnostics and biopolymer synthesis. The device can
 electronically control the transport and attachment of specific binding
 entities, such as nucleic acids and polypeptides, to specific micro-
 locations. The device can subsequently control the transport and reaction
 of analytes or reactants at the addressed specific micro-locations. The
 device is able to concentrate analytes and reactants, remove non-
 specifically bound molecules, provide stringency control for DNA
 hybridization reactions and improve the detection of analytes. The
 present sequence represents a probe used to exemplify the invention
 SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAX81321 (1-19)
 QY 56 HisValGluLeuLeu 60
 DB 2 CACGTAGACTGCTC 16
 RESULT 208
 AAX81343/c
 ID AAX81343 standard; DNA; 19 BP.
 AC AAX81343;
 XX 20-AUG-1999 (first entry)
 XX Biotinylated capture oligonucleotide ATAS.
 KW Microelectronic device; multi-step reaction; microscopic format;

```

KW ion-permeable permeation layer; electrode; electrical control; transport;
KW attachment; binding; probe; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 19
XX /*tag= a
XX /*note= "Biotinylated"
XX
XX WO9929711-A1.
XX
XX 17-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US025475.
XX
XX 05-DEC-1997; 97US-00986065.
XX
XX (NANO-) NANOGEN INC.
XX
XX Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;
XX WPI; 1999-385567/32.
XX
XX New microelectronic device designed to carry out and control multi-step
XX and multiplex molecular biological reactions in microscopic format.
XX
XX Example 13; Page 131; 179pp; English.
XX
XX The specification describes a self-addressable, self-assembling
XX microelectronic device which is designed to actively carry out and
XX control multi-step and multiplex molecular biological reactions in
XX microscopic formats. A key aspect of this invention is played by the ion
XX permeable permeation layer which overlies the electrode. This permeation
XX layer allows attachment of nucleic acids to permit immobilization but
XX also separates the attached oligonucleotides and hybridized target DNA
XX sequences from the highly reactive electrochemical environment generated
XX immediately at the electrode surface. The microelectronic device is
XX designed and fabricated to actively carry out and control reactions such
XX as nucleic acid hybridizations, antibody/antigen reactions, sample
XX preparation, diagnostics and biopolymer synthesis. The device can
XX electronically control the transport and attachment of specific micro-
XX entities, such as nucleic acids and polypeptides, to specific micro-
XX locations. The device can subsequently control the transport and reaction
XX of analytes or reactants at the addressed specific micro-locations. The
XX device is able to concentrate analytes and reactants, remove non-
XX specifically bound molecules, provide stringency control for DNA
XX hybridization reactions and improve the detection of analytes. The
XX present sequence is used in the course of the invention
XX
XX Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 9e+03 Length: 19
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAX81343 (1-19)
XX
XX QY 56 HisValGluLeuLeu 60
XX Db 18 CACGTAGACGTGCTC 4
XX
XX RESULT 209
XX AAX81347/c
XX ID AAX81347 standard; DNA; 19 BP.
XX
XX AC AAX81347;
XX
XX 20-AUG-1999 (first entry)
XX
XX DT

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XX Oligonucleotide probe DNA2.
XX
XX Microelectronic device; multi-step reaction; microscopic format;
XX ion-permeable permeation layer; electrode; electrical control; transport;
XX attachment; binding; probe; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /*tag= a
XX /*note= "Biotinylated"
XX
XX WO9929711-A1.
XX
XX 17-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US025475.
XX
XX 05-DEC-1997; 97US-00986065.
XX
XX (NANO-) NANOGEN INC.
XX
XX Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;
XX WPI; 1999-385567/32.
XX
XX New microelectronic device designed to carry out and control multi-step
XX and multiplex molecular biological reactions in microscopic format.
XX
XX Example 13; Page 135; 179pp; English.
XX
XX The specification describes a self-addressable, self-assembling
XX microelectronic device which is designed to actively carry out and
XX control multi-step and multiplex molecular biological reactions in
XX microscopic formats. A key aspect of this invention is played by the ion
XX permeable permeation layer which overlies the electrode. This permeation
XX layer allows attachment of nucleic acids to permit immobilization but
XX also separates the attached oligonucleotides and hybridized target DNA
XX sequences from the highly reactive electrochemical environment generated
XX immediately at the electrode surface. The microelectronic device is
XX designed and fabricated to actively carry out and control reactions such
XX as nucleic acid hybridizations, antibody/antigen reactions, sample
XX preparation, diagnostics and biopolymer synthesis. The device can
XX electronically control the transport and attachment of specific binding
XX entities, such as nucleic acids and polypeptides, to specific micro-
XX locations. The device can subsequently control the transport and reaction
XX of analytes or reactants at the addressed specific micro-locations. The
XX device is able to concentrate analytes and reactants, remove non-
XX specifically bound molecules, provide stringency control for DNA
XX hybridization reactions and improve the detection of analytes. The
XX present sequence is used in the course of the invention
XX
XX Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 9e+03 Length: 19
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAX81347 (1-19)
XX
XX QY 56 HisValGluLeuLeu 60
XX Db 18 CACGTAGACGTGCTC 4
XX
XX RESULT 210
XX AAZ21065/c
XX ID AAZ21065 standard; DNA; 19 BP.

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XX AAZ21065;
XX AC
XX DT
XX 15-NOV-1999 (first entry)
XX DE Nitrosomonas europaea thiamine synthetase PCR primer LacF295.
XX KW Nitrosomonas europaea; thiamine synthetase; tryptophan synthetase; thix;
XX trpX; mutant; ammonia-oxidizing microbe; limited growth; PCR primer; ss.
XX OS Synthetic.
XX OS Nitrosomonas europaea.
XX JP11235188-A.
XX PN
XX PD
XX 31-AUG-1999.
XX PF 08-DEC-1998; 98JP-00349146.
XX PR 08-DEC-1997; 97JP-00337547.
XX PA (KURK ) KURITA WATER IND LTD.
XX DR WPI; 1999-544006/46.
XX PT Preparation of mutant of an ammonia-oxidizing microbe - comprising
XX limited growth in natural environment.
XX PS Example 4; Page 7; 17pp; Japanese.
XX CC The present invention describes the preparation of a mutant of an ammonia
XX -oxidizing microbe of limited growth in natural environment in which the
XX function of a gene participating to the limitation of growth derived from
XX an ammonia-oxidizing microbe is artificially inactivated and the gene of
XX inactivated function is exchanged with a corresponding gene on the
XX chromosome by a homologous recombination. The method is useful for the
XX preparation of a mutant of an ammonia-oxidizing microbe of limited growth
XX in natural environment easily. The present sequence represents a PCR
XX primer for Nitrosomonas europaea thiamine synthetase (thix), which is
XX used in the exemplification of the present invention
XX SQ Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ21065 (1-19)
QY 32 ValVallysArgArg 36
DB 15 GTTGTAAACGACGG 1

RESULT 211
AAZ28287
ID AAZ28287 standard; DNA; 19 BP.
XX AC AAZ28287;
XX 17-JUN-1999 (first entry)
XX DE Human CYP3A4 gene polymorphism #1.
XX KW CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism;
XX CYP3A4 substrate; drug-drug interaction identification; toxin exposure;
XX Genetic linkage detection; phenotypic variation; ss.
XX OS Homo sapiens.
XX

XX WO9913106-A1.
XX 18-MAR-1999.
XX PF 02-SEP-1998; 98WO-US018158.
XX PR 10-SEP-1997; 97US-0058612P.
XX PA (AXYS-) AXYS PHARM INC.
XX PI Lichter JB, Guida M;
XX DR WPI; 1999-215070/18.
XX FT New isolated CYP3A4 polymorphic sequences.
XX PS Claim 2; Page 35; 40pp; English.
XX CC This sequence represents a CYP3A4 sequence polymorphism of the invention,
XX which is part of a non-naturally occurring chromosome. Nucleic acids
XX comprising the CYP3A4 polymorphic sequences can be used to screen
XX patients for altered metabolism for CYP3A4 substrates, potential drug-
XX drug interactions, and adverse/side effects as well as diseases that
XX result from environmental or occupational exposure to toxins. They can
XX also be used to establish animal, cell culture and in vitro cell-free
XX models for drug metabolism. Polymorphic CYP3A4 gene sequences can be used
XX for expression studies to determine the effect of promoter and/or intron
XX sequence variations on mRNA expression and stability. The polymorphisms
XX are also used as single nucleotide polymorphisms to detect genetic
XX linkage to phenotypic variation in activity and expression of CYP3A4. The
XX nucleic acids can also be used to generate genetically modified non-human
XX animals or site specific gene modifications in cell lines
XX SQ Sequence 19 BP; 7 A; 3 C; 9 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ28287 (1-19)
QY 22 LysGlyArgArgGlu 26
DB 3 AAGGGCAGGAGAGAG 17

RESULT 212
AAV72008/C
ID AAV72008 standard; DNA; 19 BP.
XX AC AAV72008;
XX 29-MAR-1999 (first entry)
XX DE Electronic perturbation catalysis oligonucleotide probe HLA 241.
XX KW Electronic perturbation analysis; hybridisation analysis; match hybrid;
XX mismatch hybrid; detection; clinical assay; optoelectronic device;
XX optical memory; nanofabrication; synthesis; self-assembly; denaturation;
XX self-organising; fluorescence; dehybridisation; probe; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 19
XX FT /*tag= a
XX FT /note= "3'-end modified by presence of Biotin"
XX PN WO9851819-A1.
XX

```

```

PD 19-NOV-1998.
XX
XX 07-MAY-1998; 98WO-US009357.
XX
XX 14-MAY-1997; 97US-00855058.
XX
XX (NANO-) NANOGEN INC.
XX
XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;
XX WPI; 1999-059702/05.
XX
XX Hybridisation analysis using electronic stringency control device based
XX on changes in fluorescence - when an electric field is applied to the
XX hybrid, used e.g. for sequencing or for detecting single mismatch
XX mutations, also electronic perturbation catalysis.
XX
XX Example 1; Page 28; 56pp; English.
XX
XX This sequence represents a probe used in a method for studying
XX hybridisation analysis by detecting electronic denaturation using
XX electronic perturbation analysis. The method is particularly used for
XX sequencing and to discriminate between match and mismatch hybrids,
XX particularly to detect point mutations, deletions, inserts, repeat
XX regions, single nucleotide polymorphisms, translocations, intron/exon
XX junctions, etc. The same principle may be used for most molecular
XX biological processes, e.g. antibody-antigen reactions, cell typing and
XX separation, enzymatic and other clinical assays, also in optoelectronic
XX devices and optical memory materials. The method is applicable to any
XX type of reaction, e.g. nanofabrication or other self-assembling or self-
XX organising processes, synthesis of nucleic acids, peptides, polymers etc.
XX The method relies on the observation that perturbation of a fluorescence
XX signal (particularly a peak) occurs at the electric power level which
XX causes denaturation or dehybridisation. The method is very rapid, e.g.
XX match/mismatch hybrids can be distinguished in less than a minute, e.g.
XX sec. It permits use of long probes (over 20 bases) and probe specificity
XX is determined by the position of the label. Since analysis does not
XX require removal of mismatched probes, the sample can be analysed
XX repeatedly to improve assay statistics
XX
XX Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72008 (1-19)

QY 56 HisValGlutLeuLeu 60
DB 18 CACGTAGAACTGCTC 4

RESULT 213
AAV72007
ID AAV72007 standard; DNA; 19 BP.
XX
XX AAV72007;
XX
XX 29-MAR-1999 (first entry)
XX
XX Electronic perturbation catalysis oligonucleotide probe HLA 253.
XX
XX Electronic perturbation analysis; hybridisation analysis; match hybrid;
XX mismatch hybrid; detection; clinical assay; optoelectronic device;
XX optical memory; nanofabrication; synthesis; self-assembly; denaturation;
XX self-organising; fluorescence; dehybridisation; probe; ss.
XX
XX Synthetic.
XX

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FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "5'-end modified by presence of Bodipy Texas Red"
XX
XX W09851819-A1.
XX
XX 19-NOV-1998.
XX
XX 07-MAY-1998; 98WO-US009357.
XX
XX 14-MAY-1997; 97US-00855058.
XX
XX (NANO-) NANOGEN INC.
XX
XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;
XX WPI; 1999-059702/05.
XX
XX Hybridisation analysis using electronic stringency control device based
XX on changes in fluorescence - when an electric field is applied to the
XX hybrid, used e.g. for sequencing or for detecting single mismatch
XX mutations, also electronic perturbation catalysis.
XX
XX Example 1; Page 28; 56pp; English.
XX
XX This sequence represents a probe used in a method for studying
XX hybridisation analysis by detecting electronic denaturation using
XX electronic perturbation analysis. The method is particularly used for
XX sequencing and to discriminate between match and mismatch hybrids,
XX particularly to detect point mutations, deletions, inserts, repeat
XX regions, single nucleotide polymorphisms, translocations, intron/exon
XX junctions, etc. The same principle may be used for most molecular
XX biological processes, e.g. antibody-antigen reactions, cell typing and
XX separation, enzymatic and other clinical assays, also in optoelectronic
XX devices and optical memory materials. The method is applicable to any
XX type of reaction, e.g. nanofabrication or other self-assembling or self-
XX organising processes, synthesis of nucleic acids, peptides, polymers etc.
XX The method relies on the observation that perturbation of a fluorescence
XX signal (particularly a peak) occurs at the electric power level which
XX causes denaturation or dehybridisation. The method is very rapid, e.g.
XX match/mismatch hybrids can be distinguished in less than a minute, e.g.
XX sec. It permits use of long probes (over 20 bases) and probe specificity
XX is determined by the position of the label. Since analysis does not
XX require removal of mismatched probes, the sample can be analysed
XX repeatedly to improve assay statistics
XX
XX Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72007 (1-19)

QY 56 HisValGlutLeuLeu 60
DB 2 CACGTAGAACTGCTC 16

RESULT 214
AAV72011/C
ID AAV72011 standard; DNA; 19 BP.
XX
XX AAV72011;
XX
XX 29-MAR-1999 (first entry)
XX
XX Electronic perturbation catalysis oligonucleotide probe HLA 376.
XX

```

KW Electronic perturbation analysis; hybridisation analysis; match hybrid;
KW mismatch hybrid; detection; clinical assay; optoelectronic device;
KW optical memory; nanofabrication; synthesis; self-assembly; denaturation;
KW self-organising; fluorescence; dehybridisation; probe; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 19
FT /*tag= a
FT /note= "3'-end modified by presence of Biotin"
XX
XX WO9851819-A1.
XX
XX 19-NOV-1998.
XX
XX 07-MAY-1998; 98WO-US009357.
XX
XX 14-MAY-1997; 97US-00855058.
XX
XX (NANO-) NANOGEN INC.
XX
XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;
XX WPI; 1999-059702/05.
XX
XX Hybridisation analysis using electronic stringency control device based
XX on changes in fluorescence - when an electric field is applied to the
XX hybrid, used e.g. for sequencing or for detecting single mismatch
XX mutations, also electronic perturbation catalysis.
XX
XX Example 1; Page 28; 56pp; English.
XX
XX This sequence represents a probe used in a method for studying
XX hybridisation analysis by detecting electronic denaturation using
XX electronic perturbation analysis. The method is particularly used for
XX sequencing and to discriminate between match and mismatch hybrids,
XX particularly to detect point mutations, deletions, inserts, repeat
XX regions, single nucleotide polymorphisms, translocations, intron/exon
XX junctions, etc. The same principle may be used for most molecular
XX biological processes, e.g. antibody-antigen reactions, cell typing and
XX separation, enzymatic and other clinical assays, also in optoelectronic
XX devices and optical memory materials. The method is applicable to any
XX type of reaction, e.g. nanofabrication or other self-assembling or self-
XX organising processes, synthesis of nucleic acids, peptides, polymers etc.
XX The method relies on the observation that perturbation of a fluorescence
XX signal (particularly a peak) occurs at the electric power level which
XX causes denaturation or dehybridisation. The method is very rapid, e.g.
XX match/mismatch hybrids can be distinguished in less than a minute, e.g. 5
XX sec. It permits use of long probes (over 20 bases) and probe specificity
XX is determined by the position of the label. Since analysis does not
XX require removal of mismatched probes, the sample can be analysed
XX repeatedly to improve assay statistics

XX Sequence 19 BP; 4 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72011 (1-19)

Qy 56 HisValGluLeuLeu 60
|||||
Db 18 CACGTAGACTGCTC 4

RESULT 215
AAV72009/C
ID AAV72009 standard; DNA; 19 BP.

XX
AC AAV72009;
XX
XX 29-MAR-1999 (first entry)
XX
XX DE Electronic perturbation catalysis oligonucleotide probe HLA 378.
XX
XX Electronic perturbation analysis; hybridisation analysis; match hybrid;
KW mismatch hybrid; detection; clinical assay; optoelectronic device;
KW optical memory; nanofabrication; synthesis; self-assembly; denaturation;
KW self-organising; fluorescence; dehybridisation; probe; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 19
FT /*tag= a
FT /note= "3'-end modified by presence of Biotin"
XX
XX WO9851819-A1.
XX
XX 19-NOV-1998.
XX
XX 07-MAY-1998; 98WO-US009357.
XX
XX 14-MAY-1997; 97US-00855058.
XX
XX (NANO-) NANOGEN INC.
XX
XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;
XX WPI; 1999-059702/05.
XX
XX Hybridisation analysis using electronic stringency control device based
XX on changes in fluorescence - when an electric field is applied to the
XX hybrid, used e.g. for sequencing or for detecting single mismatch
XX mutations, also electronic perturbation catalysis.
XX
XX Example 1; Page 28; 56pp; English.
XX
XX This sequence represents a probe used in a method for studying
XX hybridisation analysis by detecting electronic denaturation using
XX electronic perturbation analysis. The method is particularly used for
XX sequencing and to discriminate between match and mismatch hybrids,
XX particularly to detect point mutations, deletions, inserts, repeat
XX regions, single nucleotide polymorphisms, translocations, intron/exon
XX junctions, etc. The same principle may be used for most molecular
XX biological processes, e.g. antibody-antigen reactions, cell typing and
XX separation, enzymatic and other clinical assays, also in optoelectronic
XX devices and optical memory materials. The method is applicable to any
XX type of reaction, e.g. nanofabrication or other self-assembling or self-
XX organising processes, synthesis of nucleic acids, peptides, polymers etc.
XX The method relies on the observation that perturbation of a fluorescence
XX signal (particularly a peak) occurs at the electric power level which
XX causes denaturation or dehybridisation. The method is very rapid, e.g.
XX match/mismatch hybrids can be distinguished in less than a minute, e.g. 5
XX sec. It permits use of long probes (over 20 bases) and probe specificity
XX is determined by the position of the label. Since analysis does not
XX require removal of mismatched probes, the sample can be analysed
XX repeatedly to improve assay statistics

SQ Sequence 19 BP; 4 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72009 (1-19)

QY 56 Hisvalgluleu 60
 Db 18 CACGTAGACTGCTC 4

RESULT 216
 AAV72012/c
 ID AAV72012 standard; DNA; 19 BP.
 XX AAV72012;
 AC AAV72012;
 DT 29-MAR-1999 (first entry)
 DE Electronic perturbation catalysis oligonucleotide probe HLA 401.
 KW Electronic perturbation analysis; hybridisation analysis; match hybrid;
 KW mismatch hybrid; detection; clinical assay; optoelectronic device;
 KW optical memory; nanofabrication; synthesis; self-assembly; denaturation;
 KW self-organising; fluorescence; dehybridisation; probe; ss.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH modified_base 1
 FT /*tag= a
 FT /note= "5'-end modified by presence of Biotin"
 XX WO9851819-A1.
 XX 19-NOV-1998.
 XX 07-MAY-1998; 98WO-US009357.
 XX 14-MAY-1997; 97US-00855058.
 XX (NANO-) NANOGEN INC.
 XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;
 XX WPI; 1999-059702/05.
 XX Hybridisation analysis using electronic stringency control device based
 PT on changes in fluorescence - when an electric field is applied to the
 PT hybrid, used e.g. for sequencing or for detecting single mismatch
 PT mutations, also electronic perturbation catalysis.
 XX Example 1; Page 28; 56pp; English.
 PS This sequence represents a probe used in a method for studying
 CC hybridisation analysis by detecting electronic denaturation using
 CC electronic perturbation analysis. The method is particularly used for
 CC sequencing and to discriminate between match and mismatch hybrids,
 CC particularly to detect point mutations, deletions, insertions, repeat
 CC regions, single nucleotide polymorphisms, translocations, intron/exon
 CC junctions, etc. The same principle may be used for most molecular
 CC biological processes, e.g. antibody-antigen reactions, cell typing and
 CC separation, enzymatic and other clinical assays, also in optoelectronic
 CC devices and optical memory materials. The method is applicable to any
 CC type of reaction, e.g. nanofabrication or other self-assembling or self-
 CC organising processes, synthesis of nucleic acids, peptides, polymers etc.
 CC The method relies on the observation that perturbation of a fluorescence
 CC signal (particularly a peak) occurs at the electric power level which
 CC causes denaturation or dehybridisation. The method is very rapid, e.g.
 CC match/mismatch hybrids can be distinguished in less than a minute, e.g. 5
 CC sec. It permits use of long probes (over 20 bases) and probe specificity
 CC is determined by the position of the label. Since analysis does not
 CC require removal of mismatched probes, the sample can be analysed
 CC repeatedly to improve assay statistics
 XX SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 Db: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72012 (1-19)
 QY 56 Hisvalgluleu 60
 Db 18 CACGTAGACTGCTC 4

RESULT 217
 AAV72003
 ID AAV72003 standard; DNA; 19 BP.
 XX AAV72003;
 AC AAV72003;
 DT 29-MAR-1999 (first entry)
 DE Electronic denaturation experiment 19-mer DNA probe.
 KW Electronic denaturation; hybridisation analysis; match hybrid;
 KW mismatch hybrid; detection; clinical assay; optoelectronic device;
 KW optical memory; nanofabrication; synthesis; self-assembly; perturbation;
 KW self-organising; fluorescence; dehybridisation; probe; ss.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH modified_base 1
 FT /*tag= a
 FT /note= "nucleotide is modified by the presence of Bodipy
 Texas Red"
 XX WO9851819-A1.
 XX 19-NOV-1998.
 XX 07-MAY-1998; 98WO-US009357.
 XX 14-MAY-1997; 97US-00855058.
 XX (NANO-) NANOGEN INC.
 XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;
 XX WPI; 1999-059702/05.
 XX Hybridisation analysis using electronic stringency control device based
 PT on changes in fluorescence - when an electric field is applied to the
 PT hybrid, used e.g. for sequencing or for detecting single mismatch
 PT mutations, also electronic perturbation catalysis.
 XX Disclosure; Page 12; 56pp; English.
 PS This sequence represents a probe used in a method for studying
 CC hybridisation analysis by detecting electronic denaturation. The method
 CC is particularly used for sequencing and to discriminate between match and
 CC mismatch hybrids, particularly to detect point mutations, deletions,
 CC insertions, repeat regions, single nucleotide polymorphisms, translocations,
 CC intron/exon junctions, etc. The same principle may be used for most
 CC molecular biological processes, e.g. antibody-antigen reactions, cell
 CC typing and separation, enzymatic and other clinical assays, also in
 CC optoelectronic devices and optical memory materials. The method is
 CC applicable to any type of reaction, e.g. nanofabrication or other self-
 CC assembling/self-organising processes, synthesis of nucleic acids,
 CC peptides, polymers etc. The method relies on the observation that
 CC perturbation of a fluorescence signal (particularly a peak) occurs at the
 CC electric power level which causes denaturation or dehybridisation. The
 CC method is very rapid, e.g. 5 sec. It permits use of long probes (over 20
 CC bases) and probe specificity is determined by the position of the label.
 CC Since analysis does not require removal of mismatched probes, the sample

CC can be analysed repeatedly to improve assay statistics
 XX
 SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAV72003 (1-19)
 QY 56 HisValGluLeuLeu 60
 DB 2 CACGTAGACTGCTC 16
 RESULT 218
 AAV72010/c
 ID AAV72010 standard; DNA; 19 BP.
 XX
 AC AAV72010;
 XX
 DT 29-MAR-1999 (first entry)
 XX
 DE Electronic perturbation catalysis oligonucleotide probe HLA 375.
 XX
 KW Electronic perturbation analysis; hybridisation analysis; match hybrid;
 KW mismatch hybrid; detection; clinical assay; optoelectronic device;
 KW optical memory; nanofabrication; synthesis; self-assembly; denaturation;
 KW self-organising; fluorescence; denaturation; probe; ss.
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT modified_base 19
 FT /*tag= a
 FT /note= "3'-end modified by presence of Biotin"
 XX
 PN WO9851819-A1.
 XX
 XX 19-NOV-1998.
 PD
 PF 07-MAY-1998; 98WO-US009357.
 XX
 PR 14-MAY-1997; 97US-00855058.
 XX
 PA (NANO-) NANOGEN INC.
 XX
 PI Heller MJ, Tu E, Sosnowski RG, Oconnell JP;
 XX
 DR WPI; 1999-059702/05.
 XX
 XX Hybridisation analysis using electronic stringency control device based
 PT on changes in fluorescence - when an electric field is applied to the
 PT hybrid, used e.g. for sequencing or for detecting single mismatch
 PT mutations, also electronic perturbation catalysis.
 XX
 XX Example 1; Page 28; 56pp; English.
 PS
 CC This sequence represents a probe used in a method for studying
 CC hybridisation analysis by detecting electronic denaturation using
 CC electronic perturbation analysis. The method is particularly used for
 CC sequencing and to discriminate between match and mismatch hybrids,
 CC particularly to detect point mutations, deletions, inserts, repeat
 CC regions, single nucleotide polymorphisms, translocations, intron/exon
 CC junctions, etc. The same principle may be used for most molecular
 CC biological processes, e.g. antibody-antigen reactions, cell typing and
 CC separation, enzymatic and other clinical assays, also in optoelectronic
 CC devices and optical memory materials. The method is applicable to any
 CC type of reaction, e.g. nanofabrication or other self-assembling or self-
 CC organising processes, synthesis of nucleic acids, peptides, polymers etc.

CC The method relies on the observation that perturbation of a fluorescence
 CC signal (particularly a peak) occurs at the electric power level which
 CC causes denaturation or dehybridisation. The method is very rapid, e.g.
 CC match/mismatch hybrids can be distinguished in less than a minute, e.g. 5
 CC sec. It permits use of long probes (over 20 bases) and probe specificity
 CC is determined by the position of the label. Since analysis does not
 CC require removal of mismatched probes, the sample can be analysed
 CC repeatedly to improve assay statistics
 XX
 SQ Sequence 19 BP; 4 A; 3 C; 6 G; 6 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAV72010 (1-19)
 QY 56 HisValGluLeuLeu 60
 DB 18 CACGTAGACTGCTC 4
 RESULT 219
 AAA88263/c
 ID AAA88263 standard; DNA; 19 BP.
 XX
 AC AAA88263;
 XX
 DT 06-AUG-2003 (revised)
 DT 15-DEC-2000 (first entry)
 XX
 DE Nitrosomonas europaea IF014298 tryptophan synthase PCR primer #3.
 XX
 KW Nitrosomonas europaea; nitrification; inhibition; waste water; sludge;
 KW ammonia oxidising microbe; bioluminescence; tryptophan synthase;
 KW PCR primer; ss.
 XX
 OS Nitrosomonas europaea.
 XX
 PN JP2000184898-A.
 XX
 PD 04-JUL-2000.
 XX
 PF 21-DEC-1998; 98JP-00362680.
 XX
 PR 21-DEC-1998; 98JP-00362680.
 XX
 PA (KURK) KURITA WATER IND LTD.
 XX
 DR WPI; 2000-494007/44.
 XX
 XX Evaluation of nitrification inhibiting activity of waste water against
 PT active sludge.
 PT
 XX Example 4; Page 10; 16pp; Japanese.
 PS
 CC The present invention describes a method for the evaluation of
 CC nitrification inhibiting activity of waste water against active sludge in
 CC which an ammonia oxidising microbe recombinant body which has
 CC bioluminescence activity and growth of which is restricted in natural
 CC environment is mixed with waste water and the luminescence of the mixture
 CC is used as the index. The method can be used for the rapid and easy
 CC measurement of the extent of nitrification inhibiting activity of waste
 CC water against active sludge. The present sequence represents a PCR primer
 CC for Nitrosomonas europaea IF014298 tryptophan synthase, which is used in
 CC an example from the present invention. (Updated on 06-AUG-2003 to correct
 CC OS field.)
 XX
 SQ Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA88263 (1-19)

Qy 32 ValVallysArgArg 36
 Db 15 GTTGTAAACGACG 1

RESULT 220

AAA82679
 ID AAA82679 standard; DNA; 19 BP.

XX AAA82679;

XX 04-DEC-2000 (first entry)

XX cdk2 ribozyme binding site #116.

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

XX Mammalia.

XX WO200032765-A2.

XX 08-JUN-2000.

XX 06-DEC-1999; 99WO-US028772.

XX 04-DEC-1998; 98US-0110954P.

XX (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.

XX Disclosure; Page 50; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment

XX Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA82679 (1-19)

Qy 193 PheArgThrLeuGly 197

Db 1 TTTCCGACTCTGGGG 15

RESULT 221

AAA84087
 ID AAA84087 standard; DNA; 19 BP.

XX AAA84087;

XX 04-DEC-2000 (first entry)

XX Cyclin C ribozyme binding site #59.

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

XX Mammalia.

XX WO200032765-A2.

XX 08-JUN-2000.

XX 06-DEC-1999; 99WO-US028772.

XX 04-DEC-1998; 98US-0110954P.

XX (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.

XX Disclosure; Page 71; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment

XX Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA84087 (1-19)

Qy 62 LeuArgTyrIleSer 66

Db 1 CTACGGTATATTCA 15

RESULT 222

AAA84086
 ID AAA84086 standard; DNA; 19 BP.

XX AAA84086;

XX 04-DEC-2000 (first entry)

XX Cyclin C ribozyme binding site #58.

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

XX Mammalia.

PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
XX 06-DEC-1999; 99WO-US028772.
XX PF
XX 04-DEC-1998; 98US-0110954P.
XX PR
XX (IMMU-) IMMUSOL INC.
XX PA
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX PI
XX WPI; 2000-412314/35.
XX DR
XX
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis. cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
XX Disclosure; Page 71; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
XX Sequence 19 BP; 5 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA84086 (1-19)

QY 62 LeuArgTyrIleSer 66
DB 3 CTACGGTATATTCA 17

RESULT 223
AAZ87624
ID AAZ87624 standard; DNA; 19 BP.
XX AC
XX AAZ87624;
XX
DT 04-MAY-2000 (first entry)
XX
XX Bovine alphaS1 casein gene specific primer.
XX
XX Transgenic bovine; transgene; milk; serum protein; industrial enzyme;
KW infant formulation; lactoferrin; intestinal tract infection; lysozyme;
KW iron absorption; albumin; antibacterial; iron sequestration; PCR primer;
KW alphaS1 casein; ss.
XX
OS Bos sp.
XX
XX US6013857-A.
XX
XX 11-JAN-2000.
XX
XX 05-JUN-1995; 95US-00464167.
XX
XX 01-DEC-1989; 89US-00444745.
XX PR 27-NOV-1990; 90US-00619131.
XX PR 15-JUN-1992; 92US-00898956.
XX PR 15-JUN-1993; 93US-00077788.
XX PR 16-NOV-1993; 93US-00154019.

XX (PHAR-) PHARMING BV.
XX
XX Deboer HA, Heyneker HL, Platenburg G, Krimpenfort PJA, Lee SH;
XX Pieper F, Strijker R;
XX
XX WPI; 2000-146563/13.
XX
XX Transgenic cattle containing transgene controlled by mammary-specific
PT regulator, for expressing proteins in the milk, particularly human
PT lactoferrin for infant feeding formulations.
XX
XX Example 16; Col 45; 92pp; English.
XX
XX The invention provides a transgenic bovine in which the somatic and germ
CC cells contain a transgene comprising a regulatory sequence from a gene
CC expressed in mammary glands, DNA encoding a signal sequence and DNA
CC encoding a naturally occurring heterologous polypeptide. The transgenic
CC bovine, or its descendants, produce milk containing the heterologous
CC polypeptide. The transgenic bovines are used to express human milk and
CC serum proteins or industrial enzymes, specifically for infant
CC formulations that contain human lactoferrin for control of intestinal
CC tract infections and to improve iron absorption, particularly when
CC potentiated by human lysozyme. The polypeptide expressed may also be
CC human albumin, used as a plasma extender. The polypeptide expressed in
CC milk of the transgenic bovine requires little if any purification before
CC human consumption and is expressed at significantly higher levels than in
CC transgenic mice or sheep. Large polypeptides that are difficult to
CC express in other systems can also be expressed. Sequences AAZ87624-25
CC represent primers for amplifying bovine alphaS1 casein gene fragments
XX
XX Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ87624 (1-19)

QY 32 ValVallysArgArg 36
DB 5 GTTGTAAACGACGG 19

RESULT 224
AAZ88066/c
ID AAZ88066 standard; DNA; 19 BP.
XX AC AAZ88066;
XX
XX 20-APR-2000 (first entry)
XX
XX MLV proviral long terminal repeat DNA PCR primer #4.
DE
XX Lentiviral vector; packaging; gag; pol; gene therapy; infection;
KW gene expression; PCR primer; ss.
XX
XX Murine leukemia virus.
XX
XX WO200000600-A2.
XX
XX 06-JAN-2000.
XX
XX 26-MAY-1999; 99WO-US011516.
XX PF
XX 26-MAY-1998; 98US-0086635P.
XX PR
XX (CHAN/) CHANG L.
XX PA
XX Chang L;
PI

XX WPI; 2000-137067/12.
DR
XX
XX New packaging vector comprising a nucleotide sequence encoding Gag and
PT Pol proteins of a reference lentivirus useful for the delivery of non-
PT lentiviral genes to target cells.
XX
XX
PS Example; Page 132; 311pp; English.
PS
XX
XX The present invention describes a packaging vector (PV) comprising a
CC nucleotide sequence encoding Gag and Pol proteins of a reference
CC lentivirus that differs from the reference lentivirus at least in that:
CC (a) its major splice donor site is either deleted or is insufficiently
CC different from the reference lentivirus so that it is not a potential
CC site for homologous recombination; and (b) it lacks a functional major
CC packaging signal so that the introduced vector causes the host cell to
CC produce packaging vector particles comprising functional Gag and Pol
CC proteins. The vectors are useful for transforming (eukaryotic) cells to
CC express specific genes at high levels, e.g. for gene therapy. The
CC improved vectors are safer, yet permit increased efficiency of packaging
CC the recombinant viral genome and increased long-term gene expression.
CC These properties are required for gene therapy as a means of treating
CC infectious and non-infectious diseases. Unlike other retroviruses, the
CC lentiviruses are able to infect non-dividing cells. The present sequence
CC represents an HIV proviral long terminal repeat DNA PCR primer which is
CC used in the exemplification of the present invention
XX
SQ Sequence 19 BP; 8 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ88066 (1-19)

Qy 169 SerValArgLeuSer 173
Db 18 TCTGTCCGATGTCT 4

RESULT 225
AAA49122
ID AAA49122 standard; DNA; 19 BP.
XX
AC AAA49122;
XX
XX 16-NOV-2000 (first entry)
XX
XX pMOS-R primer used in the construction of piece for HIV vaccine.
XX
KW HIV; human immunodeficiency virus; vaccine; AIDS; PCR primer; snut;
KW silent nucleotide substitution; ss.
XX
XX Synthetic.
XX
XX WO200029561-A2.
XX
XX 25-MAY-2000.
XX
XX 27-MAR-2000; 2000WO-DK000144.
XX
XX 29-MAR-1999; 99DX-00000427.
XX
XX 09-APR-1999; 99US-0128558P.
XX
XX (STAT-) STATENS SERUM INST.
XX
XX Fomsgaard A;
XX
XX WPI; 2000-387778/33.
XX
XX

PT Producing nucleotide sequence construct with optimized codons for human
PT immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
PT nucleotide sequence from a HIV patient, redesigning and assembling it
XX with snuts.
XX
PS Example 4; Page 33; 150pp; English.
XX
XX The present invention relates to a nucleotide construct with optimised
CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
CC construct uses codons from highly expressed mammalian proteins to code
CC for each derivative of an early, primary HIV envelope gene. The first
CC stage in the production of the construct was the cloning of an HIV
CC envelope gene. A nucleotide sequence encoding this gene was then created
CC using codons from highly expressed mammalian genes. The next stage was
CC the creation of snuts (AAA49060-A49079) by redesigning this nucleotide
CC construct so that restriction enzyme sites surrounded functional regions
CC of the sequence. The snuts were then assembled into pieces (AAA49080-
CC A49092). The present sequence is a PCR primer that was used in the
CC assembly of the pieces. Each derivative of the envelope gene (AAA49093-
CC A49097) was then built using the pieces. The HIV DNA vaccine may be used
CC as a prophylactic vaccine and as a therapeutic vaccine in HIV infected
XX patients
SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA49122 (1-19)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 226
AAC70391
ID AAC70391 standard; DNA; 19 BP.
XX
XX AAC70391;
XX
XX 09-FEB-2001 (first entry)
XX
XX Single nucleotide polymorphism PCR primer #148.
XX
XX Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200058519-A2.
XX
XX 05-OCT-2000.
XX
XX 30-MAR-2000; 2000WO-US008440.
XX
XX 31-MAR-1999; 99US-0127248P.
XX
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
XX WPI; 2000-611722/58.
XX
XX Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful

PT for phenotypic correlations, forensics, paternity testing, medicine and
 PT genetic analysis.
 XX
 XX Claim 8; Fig 5; 214pp; English.
 XX
 CC The present invention is concerned with a number of human single
 CC nucleotide polymorphisms (SNPs) which the inventors identified in human
 CC genes. These SNPs can be used in disease diagnosis and prediction of an
 CC individual's susceptibility to disease, in forensic and paternity testing
 CC and in genetic mapping. In particular, the SNPs of the invention can be
 CC used to diagnose susceptibility to diseases of the cardiovascular,
 CC endocrine and neurological systems, such as coronary artery disease,
 CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
 CC diseases
 XX
 SQ Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0
 US-09-966-880A-8 (1-198) x AAC70391 (1-19)
 QY 101 AsnProAsnLeuSer 105
 Db 2 AACCCCAACCTTCT 16
 RESULT 227
 AAC70385
 ID AAC70385 standard; DNA; 19 BP.
 AC AAC70385;
 XX
 XX 09-FEB-2001 (first entry)
 DT
 DE Single nucleotide polymorphism PCR primer #144.
 XX
 XX Single nucleotide polymorphism; SNP; human; genetic disease;
 KW disease susceptibility; cardiovascular system; endocrine system;
 KW neurological system; forensic testing; paternity testing; PCR primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200058519-A2.
 PN
 XX 05-OCT-2000.
 PD
 XX 30-MAR-2000; 2000WO-US008440.
 PF
 XX 31-MAR-1999; 99US-0127248P.
 PR
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 PA
 XX Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
 PI Lipshutz RJ, Patil N, Sklar P;
 XX
 XX WPI; 2000-611722/58.
 DR
 XX
 XX Nucleic acid selected from one of 106 genes comprising single nucleotide
 PT polymorphisms, allele-specific oligonucleotides to the genes are useful
 PT for phenotypic correlations, forensics, paternity testing, medicine and
 PT genetic analysis.
 XX
 XX Claim 8; Fig 5; 214pp; English.
 PS
 XX The present invention is concerned with a number of human single
 CC nucleotide polymorphisms (SNPs) which the inventors identified in human
 CC genes. These SNPs can be used in disease diagnosis and prediction of an

CC individual's susceptibility to disease, in forensic and paternity testing
 CC and in genetic mapping. In particular, the SNPs of the invention can be
 CC used to diagnose susceptibility to diseases of the cardiovascular,
 CC endocrine and neurological systems, such as coronary artery disease,
 CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
 CC diseases
 XX
 SQ Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0
 US-09-966-880A-8 (1-198) x AAC70385 (1-19)
 QY 101 AsnProAsnLeuSer 105
 Db 2 AACCCCAACCTTCT 16
 RESULT 228
 AAC70388
 ID AAC70388 standard; DNA; 19 BP.
 AC AAC70388;
 XX
 XX 09-FEB-2001 (first entry)
 DT
 DE Single nucleotide polymorphism PCR primer #146.
 XX
 XX Single nucleotide polymorphism; SNP; human; genetic disease;
 KW disease susceptibility; cardiovascular system; endocrine system;
 KW neurological system; forensic testing; paternity testing; PCR primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200058519-A2.
 PN
 XX 05-OCT-2000.
 PD
 XX 30-MAR-2000; 2000WO-US008440.
 PF
 XX 31-MAR-1999; 99US-0127248P.
 PR
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 PA
 XX Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
 PI Lipshutz RJ, Patil N, Sklar P;
 XX
 XX WPI; 2000-611722/58.
 DR
 XX
 XX Nucleic acid selected from one of 106 genes comprising single nucleotide
 PT polymorphisms, allele-specific oligonucleotides to the genes are useful
 PT for phenotypic correlations, forensics, paternity testing, medicine and
 PT genetic analysis.
 XX
 XX Claim 8; Fig 5; 214pp; English.
 PS
 XX The present invention is concerned with a number of human single
 CC nucleotide polymorphisms (SNPs) which the inventors identified in human
 CC genes. These SNPs can be used in disease diagnosis and prediction of an
 CC individual's susceptibility to disease, in forensic and paternity testing
 CC and in genetic mapping. In particular, the SNPs of the invention can be
 CC used to diagnose susceptibility to diseases of the cardiovascular,
 CC endocrine and neurological systems, such as coronary artery disease,
 CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
 CC diseases
 XX
 SQ Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Alignment Scores: 9e+03 Length: 19
 Pred. No.: 5.00 Matches: 5
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 3

US-09-966-880A-8 (1-198) x AAC70388 (1-19)

OY 101 AsnProAsnLeuSer 105
 DB 2 AACCCCAAGCTTCT 16

RESULT 229
 AAA59922
 ID AAA59922 standard; DNA; 19 BP.
 AC AAA59922;
 XX
 XX
 DT 16-OCT-2000 (first entry)
 XX
 DE PCR primer used in hLF transgene expression cassette construction.
 XX
 KW Lactoferrin; transgenic bovine species; milk; infant formula;
 KW alphaS1-casein expression regulatory sequence; PCR primer; ss.
 XX
 OS Bos sp.
 PN US6066725-A.
 XX
 XX 23-MAY-2000.
 PD
 XX 21-SEP-1998; 98US-00158313.
 PF
 XX 01-DEC-1989; 89US-00444745.
 PR 27-NOV-1990; 90US-00619131.
 PR 15-JUN-1992; 92US-00898956.
 PR 15-JUN-1993; 93US-00077788.
 PR 16-NOV-1993; 93US-00154019.
 PR 07-JUN-1995; 95US-00476798.
 XX
 XX (PHAR-) PHARMING BV.
 XX
 XX Deboer HA, Heyneker HL, Lee SH, Krimpenfort PJA, Platenburg G;
 PI Pieper F, Strijker R;
 XX
 XX WPI; 2000-450654/39.
 XX
 XX New isolated cDNA sequence encoding the mature human lactoferrin protein,
 PT useful for generating higher amounts of lactoferrin in bovine milk, which
 PT are beneficial and safe for human consumption.
 XX
 XX Example 16; Col 45; 89pp; English.
 PS
 XX This invention relates to a cDNA sequence encoding the mature human
 CC lactoferrin (hLF) protein. Lactoferrin is the major iron binding protein
 CC in human milk, and may play a role in the absorption of iron by the small
 CC intestine. The invention concerns the expression of hLF in bovine milk.
 CC Included in the invention are methods for the production of transgenic
 CC bovine species, which produce milk with high lactoferrin levels. The hLF
 CC coding sequence is placed under the control of bovine alphaS1-casein
 CC expression regulation sequences. The transgenic milk may be either used
 CC as normal milk, or further treated to purify the recombinant polypeptide.
 CC Purified hLF obtained from the transgenic cows may be used in food
 CC formulations such as infant formula. The methods contained in the
 CC invention may be used to obtain milk from transgenic cows which has
 CC nutritional or other beneficial value. The advantage of the production of
 CC transgenic bovine milk using the isolated lactoferrin cDNA sequence, is
 CC that it provides a matrix where little or no purification is necessary
 CC prior to human consumption. The present sequence represents a PCR primer
 CC used to amplify the alphaS1-casein DNA sequence for use in the

CC construction of a hLF transgene cassette
 XX
 SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
 Alignment Scores: 9e+03 Length: 19
 Pred. No.: 5.00 Matches: 5
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 3

US-09-966-880A-8 (1-198) x AAA59922 (1-19)

OY 32 ValVallysArg 36
 DB 5 GTTGTAACGACGG 19

RESULT 230
 AAC64682/C
 ID AAC64682 standard; DNA; 19 BP.
 AC AAC64682;
 XX
 XX 27-FEB-2001 (first entry)
 DT
 XX Nitrosomonas europaea trpX PCR primer SEQ ID NO:5.
 DE
 XX Nitrosomonas europaea; trpX; TRPA-1; TRPA-2; frozen microbe body;
 KW ammonia-oxidising microbe; inhibition; nitrification; luciferase;
 KW PCR primer; ss.
 XX
 XX Nitrosomonas europaea.
 OS
 XX JP2000262285-A.
 PN
 XX 26-SEP-2000.
 PD
 XX 15-MAR-1999; 99JP-00067954.
 PF
 XX 15-MAR-1999; 99JP-00067954.
 PR
 XX (KURK) KURITA WATER IND LTD.
 PA
 XX WPI; 2000-675515/66.
 DR
 XX Preparation of the frozen microbe body of an ammonia-oxidizing microbe
 PT and a frozen microbe body useful for measurement of the inhibiting rate
 PT on nitrification activity.
 XX
 XX Example 1; Page 10; 21pp; Japanese.
 PS
 XX The present invention describes a method for the preparation of the
 CC frozen microbe body of an ammonia-oxidising microbe in which a protective
 CC agent containing a protein which protects the bioluminescence activity of
 CC an ammonia-oxidising microbe having luciferase gene and protects the
 CC response ability to a nitrification-inhibiting substance is made to co-
 CC exist when the ammonia-oxidising microbe is frozen. Also described is a
 CC frozen microbe body of an ammonia-oxidising microbe prepared by freezing
 CC an ammonia-oxidising microbe having luciferase gene in the co-existence
 CC of the above protective agent. The frozen microbe body can be used for
 CC the measurement of the inhibiting rate on nitrification activity. The
 CC present sequence represents a PCR primer, which is used in an example
 CC from the present invention
 XX
 SQ Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
 Alignment Scores: 9e+03 Length: 19
 Pred. No.: 5.00 Matches: 5
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53%

DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAC64682 (1-19)

QY 32 ValVallyeArg 36
 |||||
 DB 15 GTTGTAAACGACGG 1

RESULT 231
 AAC68319
 ID AAC68319 standard; DNA; 19 BP.
 XX
 AC AAC68319;
 XX
 DT 20-FEB-2001 (first entry)
 XX
 DE Primer 1 used in construction of transgene cassette.
 XX
 KW Lactoferrin; mammary; milk; ss.
 XX
 OS Synthetic.
 XX
 PN US6140552-A.
 XX
 PD 31-OCT-2000.
 XX
 PF 07-JUN-1995; 95US-00476798.
 XX
 PR 01-DEC-1989; 89US-00444745.
 PR 27-NOV-1990; 90US-00619131.
 PR 15-JUN-1992; 92US-00898956.
 PR 15-JUN-1993; 93US-00077788.
 PR 16-NOV-1993; 93US-00154019.
 XX
 PA (PHAR-) PHARMING BV.
 XX
 PI Srijker R, Heyneker HL, Platenburg G, Pieper F, Krimpenfort PJA;
 PI Lee SH, Deboer HA;
 XX
 DR WPI; 2001-040323/05.
 XX
 PT New transgenic bovine whose mammary gland cells contain DNA encoding a
 PT signal sequence, and a polypeptide of interest and an expression
 PT regulatory sequence, for producing polypeptides in bovine milk.
 XX
 PS Example; Col 44; 88pp; English.
 XX
 CC The present invention relates to a transgenic or chimeric bovine whose
 CC mammary gland cells contain a construct encoding a signal sequence, a
 CC polypeptide of interest and a regulatory sequence that promotes
 CC expression of the DNA sequence. The transgenic or chimeric bovine is
 CC useful for producing recombinant polypeptides in milk of female
 CC transgenic mammals. The recombinant polypeptide may be used in food
 CC formulations, particularly in infant formula having either nutritional or
 CC beneficial value. An infant formula containing human lactoferrin from the
 CC transgenic bovine milk provides bacteriostatic effect, which aids in
 CC controlling diarrhoea in newborn. Recombinant polypeptides may also be
 CC used to supplement common diet formulations

Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAC68319 (1-19)

QY 32 ValVallyeArg 36
 |||||
 DB 15 GTTGTAAACGACGG 1

RESULT 232
 AAH44505
 ID AAH44505 standard; DNA; 19 BP.
 XX
 AC AAH44505;
 XX
 DT 25-OCT-2001 (first entry)
 XX
 DE Human glutaredoxin-Bio36 PCR primer 2.
 XX
 KW Human; glutaredoxin-Bio36; hGRX-Bio36; genital system disease;
 KW cardiovascular system disease; cerebral ischaemia; PCR primer;
 KW cerebral nerve cell damage; immunological disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN CN1297897-A.
 XX
 PD 06-JUN-2001.
 XX
 PF 24-NOV-1999; 99CN-00124106.
 XX
 PR 24-NOV-1999; 99CN-00124106.
 XX
 PA (SHAN-) SHANGHAI SHENGYUAN GENE DEV CO LTD.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2001-489646/54.
 XX
 PT New human oxyglutelinoid and its code sequence.
 XX
 PS Example 3; Page 13 (Disclosure); 25pp; Chinese.
 XX
 CC The present invention describes the human glutaredoxin-Bio36 (hGRX-Bio36)
 CC protein. The present invention also discloses a method of applying the
 CC protein in treating various diseases, such as genital system disease,
 CC cardiovascular system disease, cerebral ischaemia and cerebral nerve cell
 CC damage and immunological diseases. The present sequence represents a PCR
 CC primer for hGRX-Bio36, which is used in an example from the present
 CC invention

Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH44505 (1-19)

QY 108 IlePheThrAlaArg 112
 |||||
 DB 3 ATCTTCACGGCTCGC 17

RESULT 233
 AAH44651/C
 ID AAH44651 standard; DNA; 19 BP.
 XX
 AC AAH44651;
 XX
 DT 09-NOV-2001 (first entry)
 XX
 DE Hydrazide 19-mer oligonucleotide.
 XX
 KW Hydrazide; multiple attachment moiety; binding; biomolecule;
 KW phenyl boronic acid; microarray; solid-phase synthesis; diagnostic;
 KW analytical technique; immobilised reagent; hybridisation;

gene sequence identification; ss.

Synthetic.

WO200151689-A1.

19-JUL-2001.

11-AUG-2000; 2000WO-US022205.

11-JAN-2000; 2000US-0175550P.

(NANO-) NANOGEN INC.

Schweitzer M, Windhab N, Havens JR, Onofrey TJ, Greef CH, Wang D; WPI; 2001-557493/62.

Binding biomolecules to substrate by contacting with branched linking group to form branched linking structure, and contacting linking PT structure with binding group in substrate.

Example 2; Page 28; 90pp; English.

The present invention describes biomolecules which are bound to a substrate by contacting with a branched linking group to form a branched linking structure, and contacting the linking structure with a binding group contained within the substrate to form a coupled substrate binding structure. Also described are: (1) the use of branched and unbranched phenyl boronic acid containing molecules to bind biomolecules to a substrate; and (2) a microarray with binding groups coupled to biomolecules. The biomolecules can be used for solid-phase synthesis and/or synthesis of small molecule libraries e.g. deoxyribonucleic acid, ribonucleic acid, pyranosyl-ribonucleic acid, and peptides, and for analytical techniques that require immobilised reagents e.g. hybridisation based assays, diagnostics, and gene sequence identification. The present sequence represents a hydrazide 19-mer oligonucleotide which is used in an example from the present invention

Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH44651 (1-19)

QY 56 HisValGluLeuLeu 60

DB 18 CACGTAGAACTGCTC 4

RESULT 234

AAH49500/C

ID AAH49500 standard; DNA; 19 BP.

XX AC AAH49500;

XX DT 21-DEC-2001 (first entry)

XX DE Oligonucleotide containing acetyl/aldehyde modification.

XX KW Acetyl group-containing reactive monomer; phosphoramidite; nucleotide synthesis; ss.

XX OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1 /*tag= a

FT

gene sequence identification; ss.

Synthetic.

WO200151689-A1.

19-JUL-2001.

11-AUG-2000; 2000WO-US022205.

11-JAN-2000; 2000US-0175550P.

(NANO-) NANOGEN INC.

Schweitzer M, Windhab N, Havens JR, Onofrey TJ, Greef CH, Wang D; WPI; 2001-557493/62.

Binding biomolecules to substrate by contacting with branched linking group to form branched linking structure, and contacting linking PT structure with binding group in substrate.

Example 2; Page 28; 90pp; English.

The present invention describes biomolecules which are bound to a substrate by contacting with a branched linking group to form a branched linking structure, and contacting the linking structure with a binding group contained within the substrate to form a coupled substrate binding structure. Also described are: (1) the use of branched and unbranched phenyl boronic acid containing molecules to bind biomolecules to a substrate; and (2) a microarray with binding groups coupled to biomolecules. The biomolecules can be used for solid-phase synthesis and/or synthesis of small molecule libraries e.g. deoxyribonucleic acid, ribonucleic acid, pyranosyl-ribonucleic acid, and peptides, and for analytical techniques that require immobilised reagents e.g. hybridisation based assays, diagnostics, and gene sequence identification. The present sequence represents a hydrazide 19-mer oligonucleotide which is used in an example from the present invention

Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH44651 (1-19)

QY 56 HisValGluLeuLeu 60

DB 18 CACGTAGAACTGCTC 4

RESULT 234

AAH49500/C

ID AAH49500 standard; DNA; 19 BP.

XX AC AAH49500;

XX DT 21-DEC-2001 (first entry)

XX DE Oligonucleotide containing acetyl/aldehyde modification.

XX KW Acetyl group-containing reactive monomer; phosphoramidite; nucleotide synthesis; ss.

XX OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1 /*tag= a

FT

gene sequence identification; ss.

Synthetic.

WO200151689-A1.

19-JUL-2001.

11-AUG-2000; 2000WO-US022205.

11-JAN-2000; 2000US-0175550P.

(NANO-) NANOGEN INC.

Schweitzer M, Windhab N, Havens JR, Onofrey TJ, Greef CH, Wang D; WPI; 2001-557493/62.

Binding biomolecules to substrate by contacting with branched linking group to form branched linking structure, and contacting linking PT structure with binding group in substrate.

Example 2; Page 28; 90pp; English.

The present invention describes biomolecules which are bound to a substrate by contacting with a branched linking group to form a branched linking structure, and contacting the linking structure with a binding group contained within the substrate to form a coupled substrate binding structure. Also described are: (1) the use of branched and unbranched phenyl boronic acid containing molecules to bind biomolecules to a substrate; and (2) a microarray with binding groups coupled to biomolecules. The biomolecules can be used for solid-phase synthesis and/or synthesis of small molecule libraries e.g. deoxyribonucleic acid, ribonucleic acid, pyranosyl-ribonucleic acid, and peptides, and for analytical techniques that require immobilised reagents e.g. hybridisation based assays, diagnostics, and gene sequence identification. The present sequence represents a hydrazide 19-mer oligonucleotide which is used in an example from the present invention

Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH44651 (1-19)

QY 56 HisValGluLeuLeu 60

DB 18 CACGTAGAACTGCTC 4

RESULT 234

AAH49500/C

ID AAH49500 standard; DNA; 19 BP.

XX AC AAH49500;

XX DT 21-DEC-2001 (first entry)

XX DE Oligonucleotide containing acetyl/aldehyde modification.

XX KW Acetyl group-containing reactive monomer; phosphoramidite; nucleotide synthesis; ss.

XX OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1 /*tag= a

FT

gene sequence identification; ss.

Synthetic.

WO200151689-A1.

19-JUL-2001.

11-AUG-2000; 2000WO-US022205.

11-JAN-2000; 2000US-0175550P.

(NANO-) NANOGEN INC.

Schweitzer M, Windhab N, Havens JR, Onofrey TJ, Greef CH, Wang D; WPI; 2001-557493/62.

Binding biomolecules to substrate by contacting with branched linking group to form branched linking structure, and contacting linking PT structure with binding group in substrate.

Example 2; Page 28; 90pp; English.

The present invention describes biomolecules which are bound to a substrate by contacting with a branched linking group to form a branched linking structure, and contacting the linking structure with a binding group contained within the substrate to form a coupled substrate binding structure. Also described are: (1) the use of branched and unbranched phenyl boronic acid containing molecules to bind biomolecules to a substrate; and (2) a microarray with binding groups coupled to biomolecules. The biomolecules can be used for solid-phase synthesis and/or synthesis of small molecule libraries e.g. deoxyribonucleic acid, ribonucleic acid, pyranosyl-ribonucleic acid, and peptides, and for analytical techniques that require immobilised reagents e.g. hybridisation based assays, diagnostics, and gene sequence identification. The present sequence represents a hydrazide 19-mer oligonucleotide which is used in an example from the present invention

Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH44651 (1-19)

QY 56 HisValGluLeuLeu 60

DB 18 CACGTAGAACTGCTC 4

RESULT 234

AAH49500/C

ID AAH49500 standard; DNA; 19 BP.

XX AC AAH49500;

XX DT 21-DEC-2001 (first entry)

XX DE Oligonucleotide containing acetyl/aldehyde modification.

XX KW Acetyl group-containing reactive monomer; phosphoramidite; nucleotide synthesis; ss.

XX OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1 /*tag= a

FT

gene sequence identification; ss.

Synthetic.

WO200151689-A1.

19-JUL-2001.

11-AUG-2000; 2000WO-US022205.

11-JAN-2000; 2000US-0175550P.

(NANO-) NANOGEN INC.

Schweitzer M, Windhab N, Havens JR, Onofrey TJ, Greef CH, Wang D; WPI; 2001-557493/62.

Binding biomolecules to substrate by contacting with branched linking group to form branched linking structure, and contacting linking PT structure with binding group in substrate.

Example 2; Page 28; 90pp; English.

The present invention describes biomolecules which are bound to a substrate by contacting with a branched linking group to form a branched linking structure, and contacting the linking structure with a binding group contained within the substrate to form a coupled substrate binding structure. Also described are: (1) the use of branched and unbranched phenyl boronic acid containing molecules to bind biomolecules to a substrate; and (2) a microarray with binding groups coupled to biomolecules. The biomolecules can be used for solid-phase synthesis and/or synthesis of small molecule libraries e.g. deoxyribonucleic acid, ribonucleic acid, pyranosyl-ribonucleic acid, and peptides, and for analytical techniques that require immobilised reagents e.g. hybridisation based assays, diagnostics, and gene sequence identification. The present sequence represents a hydrazide 19-mer oligonucleotide which is used in an example from the present invention

Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH44651 (1-19)

QY 56 HisValGluLeuLeu 60

DB 18 CACGTAGAACTGCTC 4

RESULT 234

AAH49500/C

ID AAH49500 standard; DNA; 19 BP.

XX AC AAH49500;

XX DT 21-DEC-2001 (first entry)

XX DE Oligonucleotide containing acetyl/aldehyde modification.

XX KW Acetyl group-containing reactive monomer; phosphoramidite; nucleotide synthesis; ss.

XX OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1 /*tag= a

FT

gene sequence identification; ss.

Synthetic.

WO200151

KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antiskinning; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029500.
XX
XX 26-OCT-1999; 99US-0161532P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Robbins JM, Tritz R;
PI
XX WPI; 2001-300427/31.
DR
XX
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX
PS Example 1; Page 91; 408pp; English.
XX
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiskinning,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAH57841 (1-19)

QY 193 PheArgThrLeuGly 197
Db 1 TTTCGGACTCTGGGG 15

RESULT 236
AAH59249
ID AAH59249 standard; DNA; 19 BP.
XX
AC AAH59249;
XX
DT 10-SEP-2001 (first entry)

Cyclin C ribozyme binding site SEQ ID NO:1673.
Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
recognition site; target; ribozyme binding site; eye disease; vulnary;
proliferative disease; skin disease; psoriasis; diabetic retinopathy;
cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
antiskinning; ophthalmological; keratolytic; gene therapy; viral wart;
atopic dermatitis; actinic keratosis; squamous cell carcinoma;
basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029500.
XX
XX 26-OCT-1999; 99US-0161532P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX Robbins JM, Tritz R;
PI
XX WPI; 2001-300427/31.
DR
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX
PS Example 1; Page 193; 408pp; English.
XX
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiskinning,
CC ophthalmological, vulnary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAH59249 (1-19)

QY 62 LeuArgTyrIleSer 66
Db 1 CTACGGTATATTCA 15

RESULT 237
AAH59248
ID AAH59248 standard; DNA; 19 BP.
XX
AC AAH59248;
XX
XX 10-SEP-2001 (first entry)
XX
XX Cyclin C ribozyme binding site SEQ ID NO:1672.
XX
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnery;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; cytosolic;
KW antiproliferative; antiseborrheic; antidiabetic; virucide;
KW antiproliferative; antiseborrheic; antidiabetic; virucide;
KW antiproliferative; antiseborrheic; antidiabetic; virucide;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200130362-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029500.
XX
XX 26-OCT-1999; 99US-0161532P.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX Robbins JM, Tritz R;
PI
XX WPI; 2001-300427/31.
XX
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX Example 1; Page 193; 408pp; English.
XX
XX The present invention describes a method for treating a proliferative
XX skin or eye disease and scarring. The method involves administering a
XX ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX dependent kinase, growth factor or a reductase, or administering a
XX nucleic acid molecule (II) comprising a promoter operably linked to a
XX nucleic acid segment encoding (I). (I) can have antiproliferative,
XX dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
XX ophthalmological, vulnery, keratolytic and virucide activities, and
XX cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX in gene therapy. (I) and (II) are useful for treating proliferative skin
XX diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX also be used for treating proliferative eye diseases such as diabetic
XX retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
XX prematurity and retinal detachment, and for treating and preventing
XX scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
XX scar. AAH57577 to AAH62099 represent sequences used in the
XX exemplification of the present invention
XX
SQ Sequence 19 BP; 5 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x AAH59248 (1-19)
QY 62 LeuAtgTyrIleSer 66
Db 3 CTACGGTATATTCA 17

RESULT 238
AAH26909/c
ID AAH26909 standard; DNA; 19 BP.
XX
XX AAH26909;
XX
XX 21-DEC-2001 (first entry)
XX
XX Biotinylated DNA capture probe C2(ATA5) for electron hybridisation.
DE
XX Capture probe; hybridisation; electronics; photonics; nanotechnology; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "biotinylation"
XX
XX WO200153799-A1.
XX
XX 26-JUL-2001.
XX
XX 12-JAN-2001; 2001WO-US000926.
XX
XX 24-JAN-2000; 2000US-00489855.
XX
XX (NANO-) NANOGEN INC.
XX
XX Edman CF, Heller MJ, Gurtner C, Formosa R;
XX WPI; 2001-607116/69.
XX
XX Device for photoelectric transport of charged materials in liquid
PT environment for micro- and opto- electronic devices, has a substrate
PT generating light induced current, conductor, permeation layer and light
PT source to illuminate substrate.
XX
XX Disclosure; Page 60; 119pp; English.
XX
XX The present sequence is that of biotinylated capture probe C2(ATA5),
XX which was used to demonstrate an electron hybridisation method of the
XX invention. Mn203 stabilised n-type silicon photoelectrodes coated with a
XX streptavidin-agarose permeation layer were shown to constitute a simple
XX platform for rapid manipulation of DNA oligonucleotides by electron
XX hybridisation. In this process, a set of unlabelled oligonucleotides
XX (capture strands) are first targeted to specific locations and anchored.
XX A second set of fluorescent labeled oligonucleotides (target strands) is
XX then targeted to the same locations and actively hybridised to the
XX capture strands. In the example provided, 2 sets of biotinylated capture
XX probes, C1 (see AAH26908) and C2 (present sequence), were successively
XX transported and anchored to 4 different locations on a streptavidin-
XX agarose and Mn203 coated amorphous silicon substrate. 2 Fluorescence
XX labeled target sequences, T1 (see AAH26910) and T2 (see AAH26911), were
XX then transported to a location with complementary capture probes and a
XX location with non-complementary capture probes. This step produced 2
XX clearly detectable fluorescence signals at the 2 locations with matching
XX sequences. The ratio between signal and non-specific background was
XX better than 4. The method allows for detection of DNA oligonucleotides in
XX an extremely short time. The invention generally provides systems and
XX devices for photoelectroretro transport and hybridisation of
XX oligonucleotides. The techniques of the invention have wide use in
XX manufacture of micro electronic and opto electronic devices. Self-
XX assembly fabrication techniques based on DNA polymers enables micron, sub
XX -micron or nanoscale devices to be fabricated

XX SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x AAH26909 (1-19)
 QY 56 HisValGluLeuLeu 60
 Db 18 CACGTAGACTGCTC 4

RESULT 239
 AAS43497
 ID AAS43497 standard; DNA; 19 BP.
 XX AC AAS43497;
 XX DT 18-DEC-2001 (first entry)
 XX DE
 XX Corneodesmosin PCR primer #6.
 XX Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
 KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200162798-A2.
 FN
 XX 30-AUG-2001.
 PD
 XX 23-FEB-2001; 2001WO-GB000795.
 PF
 XX 23-FEB-2000; 2000GB-00004312.
 PR
 XX (OXAG-) OXAGEN LTD.
 PA
 XX Olaveson M, Lench N, Allen M, Tazi-Ahnni R;
 PI
 XX WPI; 2001-570627/64.
 DR
 XX Corneodesmosin protein and polynucleotide encoding it, having one or more
 PT polymorphisms useful in treating, diagnosing or determining
 PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
 PT diseases.
 PT
 XX Disclosure; Page 25; 60pp; English.

XX The invention relates to corneodesmosin protein (I) and nucleic acid (II)
 CC encoding the corneodesmosin gene, where the gene comprises a base
 CC substitution, deletion or insertion at one or more positions. (I) and
 CC (II) are useful for screening for agents for use in prognosis, diagnosis
 CC and treatment of individuals having or being susceptible to
 CC corneodesmosin-mediated diseases, by monitoring the reaction between the
 CC molecules and the agents. The nucleotide and amino acid polymorphisms are
 CC useful for diagnosing or determining susceptibility to corneodesmosin-
 CC mediated disease, which facilitates subsequent treatment of the disease
 CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
 CC are useful in diagnostic, prognostic or therapeutic methods and as
 CC research tools for e.g. in drug screening. (II) is useful as probes or
 CC primers for detecting an allele of the polymorphism or in the regulation
 CC of corneodesmosin gene. Antibodies which binds to (I) are useful for
 CC screening DNA cline libraries for cells secreting the antigen. (II) is
 CC useful as a model to investigate the role of corneodesmosin in normal
 CC skin function. AAS43497-AAS43749 represent corneodesmosin coding
 CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
 CC invention

XX SQ Sequence 19 BP; 4 A; 7 C; 5 G; 2 T; 0 U; 1 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x AAS43497 (1-19)
 QY 129 LeuHisArgAlaGly 133
 Db 4 CTCACACAGCTGGA 18

RESULT 240
 ABV73311/c
 ID ABV73311 standard; DNA; 19 BP.
 XX AC ABV73311;
 XX DT 22-JAN-2003 (first entry)
 XX DE Troponin T cDNA amplifying primer.
 XX Replacement cell; primordial stem cell; pluripotent; immunosuppressive;
 KW cell therapy; nuclear transfer; skeletal; troponin T; PCR; primer; ss.
 KW
 XX Bos taurus.
 OS
 XX WO200273188-A1.
 FN
 XX 19-SEP-2002.
 PD
 XX 13-MAR-2002; 2002WO-US007394.
 PF
 XX 13-MAR-2001; 2001US-0275104P.
 PR
 XX (ADCE-) ADVANCED CELL TECHNOLOGY INC.
 PA
 XX Lanza R;
 PI
 XX WPI; 2002-713528/77.
 DR
 XX Producing replacement cells and/or tissues for treating patients in need
 PT of replacement cells comprises exposing the pluripotent cells to
 PT environmental cues in order to encourage development along a certain
 PT path.
 PT
 XX Example 4; Page 28; 53pp; English.

XX The invention relates to producing replacement cells and/or tissues for a
 CC mammal. The method involves (a) isolating a primordial stem cell or other
 CC embryonic pluripotent cell or cells; (b) introducing into the primordial
 CC stem cell or embryonic pluripotent cells at least one selectable marker
 CC operatively linked to a cell or tissue specific promoter, enhancer or
 CC other regulatory genetic element so that the selectable marker is
 CC expressed in the cell or tissue type of interest; (c) permitting the
 CC primordial stem cell or embryonic cells to differentiate into
 CC differentiated cells and tissues; and (d) selecting for cells and tissues
 CC that express the selectable marker in order to produce replacement cells
 CC and/or tissues. The method is useful for treating patients in need of
 CC replacement cells. The method eliminates the need for in vitro isolation
 CC and differentiation of embryonic stem cells in producing isogenic
 CC replacement tissues using nuclear transfer. The present sequence
 CC represents a PCR primer for amplifying troponin T cDNA for creation of
 CC tissue-engineered cardiac tissue by nuclear transfer in Bos taurus
 XX

XX SQ Sequence 19 BP; 4 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19

Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABV73311 (1-19)

QY 126 LeuArgArgLeuHis 130

DB 17 CTTGGCGGCTACAT 3

RESULT 241

ABK68748
 ID ABK68748 standard; DNA; 19 BP.

XX

AC ABK68748;

XX

DT 02-JUL-2002 (first entry)

XX

DE Oligonucleotide #2 for detecting polymorphism in CYP3A4 gene.

XX

KW Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;
 KW ss.

XX

OS Homo sapiens.

XX

PN WO200218641-A2.

XX

PD 07-MAR-2002.

XX

XX 30-AUG-2001; 2001WO-1B001580.

PF

XX 30-AUG-2000; 2000GB-00021286.

PR

XX (GEMI-) GEMINI GENOMICS PLC.

PA

XX Risinger C, Andersson MK, Lewander T, Olaisson B;

PI

XX WPI; 2002-351712/38.

XX

PT Novel primer pairs and sequence determination oligonucleotides useful for
 PT amplifying and detecting novel single nucleotide polymorphisms in the 5'
 PT flanking regions of cytochrome p450 (CYP3A4 and CYP2C9 genes
 PT respectively.

XX

PS Disclosure; Page 3; 47pp; English.

XX

CC The present invention relates to PCR primer pairs for amplifying and
 CC sequence determination oligonucleotides for detecting single nucleotide
 CC polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450
 CC (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position
 CC 461 of a defined 1345 base pair sequence for CYP3A4 or position 957,
 CC 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9.
 CC The PCR primers are useful for amplifying the CYP sequences and the
 CC oligonucleotides are useful for detecting SNPs in the 5'-flanking regions
 CC of the CYP3A4 or CYP2C9 genes. ABK68747-ABK68750 represent previously
 CC published oligonucleotides for detecting a polymorphism in the CYP3A4
 CC gene

XX

SQ Sequence 19 BP; 7 A; 3 C; 9 G; 0 T; 0 U; 0 Other;

Alignment Scores: 9e+03 Length: 19
 Pred. No.: 5.00 Matches: 5
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 6

US-09-966-880A-8 (1-198) x ABK68748 (1-19)

QY 22 LysGlyArgArgGlu 26

Db 3 AAGCGGAGGAGAG 17

RESULT 242

ABN88432
 ID ABN88432 standard; DNA; 19 BP.

XX

AC ABN88432;

XX

DT 19-AUG-2002 (first entry)

XX

DE Mouse genome polymorphic region related PCR primer SEQ ID NO:122.

XX

KW Molecular recognition; solid support assay system; non-standard base;
 KW hybridisation; PCR primer; ss.

XX

OS Mus sp.

OS Synthetic.

XX

PN WO200233126-A2.

XX

PD 25-APR-2002.

XX

XX 15-OCT-2001; 2001WO-US031993.

XX

XX 14-OCT-2000; 2000US-0240397P.

PR

PR 10-APR-2001; 2001US-0282831P.

PR

PR 18-MAY-2001; 2001US-00861292.

PR

PR 22-MAY-2001; 2001US-0293259P.

XX

XX (ERAG-) ERAGEN BIOSCIENCES INC.

PA

XX Grenier JK, Marshall DJ, Prudent JR, Richmond CS, Roesch EB;

PI

PI Scherrer CW, Sherrill CB, Ptacin JL;

XX

XX WPI; 2002-479679/51.

XX

XX Assaying oligonucleotides in sample by using capture oligonucleotide that

PT

PT is coupled to support, and has molecular recognition sequence including

PT non-standard base, which is complementary to target oligonucleotide.

XX

XX Example 5; Page 51; 92pp; English.

XX

CC The present invention describes assaying a target oligonucleotide (T),
 CC comprising contacting a capture oligonucleotide (I) having a molecular
 CC recognition sequence (MS) with a non-standard base, under hybridising
 CC conditions, with a sample to hybridise (T) to (I), where (I) is coupled
 CC to a support and (T) has a tagging sequence complementary to MS of (I)
 CC and an analyte-specific sequence (AS) or its complement, and detecting
 CC the hybridisation of (T) to (I). The method can be used for assaying
 CC oligonucleotides. The method can also be used for simultaneously
 CC detecting at least two alleles in a sample comprising genomic DNA. The
 CC method is preferably useful for assaying oligonucleotides including DNA
 CC or RNA fragments. The present sequence represents a PCR primer for a
 CC polymorphic region of the mouse genome, which is used in an example from
 CC the present invention

XX

SQ Sequence 19 BP; 3 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Alignment Scores: 9e+03 Length: 19
 Pred. No.: 5.00 Matches: 5
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 6

US-09-966-880A-8 (1-198) x ABN88432 (1-19)

QY 111 AlaArgLeuTyPhe 115

DB 1 GCAGGGCTCTACTTC 15


```
RESULT 243
AAD38569/C
ID AAD38569 standard; DNA; 19 BP.
XX
AC AAD38569;
XX
DT 10-SEP-2002 (first entry)
XX
DE Bovine leukocyte antigen class I exon 3 specific probe, BoLA-ClEx3B18L.
XX
KW Bovine; immunological rejection; nuclear transfer; NT; immune response;
KW MHC-I; major histocompatibility complex; bovine leukocyte antigen;
KW embryo transfer; BoLA class I exon 3 DNA; probe; ss.
XX
OS Bos sp.
XX
PN WO200229000-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US030925.
XX
PR 03-OCT-2000; 2000US-0237673P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Davies CJ, Schlafer DH, Hall JR;
XX
XX WPI; 2002-444101/47.
XX
PT Minimizing immunological rejection of nuclear transfer fetuses, by
PT transferring the nuclear transfer embryo into an embryo recipient for
PT development of the fetus.
XX
PS Example 1; Page 19; 103pp; English.
XX
CC The present invention relates to a method of minimising immunological
CC rejection of a nuclear transfer (NT) foetus by transferring a nuclear
CC transfer embryo into an embryo recipient under conditions effective for
CC the development of a nuclear transfer foetus with minimal risk of
CC immunological rejection of the foetus due to maternal anti-foetal major
CC histocompatibility complex (MHC)-I immune response. The method is useful
CC for minimising immunological rejection of a NT foetus. It is also useful
CC for performing embryo transfer. The present DNA sequence is a probe
CC specific for bovine leukocyte antigen (BoLA) class I exon 3 DNA. This
CC probe is used in the exemplification of the invention
XX
SQ Sequence 19 BP; 6 A; 2 C; 9 G; 2 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AAD38569 (1-19)
QY 104 LeuSerLeuArgile 108
Db 17 CTGTCTCTCCGCATC 3

RESULT 244
ABL57055/C
ID ABL57055 standard; DNA; 19 BP.
XX
AC ABL57055;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide phosphoramidite oligonucleotide O10.
XX

KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..19
FT /tag= b
FT modified_base 1
FT /note= "phosphoramidite linkage"
FT /tag= a
FT /mod_base= OTHER
FT /note= "6-((2Cyanoethoxy)(diisopropylamino)
FT phosphanlyoxy)-N'-tritylhexanohydrazide"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
XX WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 2; Page 40; 120pp; English.
XX
CC The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC 19-mer, designated oligo O10, which was produced in an example from the
CC invention. The invention describes an improved process for immobilisation
CC of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC RNA and peptides, especially macromolecules containing multiple reactive
CC sites, to a substrate surface or other conjugation target. It also
CC describes the preparation of oligos containing one or more hydrazides,
CC which can be used for conjugation to surface binding moieties, or for
CC other conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
CC applications
XX
SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABL57055 (1-19)
QY 56 HisValGluLeuLeu 60
Db 18 CACGTAGAACTGCTC 4

RESULT 245
ABL57067/C
ID ABL57067 standard; DNA; 19 BP.
XX
AC ABL57067;
XX
DT 22-JUL-2002 (first entry)
XX
DE Phosphoramidite oligonucleotide.
XX
```

KW Macromolecule; hydrazide; immobilisation; ss.
 XX Synthetic.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..19
 FT /tag= a
 FT /note= "phosphoramidite linkage"
 FT
 XX WO200214558-A2.
 PN
 XX
 XX 21-FEB-2002.
 XX
 XX 10-AUG-2001; 2001WO-US041663.
 XX
 XX 11-AUG-2000; 2000WO-US022205.
 XX
 XX (NANO-) NANOGEN INC.
 XX
 XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;
 XX
 XX WPI; 2002-404476/43.
 DR
 XX
 XX Compound for binding macromolecule to substrate surface or conjugation
 PT targets, contains phosphorous containing reactive group, hydrazide
 PT protecting group and benzene ring, and has predefined formula.
 XX
 XX Disclosure; Fig 6; 120pp; English.
 XX
 XX The present sequence is of an oligonucleotide used to illustrate the
 CC synthetic steps using phosphoramidites to produce macromolecules with
 CC multiple reactive sites. These moieties can contain ester groups that are
 CC converted into hydrazides during the deprotection of the oligonucleotides
 CC with hydrazine. The invention describes an improved process for
 CC immobilisation of macromolecules including DNA, RNA, peptide nucleic
 CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
 CC multiple reactive sites, to a substrate surface or other conjugation
 CC target. It also describes the preparation of oligos containing one or
 CC more hydrazides, which can be used for conjugation to surface binding
 CC moieties, or for other conjugation reactions. The process is useful e.g.
 CC in nucleic acid hybridisation based assays, DNA chip technology and
 CC biosensor applications
 XX
 SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0
 US-09-966-880A-8 (1-198) x ABL57067 (1-19)
 QY 56 HisValGluLeuLeu 60
 Db 18 CACGTAGACTGCTC 4
 RESULT 246
 ABL57058/c
 ID ABL57058 standard; DNA; 19 BP.
 XX
 XX ABL57058;
 XX
 XX 22-JUL-2002 (first entry)
 DT
 XX Hydrazide precursor phosphoramidite oligonucleotide O11.
 DE
 XX Macromolecule; hydrazide; immobilisation; ss.
 KW
 XX Synthetic.

XX Key Location/Qualifiers
 FH modified_base 1..19
 FT /tag= b
 FT /note= "phosphoramidite linkage"
 FT
 FT modified_base 1
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Ethyl 6-(2-cyanoethoxy) (diisopropylamino)
 FT phosphanyloxy) hexanoate"
 FT 19
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "3' Cy3 dye"
 FT
 XX WO200214558-A2.
 PN
 XX
 XX 21-FEB-2002.
 XX
 XX 10-AUG-2001; 2001WO-US041663.
 XX
 XX 11-AUG-2000; 2000WO-US022205.
 XX
 XX (NANO-) NANOGEN INC.
 XX
 XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;
 XX
 XX WPI; 2002-404476/43.
 DR
 XX
 XX Compound for binding macromolecule to substrate surface or conjugation
 PT targets, contains phosphorous containing reactive group, hydrazide
 PT protecting group and benzene ring, and has predefined formula.
 XX
 XX Example 3; Page 42; 120pp; English.
 XX
 CC The present sequence is of a hydrazine treated hydrazide precursor
 CC phosphoramidite 19-met, designated oligo O11, which was produced in an
 CC example from the invention. The invention describes an improved process
 CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
 CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
 CC multiple reactive sites, to a substrate surface or other conjugation
 CC target. It also describes the preparation of oligos containing one or
 CC more hydrazides, which can be used for conjugation to surface binding
 CC moieties, or for other conjugation reactions. The process is useful e.g.
 CC in nucleic acid hybridisation based assays, DNA chip technology and
 CC biosensor applications
 XX
 SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0
 US-09-966-880A-8 (1-198) x ABL57058 (1-19)
 QY 56 HisValGluLeuLeu 60
 Db 18 CACGTAGACTGCTC 4
 RESULT 247
 ABQ77335
 ID ABQ77335 standard; DNA; 19 BP.
 XX
 XX ABQ77335;
 XX
 XX 08-MAY-2003 (first entry)
 DT
 XX Bovine H-PABP associated primer P2.
 DE

XX Polymerase chain reaction; PCR; hybridisation; adapter primer;
 KW extension primer; cell-free protein biosynthesis; amplification; primer;
 KW bovine; heart; fatty acid binding protein; H-FABP; ss.
 XX
 OS Bos taurus.
 XX
 PN WO200290371-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 18-MAR-2002; 2002WO-DE001047.
 XX
 PR 16-MAR-2001; 2001DE-01013265.
 XX
 PA (RINA-) RINA NETZWERK RNA TECHNOLOGIEN GMBH.
 XX
 PI Merk H, Erdmann V, Stiege W;
 XX WPI; 2003-148335/14.
 DR
 XX Preparation of long nucleic acids, useful for in vitro, cell-free protein
 PT synthesis, comprises attaching an adapter and extension primers to a base
 PT sequence.
 XX
 PS Disclosure; Fig 1; 37pp; German.
 XX
 CC This invention describes a novel method for preparing long nucleic acids
 CC by polymerase chain reaction (PCR) which comprises (i) hybridising a base
 CC sequence (I) to adapter primers (Adp) at both 3' and 5' ends, (ii)
 CC hybridising the products at both ends with extension primers (EP)
 CC containing an extension sequence (ES) and (iii) producing an amplified
 CC nucleic acid extended at both the 3' and 5' ends from the base sequence.
 CC The invention also describes a nucleic acid for cell-free protein
 CC biosynthesis, comprising a protein-encoding sequence, a ribosome-binding
 CC site (RBS) and optionally a promoter, transcription terminator, a
 CC expression enhancer, stabiliser or affinity tag. The method is useful for
 CC preparing nucleic acids for the cell-free, in vitro biosynthesis of
 CC proteins, particularly in prokaryotic systems, or for in vitro
 CC transcription systems, particularly Escherichia coli D10, for selective
 CC amplification of a sequence from a nucleic acid library and for
 CC characterisation of gene sequences, where the protein expressed is
 CC analysed for structure and/or function. The method makes the large-scale
 CC preparation of nucleic acids that contain regulatory regions (to improve
 CC transcriptional and translational efficiency) possible. It eliminates the
 CC need to prepare long extension primers for each base sequence, since each
 CC Adp contains a short, base sequence-specific region and a constant region
 CC that hybridises to the extension sequence (which is universal), so the
 CC method can be applied to any chosen sequence. This sequence represents a
 CC primer associated with bovine heart fatty acid binding protein (H-FABP),
 CC used to illustrate the method described in the disclosure of the
 CC invention
 XX
 SQ Sequence 19 BP; 6 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: Gaps: 0

US-09-966-880A-8 (1-198) x ABQ77335 (1-19)

Qy 32 ValVallysArgArg 36
 |||||
 Db 5 GTTGTAAACGACGG 19
 |||||

RESULT 248
 ACF03602/C
 ID ACF03602 standard; DNA; 19 BP.
 XX

AC ACF03602;
 XX
 DT 15-SEP-2003 (first entry)
 XX
 DE Human NOV1 reverse PCR primer SEQ ID NO:172.
 XX
 KW Human; NOVX; cytostatic; cardiant; antiinflammatory; immunosuppressive;
 KW antiallergic; haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic;
 KW anorectic; antiasthmatic; neurotropic; antidiabetic; antiparasytic;
 KW neuroprotective; neurotropic; antibacterial; virucide; antiparasytic;
 KW relaxant; anticonvulsant; hypotensive; vasotropic; antiparasytic;
 KW vulnary; angiogenic; antiangiogenic; gene therapy; vaccine; cancer;
 KW cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;
 KW autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;
 KW acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; Parkinson's disease; Goltre; infection; stroke;
 KW muscular dystrophy; epilepsy; wasting disorder; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200294870-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 02-NOV-2001; 2001WO-US051580.
 XX
 PR 02-NOV-2000; 2000US-0245291P.
 PR 02-NOV-2000; 2000US-0245317P.
 PR 07-NOV-2000; 2000US-0246562P.
 PR 08-NOV-2000; 2000US-0246871P.
 PR 26-JAN-2001; 2001US-0264389P.
 PR 26-JAN-2001; 2001US-0264423P.
 PR 29-JAN-2001; 2001US-0264799P.
 XX
 CC (CURA-) CURAGEN CORP.
 XX
 PI Grosse WM, Macdougall JR, Smithson G, Millet I, Stone DJ;
 PI Gunther E, Ellerman K, Alsobrook JP, Lepley DM, Burgess CE;
 PI Spytek KA, Edinger SR, Gangolli EA, Gorman L, Taupier RJ, Li L;
 PI Guo X, Fernandes SR, Vernet CAM, Tchernev VT, Casman SJ, Shenoy S;
 PI Mishra V, Furtak K, Baumgartner JC, Colman SD;
 XX WPI; 2003-140359/13.
 DR
 XX New NOVX polypeptide useful for preventing or treating NOVX-associated
 PT disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and
 PT in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 2; Page 232; 346pp; English.
 XX
 CC ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABR57412
 CC to ABR57435. (I) have cytostatic, cardiant, antiinflammatory, neurotropic,
 CC immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic,
 CC antiarteriosclerotic, anorectic, antiasthmatic, neurotropic, virucide,
 CC antiparasytic, hepatotropic, neuroprotective, antibacterial, relaxant,
 CC antiparasytic, anticonvulsant, hypotensive, vasotropic, antiparasytic,
 CC vulnary, angiogenic and antiangiogenic activities, and can be used in
 CC gene therapy and vaccines. The NOVX polypeptides and their antibodies can
 CC be used to determine the presence or absence of (I) in a sample. The NOVX
 CC polypeptides, polynucleotides encoding them, and antibodies against them,
 CC are useful in manufacturing a medicament for treating or preventing a
 CC syndrome associated with a NOVX-associated disorder such as hypertension,
 CC cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,
 CC autoimmune disorders, allergies, blood disorders, obesity, acquired
 CC immunodeficiency syndrome (AIDS), immunoglobulin (Ig)A nephropathy,
 CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, Goltre,
 CC infections (e.g. bacterial, viral, parasitic), stroke, muscular
 CC dystrophy, epilepsy, and other wasting disorders associated with chronic
 CC diseases. ACF03571 to ACF03644 represent PCR primers and probes for NOVX
 CC sequence, which are used in an example from the present invention
 XX
 XX Sequence 19 BP; 2 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACP03602 (1-19)

QY 122 GluProGluGlyLeu 126
DB 18 GAACCAGAGGGGTC 4
RESULT 249
AAL50790
ID AAL50790 standard; DNA; 19 BP.
XX AC AAL50790;
XX DT 30-JAN-2003 (first entry)
XX DE Exonuclease degradation stabilised coding sequence-related PCR primer 12.
XX PCR; primer; ss; exonuclease degradation stabilised coding sequence;
XX protein synthesis.
XX Unidentified.
XX WO200274952-A2.
XX PD 26-SEP-2002.
XX PF 18-MAR-2002; 2002WO-DE001048.
XX PR 16-MAR-2001; 2001DE-01013265.
XX PR 16-MAR-2001; 2001DE-01045014.
XX PR 05-OCT-2001; 2001DE-01051071.
XX PA (RINA-) RINA NETZWERK RNA TECHNOLOGIEN GMBH.
XX PI Merk H, Stiege W;
XX DR WPI; 2003-018805/01.
XX PT Nucleic acids stabilized against exonucleases, useful for protein
XX production in cell-free or cellular systems, contains molecules attached
XX to bulky specific binding partners.
XX PS Disclosure; Fig 1; 38pp; German.
XX CC The invention comprises nucleic acid coding sequences which have been
XX stabilised against exonuclease degradation. The nucleic acids of the
XX invention are useful for the preparation of an encoded protein in cell-
XX free or cellular systems - especially for characterisation of gene
XX CC sequences and for analysis of the structure/function of encoded proteins.
XX CC The present DNA sequence represents a PCR primer that was used in the
XX invention
XX SQ Sequence 19 BP; 6 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x AAL50790 (1-19)

QY 32 ValVallysArgArg 36

Db 5 GTTGTAAACGACGG 19

RESULT 250
ACC79586
ID ACC79586 standard; DNA; 19 BP.
XX AC ACC79586;
XX DT 05-AUG-2003 (first entry)
XX DE Progesterone receptor reverse PCR primer.

XX Gene expression control; regulatory peptide; selectively suppress;
XX cancer; gene therapy; gene expression; regulation; suppression;
XX modulation; progesterone receptor; PCR primer; ss.
XX Homo sapiens.
XX OS Synthetic.
XX WO2003033701-A1.
XX PD 24-APR-2003.
XX PF 11-OCT-2002; 2002WO-GB004633.
XX PR 11-OCT-2001; 2001GB-00024391.
XX PA (GENE-) GENE EXPRESSION TECHNOLOGIES LTD.
XX PI Hart S, Ali S, Pufong BT, Porter ACG, Buluwela L, Vainikka S;
XX PI Jenkinson JD, Kanda P;
XX DR WPI; 2003-372329/35.
XX PT Suppressing or modulating the expression of a selected gene in a cell
XX comprises introducing into the cell a molecule comprising a nucleic acid
XX binding portion, and an expression repressor portion or a modifying
XX portion.
XX PS Example 10; Page 70; 98pp; English.

XX CC The present invention describes a method for suppressing or modulating
XX the expression of a selected gene in a cell. The method comprises
XX introducing into the cell a molecule comprising a nucleic acid binding
XX portion which binds to a site at or associated with the selected gene
XX which site is present in a genome, and an expression repressor portion or
XX a modifying portion. The nucleic acid binding portion comprises an
XX oligonucleotide or oligonucleotide mimic or analogue. The repressor
XX portion comprises a polypeptide or peptidomimetic. The modifying portion
XX also comprises a polypeptide or peptidomimetic that is capable of
XX modulating covalent modification of nucleic acid or chromatin and is not
XX an endonuclease. The method is useful in controlling gene expression
XX using a complex of an oligonucleotide and a regulatory peptide. The
XX ability to selectively suppress the expression of a gene is useful in
XX many areas of biology, such as in methods of treatment where the
XX expression of the gene may be undesirable (e.g. cancer), in preparing
XX models of disease and in modifying the phenotype in order to produce
XX desirable properties. The molecule is useful in manufacturing an agent or
XX a medicament for modulating or suppressing the expression of the selected
XX gene in a patient or in an animal cell. The method is useful in gene
XX therapy. The present sequence represents a PCR primer for a progesterone
XX receptor, which is used in an example from the present invention

SQ Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC79586 (1-19)

Qy 178 ArgileLeuPro 182
Db 3 CGGATCTGCTTCCT 17

RESULT 251

ID ACC79583 standard; DNA; 19 BP.

XX ACC79583;

DT 05-AUG-2003 (first entry)

DE Human androgen receptor antisense PCR primer.

XX Gene expression control; regulatory peptide; selectively suppress;
KW cancer; gene therapy; gene expression; regulation; suppression;
KW modulation; androgen receptor; PCR primer; ss.

XX Homo sapiens.

OS Synthetic.

XX WO2003033701-A1.

PN 24-APR-2003.

PD 11-OCT-2002; 2002WO-GB004633.

PF 11-OCT-2001; 2001GB-00024391.

XX (GENE-) GENE EXPRESSION TECHNOLOGIES LTD.

XX Hart S, Ali S, Pufong BT, Porter ACG, Buluwela L, Vainikka S;
PI Jenkinson JD, Kanda P;

XX WPI; 2003-372329/35.

XX Suppressing or modulating the expression of a selected gene in a cell
PT comprises introducing into the cell a molecule comprising a nucleic acid
PT binding portion, and an expression repressor portion or a modifying
PT portion.

XX Example 8; Page 57; 98pp; English.

XX The present invention describes a method for suppressing or modulating
CC the expression of a selected gene in a cell. The method comprises
CC introducing into the cell a molecule comprising a nucleic acid binding
CC portion which binds to a site at or associated with the selected gene
CC which site is present in a genome, and an expression repressor portion or
CC a modifying portion. The nucleic acid binding portion comprises an
CC oligonucleotide or oligonucleotide mimic or analogue. The repressor
CC portion comprises a polypeptide or peptidomimetic. The modifying portion
CC also comprises a polypeptide or peptidomimetic that is capable of
CC modulating covalent modification of nucleic acid or chromatin and is not
CC an endonuclease. The method is useful in controlling gene expression
CC using a complex of an oligonucleotide and a regulatory peptide. The
CC ability to selectively suppress the expression of a gene is useful in
CC many areas of biology, such as in methods of treatment where the
CC expression of the gene may be undesirable (e.g. cancer), in preparing
CC models of disease and in modifying the phenotype in order to produce
CC desirable properties. The molecule is useful in manufacturing an agent or
CC a medicament for modulating or suppressing the expression of the selected
CC gene in a patient or in an animal cell. The method is useful in gene
CC therapy. The present sequence represents a PCR primer for the human
CC androgen receptor, which is used in an example from the present invention

XX Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

SQ Alignment Scores:

Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC79583 (1-19)

Qy 178 ArgileLeuPro 182
Db 3 CGGATCTGCTTCCT 17

RESULT 252

ADE27202

ID ADE27202 standard; RNA; 19 BP.

XX AC ADE27202;

XX 29-JAN-2004 (first entry)

DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:146.

XX short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; anti-diabetic;
KW anti-arteriosclerotic; cytoskeletal; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.

XX Synthetic.

XX WO2003070885-A2.

XX 28-AUG-2003.

XX 13-FEB-2003; 2003WO-US004317.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 06-JUN-2002; 2002US-0386782P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 03-SEP-2002; 2002US-0409293P.

XX 20-SEP-2002; 2002US-0412304P.

XX 15-JAN-2003; 2003US-0440129P.

XX (RIBO-) RIBOZYME PHARM INC.

XX McSwiggen J, Beigelman L, Thompson J;

XX WPI; 2003-721687/68.

XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.

XX Example 3; SEQ ID NO 146; 139pp; English.

XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, anti-diabetic, anti-arteriosclerotic, cytoskeletal and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.

XX Sequence 19 BP; 5 A; 2 C; 8 G; 0 T; 4 U; 0 Other;

CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 8 C; 2 G; 0 T; 5 U; 0 Other;
Alignment Scores: 9e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 9
US-09-966-880A-8 (1-198) x ADE27492 (1-19)
Qy 125 GlyleuargArgLeu 129
Db 15 GGCTTCAGAGGTTA 1
RESULT 254
ADE27492/c
ID ADE27492 standard; RNA; 19 BP.
XX
AC ADE27492;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:436.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytosolic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US0004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 05-JUN-2002; 2002US-0386782P.
PR 23-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 436; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity,
CC diabetes (types I and II), atherosclerosis, cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide

CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 8 C; 2 G; 0 T; 5 U; 0 Other;
Alignment Scores: 9e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 9
US-09-966-880A-8 (1-198) x ADE27202 (1-19)
Qy 125 GlyleuargArgLeu 129
Db 5 GGCUGAGGAGGUA 19
RESULT 253
ADE27492/c
ID ADE27492 standard; RNA; 19 BP.
XX
AC ADE27492;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:436.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytosolic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US0004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 05-JUN-2002; 2002US-0386782P.
PR 23-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 436; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity,
CC diabetes (types I and II), atherosclerosis, cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide

CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 8 C; 2 G; 0 T; 5 U; 0 Other;
Alignment Scores: 9e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 9
US-09-966-880A-8 (1-198) x ADE27492 (1-19)
Qy 125 GlyleuargArgLeu 129
Db 15 GGCTTCAGAGGTTA 1
RESULT 254
ADE27492/c
ID ADE27492 standard; DNA; 19 BP.
XX
AC ADE27492;
XX
DT 29-JAN-2004 (first entry)
XX
DE Transgenic bovine-related PCR primer SeqID20.
XX
KW transgene; bovine expression; transgenic bovine; enzyme production;
KW immunoglobulin production; clotting factor production; milk; PCR; primer;
XX
OS Unidentified.
XX
PN US2003192068-A1.
XX
PD 09-OCT-2003.
XX
PF 11-JUN-2002; 2002US-00170221.
XX
PR 01-DEC-1989; 89US-00444745.
PR 27-NOV-1990; 90US-00619131.
PR 15-JUN-1992; 92US-00898956.
PR 15-JUN-1993; 93US-00077788.
PR 16-NOV-1993; 93US-00154019.
PR 07-JUN-1995; 95US-00476798.
PR 26-OCT-1999; 99US-00426591.
XX
PA (PHAR-) PHARMING BV.
XX
PI Deboer HA, Strijker R, Heynecker HL, Platenburg G, Lee SH;
PI Pieper F, Krimpenfort PJA;
XX
DR WPI; 2003-831830/77.
XX
PT New transgenes for producing recombinant polypeptides in transgenic
PT bovine species (especially in milk) comprise at least the protein coding
PT sequence and an expression regulation sequence.
XX
PS Example 16; SEQ ID NO 20; 96pp; English.
XX
CC This invention relates to a novel transgene for producing a recombinant
CC polypeptide in a bovine species comprising at least one expression
CC regulation sequence functional in at least one cell-type of the bovine
CC species, in addition to a gene encoding the desired polypeptide. The
CC transgenes and methods are useful for producing transgenic bovines which
CC produce useful polypeptides (for example enzymes, immunoglobulins, etc.
CC clotting factors), especially in their milk. The present sequence is that
CC of a PCR primer which was derived from plasmid DNA and was used during
CC the construction of a transgene cassette in the exemplification of the
CC invention.

SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADE76677 (1-19)

QY 32 ValValLysArgArg 36

DB 5 GTGTAAACGACGG 19

RESULT 255

AAQ05909/c

ID AAQ05909 standard; DNA; 20 BP.

XX

AC AAQ05909;

XX

DT 10-JAN-1991 (first entry)

XX

DE HIV mRNA translation inhibiting antisense oligonucleotide (f).

XX

KW Modified antisense oligonucleotide; HIV mRNA translation inhibition;

XX HIV-1; transactivator region; leader sequence; tat gene; probe; ss.

OS Synthetic.

XX

PN EP386563-A.

XX

PD 12-SEP-1990.

XX

PF 25-FEB-1990; 90BP-00103641.

XX

PR 09-MAR-1989; 89DE-03907562.

XX

PA (FARB) BAYER AG.

XX

XX Stropp U, Baugarten J, Lobberding A, Springer W, Piel N;

PI Kretschmer A, Kolbl H, Frommer W;

XX

DR WPI; 1990-276634/37.

XX

XX Chemically modified antisense oligo-nucleotide(s) - inhibiting

PT translation of HIV MRNA.

PT

PS Claim 3(f); Page 8; 15pp; German.

XX

CC The chemically modified sequences are opposed to the HIV-1 transactivator
 CC region, leader sequences (nt 21-53, 74-161, 202-279) or exon 2 or 3 of
 CC the tat gene (nt 5369-5403, 5421-5548, 5583-5617, 7967-8366, 8385-9183).
 CC This sequence comprises nt 5604-5623 and gives 90% inhibition of HIV-1
 CC tat translation in vitro at concns. of 5-25 microm. The sequence is
 CC useful for treating HIV infections and their complementary sequences can
 CC be used as probes to detect HIV. Chemical modification comprises
 CC replacing one or more internit phosphodiester linkages by phosphorothioate
 CC or methylphosphonate linkages. See also AAQ05904-11

SQ Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ05909 (1-20)

QY 10 LysPheLeuTyrcIn 14
 DB 17 AAGTTTCTCTATCAA 3

RESULT 256

AAQ20407

ID AAQ20407 standard; DNA; 20 BP.

XX

AC AAQ20407;

XX

DT 10-APR-1992 (first entry)

XX

DE Capture probe #1 for detecting HPV-6 or HPV-11 E7 gene DNA.

XX

KW Detection probe; sandwich hybridisation assay; human papilloma virus; ss.

XX

OS Synthetic.

XX

PN WO9119812-A.

XX

PD 26-DEC-1991.

XX

PF 11-JUN-1990; 90FR-00007249.

XX

PR 11-JUN-1990; 90FR-00007249.

XX

PA (INMR) BIO MERIEUX.

XX

XX Cros P, Allibert P, Mallet F, Mabilat C, Mandrand B;

PI

DR WPI; 1992-024428/03.

XX

XX Sandwich hybridisation of single strand nucleic acid - using short
 PT immobilised capture probe and detection probe with non-radioactive label,
 PT for diagnosing e.g. human papilloma virus or HIV.

XX

PS Claim 31; Page 37; 51pp; French.

XX

CC Target DNA corresponding to the E7 gene of HPV types 6 or 11 is detected
 CC using one or both of the capture probes AAQ20407 and AAQ20408 fixed
 CC passively to a solid hydrophobic support together with one or both of
 CC detection probe(s) AAQ20409 and AAQ20410 labelled with a non-radioactive
 CC marker. The capture and detection probes are able to hybridise to non-
 CC overlapping segments of the target sequence. See AAQ20389-Q20420 and
 CC AAQ20630-Q20663

SQ Sequence 20 BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ20407 (1-20)

QY 174 ArgGlnLeuArgArg 178

DB 1 AGACAGCTCAGAGA 15

XX

RESULT 257

AAQ52874

ID AAQ52874 standard; RNA; 20 BP.

XX

AC AAQ52874;

XX

DT 25-MAR-2003 (revised)

XX

DT 26-MAY-1994 (first entry)

XX

DE Cytomegalovirus target sequence 51.

XX

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAQ51057 (1-20)

QY 104 LeuSerLeuArgIle 108
DB 18 TTGAGGCTCAGAATC 4

RESULT 259

AAQ52403
ID AAQ52403 standard; DNA; 20 BP.

XX AC AAQ52403;

XX 25-MAR-2003 (revised)

DT 13-JUN-1994 (first entry)

XX

XX Sequence used for ligand synthesis in selection process.

XX Ligand; identification; target; selection; amplification; partition;
XX detection; binding; affinity; ss.

XX Synthetic.

XX US5270163-A.

XX 14-DEC-1993.

XX 17-AUG-1992; 92US-00931473.

XX 11-JUN-1990; 90US-00536428.

XX 10-JUN-1991; 91US-00714131.

XX (UYRE-) UNIV RES CORP.

XX Tuerk C, Gold L;

XX WPI; 1993-404920/50.

XX Identifying nucleic acids which bind target ligands - by partitioning
XX increased affinity nucleic acids from candidate mixt. and amplifying
XX these nucleic acids.

XX Example 2; Col 163-164; 129pp; English.

XX A method (SELEX) for identifying nucleic acid ligands which bind target
XX ligands comprises, contacting a candidate mixture with the target ligand
XX so that nucleic acids with an increased affinity for the target can be
XX partitioned from the remainder of the candidate mixture; partitioning the
XX increased affinity nucleic acids from the remainder of the candidate
XX mixture and amplifying them. Preferably this procedure is repeated
XX numerous times to yield a desired level of ligand enrichment. A template
XX molecule is used to produce the ligands present in the candidate mixture
XX and this oligonucleotide is used as a PCR primer for the production of
XX the candidate ligands and as a reverse transcriptase primer for an
XX inhibition assay. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAQ52403 (1-20)

QY 32 ValVallylsArgArg 36

DB 4 GTTGTAAACGACGG 18

RESULT 260

AAQ62617

ID AAQ62617 standard; DNA; 20 BP.

XX AC AAQ62617;

XX 25-MAR-2003 (revised)

DT 18-JAN-1995 (first entry)

XX

XX Probe to detect nucleic acid hybrids.

XX double helical structure; interactions; detection; probes;

XX nucleic acid hybrids; ss.

XX Synthetic.

XX EP599337-A2.

XX 01-JUN-1994.

XX 26-NOV-1993; 93EP-00119103.

XX 27-NOV-1992; 92JP-00318959.

XX 30-NOV-1992; 92JP-00320500.

XX (CANO) CANON KK.

XX Yamamoto N, Okamoto T, Tomida Y, Kawaguchi M, Makino K;

XX Murakami A;

XX WPI; 1994-169656/21.

XX Detection of nucleic acid hybrids - using a probe or reagent which causes
XX a detectable change by interaction through a double helical structure.

XX Example 1; Page 10; 22pp; English.

XX The probes (AAQ62617-20) were used in detection of a nucleic acid, in the
XX examples the M13mp18DNA (single stranded) is the target sequence. The
XX probe is labelled eg, with a spin labeling agent, and added to the sample
XX contg. the target nucleic acid. The detection of the target depends on
XX the formation of a double helical structure of a hybrid formed between
XX the probe and the target. Two or more reagents capable of causing a
XX detectable change by interaction through the double helical structure are
XX required, and at least one of these is attached to the probe. In this
XX example the reagent is 4-aminohexylamino-2,2',6,6'-tetramethylpiperidine-N-
XX oxyl (TEMPO), and the probe is partially complementary to the target. The
XX ESR spectrum was measured and showed that the spin of the TEMPO
XX disappeared as the result of the charge transfer from fluorescein to
XX TEMPO linked to the probe through the double helix formed from the probe
XX and the M13mp18DNA. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAQ62617 (1-20)

QY 32 ValVallylsArgArg 36

DB 1 GTTGTAAACGACGG 15

RESULT 261
AAQ62619
ID AAQ62619 standard; DNA; 20 BP.
XX AC AAQ62619;
XX DT 25-MAR-2003 (revised)
XX DT 18-JAN-1995 (first entry)
XX DE Probe to detect nucleic acid hybrids.
XX KW double helical structure; interactions; detection; probes;
XX KW nucleic acid hybrids; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*notes= "thiol-G"
FT modified_base 20 /*tag= b
FT /*note= "T-NH2"
XX EP599337-A2.
XX PD 01-JUN-1994.
XX PF 26-NOV-1993; 93EP-00119103.
XX PR 27-NOV-1992; 92JP-00318959.
XX PR 30-NOV-1992; 92JP-00320500.
XX XX (CANO) CANON KK.
XX YAMAMOTO N, OKAMOTO T, TOMIDA Y, KAWAGUCHI M, MAKINO K;
XX MURAKAMI A;
XX WPI; 1994-169656/21.
XX Detection of nucleic acid hybrids - using a probe or reagent which causes
XX FT a detectable change by interaction through a double helical structure.
XX PS Example 8; Page 14; 22pp; English.
XX CC The probes (AAQ62617-20) were used in detection of a nucleic acid, in the
XX CC examples the M13mp18DNA (single stranded) is the target sequence. The
XX CC probe is labelled eg, with a spin labeling agent, and added to the sample
XX CC contg. the target nucleic acid. The detection of the target depends on
XX CC the formation of a double helical structure of a hybrid formed between
XX CC the probe and the target. Two or more reagents capable of causing a
XX CC detectable change by interaction through the double helical structure are
XX CC required, and at least one of these is attached to the probe. In the
XX CC synthesis of this probe an amino group was introduced to the 3'terminal
XX CC end and a thiol group to the 5'terminal end. DAP2+ was linked to the
XX CC 3'end and acridine to the 5' end of the probe. The fluorescence of the
XX CC acridine was quenched as the result of charge transfer from acridine to
XX CC DAP2+ through the aid of the ds of the complex hybrid. (Updated on 25-MAR-
XX CC -2003 to correct PN field.)
XX SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0
US-09-966-880A-8 (1-198) x AAQ62619 (1-20)

QY 32 ValVallysArgArg 36
|||||
Db 1 GTTGTAAACGACGG 15
RESULT 262
AAQ82646/C
ID AAQ82646 standard; DNA; 20 BP.
XX AC AAQ82646;
XX DT 25-MAR-2003 (revised)
XX DT 14-SEP-1995 (first entry)
XX DE Chromosome 11 (locus GIF) STS primer GIF-Z.
XX KW sequence sampled mapping; genomic analysis; complex genome mapping;
XX KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX OS Synthetic.
XX XX W09429486-A1.
XX PD 22-DEC-1994.
XX PF 15-JUN-1994; 94WO-US006810.
XX PR 15-JUN-1993; 93US-00078471.
XX PR 07-SEP-1993; 93US-00117952.
XX PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX EVANS GA, SMITH MW;
XX WPI; 1995-036506/05.
XX Sequencing complex genomes, present as fragments in a cosmid library - by
XX FT sequencing end-specific nucleotides of each clone then correlating with
XX FT spatial relationship of cosmid, esp. for mammalian chromosomes.
XX PS Example 4; Page 91; 128pp; English.
XX CC Sequences were determined from the ends of chromosome 11-specific cosmids
XX CC by automated sequencing without intermediate subcloning. A sample of 371
XX CC DNA sequence fragments were determined and of these, 277 were suitable
XX CC for STS primer prediction by computer analysis (using the "Primer"
XX CC program available from E.lander, MIT). The STSs and cosmids were mapped
XX CC by in situ hybridisation, somatic cell hybrid analysis or both. Using
XX CC this method, 370 STSs specific for human chromosome 11 were generated and
XX CC most of them were regionally mapped. This procedure illustrates a novel
XX CC method for sequencing complex genomes, designated "sequence sampled
XX CC mapping". The sequence sampled mapping method is useful for the
XX CC completion of high density sequence-based maps, and ultimately, for the
XX CC complete sequencing of genomic DNA directly from cosmid clones. See
XX CC AAQ82001-Q82706 and AAQ91325-Q91358 for STS primers. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
XX SQ Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0
US-09-966-880A-8 (1-198) x AAQ82646 (1-20)
QY 57 ValGluleuLeuphe 61
|||||
Db 18 GTTGTAGCTGCTCTC 4
RESULT 263

```

AAQ82475/c
ID AAQ82475 standard; DNA; 20 BP.
XX
AC AAQ82475;
XX
DT 25-MAR-2003 (revised)
DT 13-SEP-1995 (first entry)
XX
DE Chromosome 11 (locus D11S1222) STS primer cSRL-6b1-tA.
XX
KW sequence sampled mapping; genomic analysis; complex genome mapping;
KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX
OS Synthetic.
XX
PN WO9429486-A1.
XX
PD 22-DEC-1994.
XX
PF 15-JUN-1994; 94WO-US006810.
XX
PR 15-JUN-1993; 93US-00078471.
PR 07-SEP-1993; 93US-00117952.
XX
(SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PA Evans GA, Smith MW;
XX
PI WPI; 1995-036508/05.
XX
PT Sequencing complex genomes, present as fragments in a cosmid library - by
PT sequencing end-specific nucleotides of each clone then correlating with
PT spatial relationship of cosmid, esp. for mammalian chromosomes.
XX
PS Example 4; Page 83; 128pp; English.
XX
CC Sequences were determined from the ends of chromosome 11-specific cosmids
CC by automated sequencing without intermediate subcloning. A sample of 371
CC DNA sequence fragments were determined and of these, 277 were suitable
CC for STS primer prediction by computer analysis (using the "Primer"
CC program available from E.Lander, MIT). The STSs and cosmids were mapped
CC by in situ hybridisation, somatic cell hybrid analysis or both. Using
CC this method, 370 STSs specific for human chromosome 11 were generated and
CC most of them were regionally mapped. This procedure illustrates a novel
CC method for sequencing complex genomes, designated "sequence sampled
CC mapping". The sequence sampled mapping method is useful for the
CC completion of high density sequence-based maps, and ultimately, for the
CC complete sequencing of genomic DNA directly from cosmid clones. See
CC AAQ82001-Q82705 for STS primers. (Also see AAQ91325-58). (Updated on 25-
CC MAR-2003 to correct FN field.)
XX
SQ Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e-03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ82475 (1-20)
Oy 127 ArgArgLeuHisArg 131
Db 18 AGAAGACTGCACAGA 4

RESULT 264
AAQ99196
ID AAQ99196 standard; DNA; 20 BP.
XX
AC AAQ99196;
XX
DT 07-MAR-1996 (first entry)
XX
DE Phage M13 DNA primer.
XX
KW Artificial male sterility; transgenic plant; barnase; toxin;
KW crop improvement; ribonuclease; DNA primer; ss.
XX
OS Synthetic.
XX
PN WO9520668-A1.
XX
PD 03-AUG-1995.
XX
PF 31-JAN-1995; 95WO-GB000188.
PF 31-JAN-1994; 94GB-00001780.
XX
(NICK-) NICKERSON BIOCHEM LTD.
(GENE-) GENE SHEARS PTY LTD.
XX
PI Paul W, Scott RJ, Betzner A, Huttner E, Lenee P, Perez P;
XX
WPI; 1995-275453/36.
XX
PT Prodn. of plants having a desired phenotypic trait - by crossing first
PT and second lines which lack the trait, where one of the lines is
PT transgenic.
XX
PS Disclosure; Page 45; 78pp; English.
XX
CC This phage M13 DNA primer and a phage T7 primer were used in a PCR to
CC obtain a mutant T7 promoter TEV leader Prglu' fragment from pWP178-TEV,
CC that is cloned into pluescriptII KS- as an XhoI, HindIII fragment,
CC forming plasmid pWP188-T7mut
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e-03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ99196 (1-20)
Oy 32 ValVallyshArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 265
AAQ99198
ID AAQ99198 standard; DNA; 20 BP.
XX
AC AAQ99198;
XX
DT 07-MAR-1996 (first entry)
XX
DE Phage M13 DNA primer.
XX
KW Artificial male sterility; transgenic plant; barnase; toxin;
KW crop improvement; ribonuclease; DNA primer; ss.
XX
OS Synthetic.
XX
PN WO9520668-A1.
XX
PD 03-AUG-1995.
XX
PF 31-JAN-1995; 95WO-GB000188.
PF 31-JAN-1994; 94GB-00001780.
XX

```


Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ90396 (1-20)

QY 56 HisValGluLeuLeu 60
 DB 18 CACGTAGAACTGCTC 4

RESULT 268

AAQ95469

ID AAQ95469 standard; DNA; 20 BP.

XX

AC AAQ95469;

XX

DT 14-FEB-1996 (first entry)

XX

DE Primer A5 (Group 4, set A) for a human chromosomal marker.

XX

KW primer; polymerase chain reaction; PCR; linkage study; locus;

KW

KW microsatellite marker sequence; automated genotyping; allele;

KW

XX polymorphism; detection; Homo sapiens; ss.

XX

OS Synthetic.

XX

PN WO9515400-A1.

XX

PD 08-JUN-1995.

XX

PF 05-DEC-1994; 94WO-US013945.

XX

PR 03-DEC-1993; 93US-00160837.

XX

PA (UYJO) UNIV JOHNS HOPKINS.

XX

PI Levitt RC;

XX

DR WPI; 1995-215278/28.

XX

PT Kit for automated genotyping contg. pairs of PCR primers - designed to amplify polymorphic nucleotide repeat sequences, arranged in sets each with a characteristic fluorescence label, useful e.g. in detection of disease related genetic rearrangement.

PT

PS Disclosure; Fig 7D-2; 104pp; English.

XX

CC The method aims to provide a collection of highly reproducible microsatellite marker sequences (WMS) at approx. 10-50 cm intervals throughout the human genome which can be detectably labelled. The WMS are polymorphic, simple sequence repeats and can be used in automated genotyping. esp. fluorescence-based. The primers correspond to the unique DNA sequence surrounding each marker, and PCR is used to detect each polymorphism. When the WMS show considerable polymorphism (ie. a difference in the number of repeats) between individuals, the markers can be particularly informative. The WMS can be ideal for linkage studies. CC Kits comprise at least 4 groups, of at least 3 sets, each comprising labelled primers for PCR amplification of the DNA. Group 4 primer pairs are shown in AAQ95465-480 and AAQ95559-530. The chromosomal markers, CC published size range of the allele and degree of heterozygosity in the CC population for the markers covered by these primer pairs are not given in CC the specification

XX

SQ Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ95469 (1-20)

QY 172 LeuSerArgGlnLeu 176

DB 2 CTAAGTAGGCAGTTG 16

RESULT 269

AAT07712

ID AAT07712 standard; DNA; 20 BP.

XX

AC AAT07712;

XX

DT 25-MAR-2003 (revised)

XX

DT 16-JUL-1996 (first entry)

XX

DE Oligonucleotide 9 used for selection of HIV-1 RT inhibitor.

XX

KW DNA polymerase; gp43; ligand; cell sorting; inhibitor; probe; T4; HIV-1; systematic evolution of ligands by exponential enrichment; SELEX; primer; bacteriophage coat protein; serine protease; mammalian receptor; amplify; mammalian hormone; mammalian growth factor; ribosomal protein; T7; PCR; viral rev protein; nerve growth factor; HSV; reverse transcriptase; polymerase chain reaction; ss.

XX

OS Synthetic.

XX

PN US5475096-A.

XX

PD 12-DEC-1995.

XX

PF 10-JUN-1991; 91US-00714131.

XX

PR 11-JUN-1990; 90US-00536428.

XX

PA (UYRE-) UNIV RES CORP.

XX

PI Tuerk C, Gold L;

XX

DR WPI; 1996-039557/04.

XX

PT Artificial nucleic acid ligands - for selected target proteins.

PT

PS Example 2; Col 171-172; 133pp; English.

XX

CC AAT07705-T07712 represent oligonucleotides used in the creation of a template for a systematic evolution of ligands by exponential enrichment (SELEX) reaction on HIV-1 reverse transcriptase (HIV-1 RT). This sequence was used as a 3' PCR primer and RT extension primer for the constructed sequence. In a SELEX reaction, a target molecule (such as HIV-1 RT) is contacted with a mixture of random nucleic acids under conditions favourable for binding. Unbound nucleic acids are then separated from those bound to the target, and the nucleic acid-target pairs are dissociated. The dissociated nucleic acids are amplified to give a ligand enriched mixture. These steps are repeated until the specific ligand is obtained. This procedure can also be carried out for ligands for bacteriophage coat proteins, serine proteases, mammalian receptors, mammalian hormones, mammalian growth factors, ribosomal proteins, DNA polymerases and viral rev proteins. The ligands identified (such as AAT07653-T07660) may be used in assays, diagnostic procedures, or cell sorting as an inhibitor of the target molecule function. It may also be used as a probe or sequestering agent, and also possess catalytic activity. (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT07712 (1-20)

QY 32 ValVallyeArgArg 36
|||||

Db 4 GTTGTAACGACGG 18

RESULT 270

AAT12093

ID AAT12093 standard; DNA; 20 BP.

XX AC AAT12093;

XX 10-JUL-1996 (first entry)

XX M. tuberculosis rpoB gene fragment amplification primer P3.

XX Antibiotic; resistance; spectrum; gene; mycobacterium; determination;

KW amplification; tuberculosis; rpoB; fragment; primer; differential;

KW hybridisation; pattern; rifampicin; rifabutin; species identification;

ss.

XX Synthetic.

OS WO9533851-A2.

XX 14-DEC-1995.

XX 09-JUN-1995; 95WO-EP002230.

XX 09-JUN-1994; 94EP-00870093.

XX (INNO-) INNOGENETICS NV.

XX De Beenhouwer H, Portaeels F, Machtelinckx L, Jannes G, Rossau R;

PI WPI; 1996-040250/04.

XX Probes and primers for determ. of antibiotic resistance spectrum of

PT Mycobacterium, opt. coupled with species identification - from different

PT patterns of hybridisation with rpoB gene.

XX Claim 22; Page 39; 69pp; English.

XX The antibiotic resistance spectrum (ARS) of a mycobacterium can be

CC determined by amplifying the relevant part of the antibiotic resistance

CC gene, i.e. the M. tuberculosis rpoB gene fragment amplified using the

CC primer set AAT12091-98, hybridising it with at least 1 rpoB gene probe,

CC detecting the hybrids formed and inferring the ARS, and opt. the spp.,

CC from the differential hybridisation patterns. The method is partic.

CC useful for the detection of rifampicin and/or rifabutin resistance in M.

CC leprae or M. tuberculosis, and mycobacterial spp. identification. The

CC method is rapid and reliable and provides simultaneous determ. of ARS

CC and spp. identity

XX SQ Sequence 20 BP; 2 A; 4 C; 10 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.44e+03 Length: 20

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT12093 (1-20)

QY 92 ArchHisValAlaAap 96
|||||

Db 4 CGGATGTCGGGAT 18

RESULT 271

AAT11459

ID AAT11459 standard; DNA; 20 BP.

XX AC AAT11459;

XX 10-SEP-1996 (first entry)

XX Retinoblastoma gene, RB1, exon 21 PCR 3' primer.

DE Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening;

KW mutation; polymerase chain reaction; PCR; ss.

XX Synthetic.

OS WO9601908-A1.

XX 25-JAN-1996.

XX 07-JUL-1995; 95WO-US008604.

XX 08-JUL-1994; 94US-00271942.

XX (VISI-) VISIBLE GENETICS INC.

FA (HSCR-) HSC RES & DEV LP.

XX Gallie BL, Dunn JM, Stevens JK, Hui M;

PI WPI; 1996-097637/10.

XX Identifying mutation(s) in RB1 exons by quantitative amplification - and

PT by comparing length of amplification products and sequencing, for

PT diagnosis and genetic screening of retinoblastoma.

XX Claim 12; Page 23; 48pp; English.

XX AAT11420-T11473 are PCR amplification primers used for the amplification

CC of exons 1 to 27 and the promoter of the human retinoblastoma RB1 gene,

CC used to amplify RB1 exons for use in a method of diagnosing mutations in

CC the RB1 gene. By comparing the lengths of amplification products of RB

CC exons from a suspected RB patient with those of RB wild-type DNA,

CC patients can be diagnosed early which may avoid the need for

CC radiotherapy. Any difference in length of exons between a suspected RB

CC patient and those from wild-type RB1 indicates either a deletion or

CC insertion mutation. Further sequencing of suspect exons can pinpoint the

CC mutation. The method is directed to the diagnosis of and targeted genetic

CC screening for retinoblastoma in family members of a retinoblastoma

CC patient

XX SQ Sequence 20 BP; 4 A; 2 C; 4 G; 10 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.44e+03 Length: 20

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT11459 (1-20)

QY 28 TyrLeuCysTyrVal 32
|||||

Db 2 TACCTATGTTATGTT 16
|||||

RESULT 272

AA32599

ID AA32599 standard; DNA; 20 BP.

XX AC AA32599;

XX 30-JUN-1999 (first entry)

XX Target DNA partly complementary to M13mp18 DNA.

XX Nucleic acid detection; pyrylium; virus; microbe; mutation detection;
KW infectious disease; diagnosis; target; ss.
XX Synthetic.
OS
XX EP684239-A1.
PN
XX 29-NOV-1995.
PD
XX 25-MAY-1995; 9SEP-00303567.
PF
XX 26-MAY-1994; 94JP-00112626.
PR
XX 07-JUN-1994; 94JP-00125040.
PR
XX (CANO) CANON KK.
PA
XX Yamamoto N, Okamoto T;
PI
XX WPI; 1996-000982/01.
DR
XX Detection of target substances such as DNA in samples - using at least
PT two reagents, one or more of these being a pyrylium cpd., which can
PT interact in the presence of the target cpd.
PT
XX Example 1; Page 70; 87pp; English.
PS
XX The invention relates to the detection of a target substance in a sample.
CC The method comprises: (a) providing at least two reagents (at least one
CC of which is a pyrylium cpd. of a specified formula) which can form a
CC reaction system for causing changes as a result of an interaction between
CC the reagents, the interaction being caused only when the target substance
CC is present in the sample; (b) reacting the reagents with the target
CC substance; and (c) measuring the resulting changes based on the
CC interaction. The methods allow detection of target substances using a
CC number of reagents which can form a reaction system causing a change
CC based on an interaction which mediates the target substance. They may be
CC used e.g. for detection and identification of desired base sequences of
CC nucleic acids (DNA or RNA) of viruses, microbes, animals, plants and
CC humans and detection of mutation in base sequences; for detection of
CC various substances with immune reactions such as immunoassays; and for
CC diagnosis of hereditary or infectious diseases. The methods do not
CC require B/F separation for detection of hybrid, comprise simple steps and
CC are highly sensitive. They allow accurate detection of desired hybrid
CC only, even when mismatched hybrid is present
XX
SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX32599 (1-20)

QY 32 ValValValysArgArg 36
Db 1 GTTGTAACACGCGG 15

RESULT 273
AAT12858
ID AAT12858 standard; DNA; 20 BP.
XX
AC AAT12858;
XX
DT 22-OCT-1996 (first entry)
XX
DE PCR 3' primer for exon 21 of human RB1 (retinoblastoma-1) gene.
XX PCR; polymerase chain reaction; retinoblastoma; tumour suppressor;
KW

KW cancer; mutation; identification; diagnosis; cystic fibrosis;
KW hierarchy assay; method; specificity; ss.
XX
OS Homo sapiens.
XX
PN WO9607761-A2.
XX
XX 14-MAR-1996.
PD
XX 07-JUL-1995; 95WO-US008606.
PF
XX 08-JUL-1994; 94US-00271946.
PR
XX (VISI-) VISIBLE GENETICS INC.
PA
XX Dunn JM, Stevens JK, Capatos D, Matthews DE;
PI WPI; 1996-171632/17.
XX
XX Testing for a disease-associated mutation in a gene - using a hierarchy
PT of tests selected to optimise performance while minimising cost.
PT
XX Example 1; Page 32; 63pp; English.
PS
XX AAT12839-T12899 (excluding AAT12878) are PCR primers used to amplify
CC various regions of the RB-1 genome, including exons 1-27, the promoter
CC region and a control sequence unrelated to RB-1 from chromosome 15. The
CC primers are used in an example of a method for testing a disease-
CC associated mutation in a gene, the gene may not necessarily be a tumour
CC suppressor gene like the retinoblastoma gene another example is the
CC cystic fibrosis transmembrane conductance regulator (CFTR) gene which may
CC be analysed using the same method. The primers are used in various
CC groupings to produce a hierarchical assay useful to test a group of
CC patients suspected to have a hierarchical mutation. The method allows the
CC optimum (or near optimum) diagnostic algorithm by considering the cost
CC and the sensitivity and specificity of each test
XX
SQ Sequence 20 BP; 4 A; 2 C; 4 G; 10 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT12858 (1-20)

QY 28 TyLeuCysTyrVal 32
Db 2 TACCTATGTTATGTT 16

RESULT 274
AAX01439
ID AAX01439 standard; DNA; 20 BP.
XX
AC AAX01439;
XX
DT 27-AUG-2003 (revised)
DT 28-APR-1999 (first entry)
XX
XX PCR primer #4 for M13 template.
DE
XX PCR primer; chain terminating nucleotide; protected 3'-hydroxyl group;
KW nucleic acid sequencing; nucleic acid synthesis; ss.
XX
OS Synthetic.
OS Enterobacteria phage M13.
XX
XX WO9623807-A1.
PN
XX 08-AUG-1996.
PD

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XX PF 30-JAN-1996; 96WO-SE0000096.
XX XX
XX PR 31-JAN-1995; 95SE-00000342.
XX XX
XX PA (KWIA/) KWIATKOWSKI M.
XX XX
XX PI Kwiatkowski M;
XX XX
XX DR WPI; 1996-371367/37.
XX XX
XX PT New nucleotide cpds. with a 3'-acetal function - useful as chain
XX PT terminating nucleotide(s) in the sequencing and synthesis of nucleic
XX PT acids.
XX XX
XX PS Example 6; Page 17; 32pp; English.
XX XX
XX CC This sequence represents a labelled PCR primer for a bacteriophage M13
XX CC sequence, the position of the label on this sequence is not specified.
XX CC The invention relates to novel nucleotide compounds, which can be used as
XX CC chain terminating nucleotides which have a protected 3'-hydroxyl group
XX CC which is readily deprotected by acid hydrolysis. As chain terminators
XX CC they can be deprotected to form nucleotides that may be further extended.
XX CC They can be used for sequencing of nucleic acids or for nucleic acid
XX CC synthesis. (Updated on 27-AUG-2003 to correct OS field.)
XX XX
XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX01439 (1-20)
QY 32 ValValLysArgArg 36
DB 5 GTTGTAACGACGG 19

RESULT 275
AAT10748/C
ID AAT10748 standard; RNA; 20 BP.
XX AC
XX AC AAT10748;
XX XX
XX DT 09-SEP-1996 (first entry)
XX XX
XX DE Oligonucleotide probe, A1-A5.
XX XX
XX KW Electronically self-addressable device; ED; electrode; current source;
XX KW attachment layer; permeable; counterion; genetic typing; probe;
XX KW detection; ss.
XX OS
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT modified_base 20
XX FT /*tag= a
XX FT /note= "3'-ribonucleoside terminus"
XX PN
XX PN WO9601836-A1.
XX XX
XX PD 25-JAN-1996.
XX XX
XX PF 05-JUL-1995; 95WO-US008570.
XX XX
XX PR 07-JUL-1994; 94US-00271882.
XX XX
XX PA (NANO-) NANOGEN INC.
XX XX

PI Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX WPI; 1996-097582/10.
XX XX
XX PT Electronically self-addressable device - used for electronic control of,
XX PT e.g. nucleic acid hybridisation.
XX XX
XX PS Example 1; Page 60; 155pp; English.
XX XX
XX CC The sequences given in AAT10742-67 are synthetic oligonucleotides which
XX CC are used in the construction of the electronically self-addressable
XX CC device (SD) of the invention. The SD comprises a substrate, an electrode
XX CC or opt. a number of electrodes supported by the substrate, a current
XX CC source operatively connected to the electrode and an attachment layer
XX CC adjacent to the electrode which is permeable to a counterion but not
XX CC permeable to a molecule capable of insulating or binding to the
XX CC electrode. The attachment layer is capable of attaching a macromolecule.
XX CC The SD is used for genetic typing and comprises a number of
XX CC electronically addressable locations each comprising an electrode, and a
XX CC binding entity, such as one of these probes, attached to each of the
XX CC locations capable of detecting the presence of a genetic sequence
XX XX
XX SQ Sequence 20 BP; 4 A; 3 C; 7 G; 5 T; 1 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT10748 (1-20)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGACTGCTC 4

RESULT 276
AAT58736
ID AAT58736 standard; cDNA; 20 BP.
XX AC
XX AC AAT58736;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 18-MAR-1997 (first entry)
XX XX
XX DE Alexandrium LsrDNA reverse primer, D2C.
XX KW
XX KW Probe; detection; Alexandrium; large-subunit ribosomal RNA gene; LsrDNA;
XX KW marine dinoflagellate; hypervariable domain; D1; D2; A. tamarense;
XX KW A. catenella; A. fundyense; ribotype; North American; Western European;
XX KW Temperate Asian; Tasmanian; Tropical Asian; Affine; Minutum; Andersoni;
XX KW ss.
XX OS
XX OS Synthetic.
XX XX
XX PN US5582983-A.
XX PD 10-DEC-1996.
XX XX
XX PF 14-JUN-1994; 94US-00259745.
XX XX
XX PR 28-OCT-1992; 92US-00967637.
XX XX
XX PA (WOOD-) WOODS HOLE OCEANOGRAPHIC INST.
XX XX
XX PI Scholin CA, Anderson DM;
XX XX
XX DR WPI; 1997-042301/04.
XX XX
XX PT Detection of Alexandrium dinoflagellates by nucleic acid hybridisation -
XX PT uses oligo:nucleotide(s) directed to the D2 hyper-variable domain of

```


PT large sub-unit of rRNA gene.
XX Example 1; Col 7; 48pp; English.

XX The sequences given in AAT58735-36 represent primers which were used in
CC the amplification of the large-subunit ribosomal RNA genes (LSrDNA) from
CC various strains of the marine dinoflagellates. The primers are targeted
CC to conserved elements at positions 24-45 (forward primer) and 733-714
CC (reverse primer) relative to the Procentrum micans LSrRNA. The
CC amplified fragment contains the evolutionarily variable domains D1 and
CC D2. Analysis of the LSrDNA has revealed hypervariable domains which
CC provide highly specific signature sequences useful in identifying and
CC detecting similar populations of Alexandrium. Analysis of the LSrDNA
CC sequence lead to the identification of five distinct Alexandrium
CC tamarensis/catenella/fundense ribotypes which were named with reference
CC to the geographic origin of the isolates: North American, Western
CC European and Temperate Asian designations reflect the origins of the
CC majority of cultures within each cluster. Tasmanian and Tropical Asian
CC designations reflect the origins of single A. tamarensis cultures.
CC Alexandrium species designations were used to identify the three
CC remaining ribotypes. Affine and Minutum were chosen for two of these
CC since their representatives are the most prominent within their
CC respective clusters. Andersoni was chosen to delineate the final
CC ribotype, reflecting both its unique LSrDNA sequence and the isolates
CC taxonomic classification. (Updated on 25-MAR-2003 to correct PF field.)
XX

SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT58736 (1-20)

QY 170 ValArgLeuSerArg 174
DB |||||
6 GTCCGCTCTTCAAGA 20

RESULT 277
AAT62432
ID AAT62432 standard; cDNA; 20 BP.
XX
AC AAT62432;
XX
DT 08-JUL-1997 (first entry)
XX
DE Bovine beta-mannosidosis carrier test sense primer MJ-124.
XX
KW Bovine; beta-mannosidase; enzyme; kidney; affinity chromatography;
KW antibody; primer; probe; PCR; polymerase chain reaction; amplification;
KW thyroid; hybridisation; detection; point mutation; beta-mannosidosis;
KW cattle; carrier; Saler breed; ss.
XX
OS Synthetic.
XX
PN US5605797-A.
XX
PD 25-FEB-1997.
XX
PF 15-SEP-1994; 94US-00306546.
XX
PR 15-SEP-1994; 94US-00306546.
XX
PA (UNMS) UNIV MICHIGAN STATE.
XX
PI Cavanagh KT, Chen H, Friderici K, Jones MZ;
XX
DR WPI; 1997-153571/14.
XX

PT Oligo:nucleotide fragments of bovine beta-mannosidase gene - for
PT detecting mutation associated with beta-mannosidosis.
XX
PS Example 2; Col 18; 39pp; English.

XX The primers AAT62432-3 were used to detect beta-mannosidosis carriers by
CC detecting a mutation in the beta-mannosidase gene (AAT62419). The method
CC of detection is artificial introduction of restriction site (AIRS) which
CC involves amplifying a 187 bp fragment of the genomic sequence around the
CC point mutation and selectively introducing a BstNI restriction enzyme
CC site, especially in the wild type sequence. The mutant sequence will not
CC contain this site after amplification. Thus upon restriction digestion
CC with BstNI, wild type and mutant sequences can be separated. This primer
CC corresponds to bases 2554-2573 of the bovine beta-mannosidase gene
CC sequence. The assays can be used to identify cattle that are carriers of
CC beta-mannosidosis, e.g. in the Saler breed

SQ Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT62432 (1-20)

QY 179 IleuLeuProLeu 183
DB |||||
6 ATTCCTTTACCCCTG 20

RESULT 278
AAV00799
ID AAV00799 standard; RNA; 20 BP.
XX
AC AAV00799;
XX
DT 25-MAR-1998 (first entry)
XX
DE 3' PCR primer for SELEX ligands to HIV-1 RT.

XX Systematic evolution of ligands by exponential enrichment; SELEX; PCR;
KW binding affinity; diagnosis; inhibitor; probe; catalyst; template; ss;
KW human immunodeficiency virus type 1; reverse transcriptase; primer;
KW amplification.
XX
OS Synthetic.
XX
PN US5670637-A.
XX
PD 23-SEP-1997.
XX
PF 27-MAR-1995; 95US-00412110.
XX
PR 11-JUN-1990; 90US-00536428.
PR 10-JUN-1991; 91US-00714131.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Tuerk C, Gold L;
XX
DR WPI; 1997-479527/44.
XX
PT Nucleic acid ligands for binding proteins - obtained by systematic
PT evolution of ligands by exponential enrichment procedures.

XX Example 2; Col 55; 133pp; English.
XX This oligonucleotide is used in the generation of a template for the
CC isolation of nucleic acid ligands which bind the human immunodeficiency
CC virus type 1 (HIV-1) reverse transcriptase. The ligands are isolated by

CC the systematic evolution of ligands by exponential enrichment (SELEX)
 CC method of the invention. This method is especially used to isolate novel
 CC non-naturally occurring nucleic acid ligands having a specific binding
 CC affinity for a target molecule, where the target molecule is a protein
 CC and the nucleic acid ligand is not a nucleic acid known to bind the
 CC target molecule. The nucleic acid ligands can be used, e.g. in assay
 CC methods, diagnostic procedures, cell sorting, as inhibitors of target
 CC molecule function, as probes, as sequestering agents, for therapy or as
 CC catalysts

SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV00799 (1-20)

QY 32 ValVallyeArgArg 36
 DB 4 GTTGTAAACGACGG 18

RESULT 279

AAV02707
 ID AAV02707 standard; DNA; 20 BP.

AC AAV02707;

DT 19-MAY-1998 (first entry)

DE Human Class I HLA-G gene exon 2 PCR primer 1.

KW Human leukocyte antigen class I gene; HLA-G; allele testing; donor;
 KW tissue matching; recipient; graft rejection; class typing; ds.

XX Synthetic.

OS Homo sapiens.

XX WO9723645-A1.

XX 03-JUL-1997.

XX 04-JAN-1996; 96WO-US000362.

XX 04-JAN-1996; 96WO-US000362.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Yang SY, Cereb N;

XX WPI; 1997-351080/32.

PT DNA-based human leukocyte antigen class I gene typing method - useful for
 PT tissue matching and prevention of graft versus host disease.

XX Claim 16; Page 18; 89pp; English.

CC AAV02707 and AAV02708 are PCR primers used to amplify the human leukocyte
 CC antigen (HLA) Class I HLA-G gene exon 2, which is used in a novel method
 CC for testing a tissue sample to determine the allelic type of a HLA class
 CC I gene in the sample. The HLA class I gene is selected from among HLA-A,
 CC -B and -C genes. The method comprises of treating the tissue sample to
 CC obtain nucleic acid polymers suitable for amplification then combining
 CC these polymers with a first primer which hybridises with a portion of
 CC intron 1 or intron 3 of the HLA Class I gene and a second primer which
 CC hybridises with a different portion of the HLA Class I gene under
 CC conditions suitable for amplification to obtain an amplified product. The
 CC product is then evaluated to determine the allelic type of the HLA-Class
 CC I gene. The method is useful for tissue matching HLA class I antigens

CC between donors and recipients and hence for preventing graft versus host
 CC disease
 XX SQ Sequence 20 BP; 2 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV02707 (1-20)

QY 35 ArgArgAspSerAla 39
 DB 5 CGACGCGACTCGCG 19

RESULT 280

AAV20877

ID AAV20877 standard; cDNA; 20 BP.

XX AAV20877;

DT 28-JUL-1998 (first entry)

DE Mouse specific 5' PCR primer.

KW Rat interferon-gamma inducing factor; IGIF; interleukin-18; IL-18;
 KW IL-18-alpha; transfection; antibody; probe; hybridisation; PCR;
 KW amplification; primer; ss.

XX Synthetic.

OS Mus sp.

XX WO9810072-A1.

XX 12-MAR-1998.

XX 08-SEP-1997; 97WO-US015891.

XX 09-SEP-1996; 96US-0025141P.

XX 08-APR-1997; 97US-0043087P.

XX (CORR) CORNELL RES FOUND INC.

XX Joh TH, Conti B;

XX WPI; 1998-193622/17.

PT Rat interferon-gamma inducing factors and related DNA - useful for
 PT quantitating stress in a mammal.

XX Example 1; Page 34; 47pp; English.

CC This is the nucleotide sequence of the mouse specific 5' PCR primer used
 CC in the amplification of the isolated rat interferon-gamma inducing factor
 CC (IGIF), also known as interleukin-18 (IL-18). It can be used to transform
 CC a cell, which upon its expression can cause the cell to produce rat IGIF,
 CC i.e. IL-18 or IL-18 alpha. The antibody to IGIF, IGIF and probes derived
 CC from it, are useful for detection of IL-18 or IL-18 alpha present in a
 CC sample. The amount of IL-18 or IL-18 alpha in a sample can be used to
 CC quantitate stress in a mammal

SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0

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DB:      2      Gaps:      0
US-09-966-880A-8 (1-198) x AAV20877 (1-20)
QY      53 AenglyCyHisVal 57
      |||||
DB      4 AATGGCTGCATGTC 18
      |||||
RESULT 281
AAV44624
ID      AAV44624 standard; DNA; 20 BP.
XX
AC      AAV44624;
XX
DT      24-NOV-1998 (first entry)
XX
DE      Human uncoupling protein-2 UCP2 gene primer hUCP2.CDSR3.
XX
KW      Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
KW      obesity; hyperinsulinaemia; glucose intolerance; diabetes; syndrome X;
KW      hypothermia; wasting; cachexia; anorexia; inflammation; fever;
KW      hyperthermia; gene therapy; diagnosis; PCR; primer; ss.
XX
OS      Synthetic.
OS      Homo sapiens.
XX
PN      M09831396-A1.
XX
PD      23-JUL-1998.
XX
PF      22-APR-1997; 97WO-US006864.
XX
PR      15-JAN-1997; 97US-0034960P.
XX
PA      (UYDU-) UNIV DUKE.
PA      (REGC) UNIV CALIFORNIA.
PA      (CNRS) CENT NAT RECH SCI.
XX
XX      Surwit RS, Collins SA, Warden CH, Seldin MF, Ricquier D;
PI      Bouillaud F;
PI      WPI; 1998-413823/35.
XX
XX      Method for treating disease associated with altered UCP-2 expression - by
PT      administering agent which enhances or inhibits UCP-2 activity,
PT      effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
PT      etc.
XX
PS      Disclosure; Fig 1F; 98pp; English.
XX
CC      Primer hUCP2.CDSR3 is used with forward primer hUCP2.CDSF3 (see AAV44623)
CC      in the PCR amplification of a 1096 bp region of the human uncoupling
CC      protein-2 (UCP2) gene coding sequence (see also AAV44595). The primers
CC      were also used in a RACE amplification of human UCP2 cDNA. The invention
CC      relates to a method for treating diseases associated with altered UCP2
CC      expression, such as obesity, diabetes, syndrome X, hypothermia,
CC      hyperinsulinaemia, glucose intolerance, wasting, anorexia, inflammation,
CC      cachexia, fever or hyperthermia
XX
SQ      Sequence 20 BP; 9 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      9.44e+03      Length:      20
Score:          5.00      Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:            2      Gaps:      0

US-09-966-880A-8 (1-198) x AAV44624 (1-20)
QY      22 LysGlyArgArgGlu 26
      |||||

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DB      5 AAGGAGAGGAGGAA 19
RESULT 282
AAV27092/C
ID      AAV27092 standard; DNA; 20 BP.
XX
AC      AAV27092;
XX
DT      25-MAR-2003 (revised)
DT      16-SEP-1998 (first entry)
XX
DE      Primer YA6.
XX
KW      ss; Human; double-stranded adenosine deaminase; neurological disorder;
KW      CNS disorder; PCR; primer; amplification.
XX
OS      Synthetic.
XX
PN      US5763174-A.
XX
PD      09-JUN-1998.
XX
PF      13-NOV-1995; 95US-00555678.
XX
PR      17-FEB-1994; 94US-00197794.
PR      25-JUL-1994; 94US-00280443.
PR      01-JUN-1995; 95US-00457459.
XX
XX      (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX      Nishikura K;
XX      WPI; 1998-347307/30.
XX
XX      Diagnosis of disorders characterised by inappropriate expression of
XX      enzyme - comprises contacting tissue sample with labelled antibodies,
XX      oligonucleotides or protein reagent and measuring association of enzyme.
XX      Example 10; Col 21; 66pp; English.
XX
XX      The primers AAV27072-V27099 were used in the isolation, amplification and
XX      characterisation of double-stranded adenosine deaminase (DRADA). DRADA is
XX      specific for double-stranded RNA and is useful for the diagnosis of
XX      disorders characterised by inappropriate double-stranded ribonucleic acid
XX      adenosine deaminase expression. Particularly for diagnosis of certain
XX      neurological or CNS disorders, e.g. Alzheimer's disease, Huntington's
XX      disease, subacute sclerosing panencephalitis, measles inclusion body
XX      encephalitis or stroke, or other neurological conditions associated with
XX      aging. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ      Sequence 20 BP; 7 A; 1 C; 9 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      9.44e+03      Length:      20
Score:          5.00      Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:            2      Gaps:      0

US-09-966-880A-8 (1-198) x AAV27092 (1-20)
QY      38 SerAlaThrSerPhe 42
      |||||
DB      17 TCAGCCACATCCTTC 3
      |||||
RESULT 283
AAV27081
ID      AAV27081 standard; DNA; 20 BP.
XX
AC      AAV27081;
XX
DT      25-MAR-2003 (revised)

```

DT 16-SEP-1998 (first entry)
 XX
 DE Primer YS5.
 XX
 KW ss; Human; double-stranded adenosine deaminase; neurological disorder;
 KW CNS disorder; PCR; primer; amplification.
 XX
 XX Synthetic.
 OS
 XX US5763174-A.
 PN
 XX 09-JUN-1998.
 PD
 XX 13-NOV-1995; 95US-00555678.
 PF
 XX 17-FEB-1994; 94US-00197794.
 PR
 XX 25-JUL-1994; 94US-00280443.
 PR
 XX 01-JUN-1995; 95US-00457459.
 XX
 XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 PA
 XX Nishikura K;
 PI
 XX WPI; 1998-347307/30.
 DR
 XX Diagnosis of disorders characterised by inappropriate expression of
 PT enzyme - comprises contacting tissue sample with labelled antibodies,
 PT oligonucleotides or protein reagent and measuring association of enzyme.
 XX
 XX Example 10; Col 21; 66pp; English.
 PS
 XX The primers AAV27072-V27099 were used in the isolation, amplification and
 CC characterisation of double-stranded adenosine deaminase (DRADA). DRADA is
 CC specific for double-stranded RNA and is useful for the diagnosis of
 CC disorders characterised by inappropriate double-stranded ribonucleic acid
 CC adenosine deaminase expression. Particularly for diagnosis of certain
 CC neurological or CNS disorders, e.g. Alzheimer's disease, Huntington's
 CC disease, subacute sclerosing panencephalitis, measles inclusion body
 CC encephalitis or stroke, or other neurological conditions associated with
 CC aging. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 20 BP; 3 A; 9 C; 1 G; 7 T; 0 U; 0 Other;
 Alignment Scores: Length: 20
 Pred. No.: 9.44e+03 Matches: 5
 Score: 5.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAV27081 (1-20)
 Qy 38 SerAlaThrSerPhe 42
 Db 4 TCAGCCACATCCTC 18
 RESULT 284
 AAV48030
 ID AAV48030 standard; DNA; 20 BP.
 XX
 AC AAV48030;
 XX
 XX 19-OCT-1998 (first entry)
 DT
 XX Murine B7-1 targetted oligonucleotide 14915.
 DE
 XX ss; mouse; B7; T cell; inflammation; autoimmune disease; cell activation;
 KW cell proliferation.
 KW
 XX Synthetic.
 OS
 XX Homo sapiens.
 XX

FH Key Location/Qualifiers
 PT modified_base 1..20
 FT /tag= a
 FT /note= "Phosphorothioate linkages"
 XX
 XX W09829124-A1.
 PN
 XX 09-JUL-1998.
 PD
 XX 16-DEC-1997; 97WO-US023270.
 PF
 XX 31-DEC-1996; 96US-00777266.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CF, Vickers TA;
 PI
 XX WPI; 1998-387783/33.
 DR
 XX New oligo:nucleotide(s) that modulate expression of B7 proteins - used
 PT for, e.g. controlling activation and proliferation of T cells,
 PT particularly for treatment, diagnosis and prevention of inflammation.
 XX
 XX Example 1; Page 36; 120pp; English.
 PS
 XX The oligonucleotides which specifically hybridise to B7 modulate its
 CC expression (and thus T cell activation and proliferation). This is
 CC particularly useful for treatment and prevention of inflammation and
 CC autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,
 CC Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,
 CC (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,
 CC rhinitis, allergy, cancer and metastases. The oligonucleotides may also
 CC be used to manipulate T cell activation ex vivo; to determine or detect
 CC B7 protein expression; for diagnosis; as assay and purification reagents,
 CC and to study physiological roles of B7 proteins
 XX
 SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;
 Alignment Scores: Length: 20
 Pred. No.: 9.44e+03 Matches: 5
 Score: 5.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAV48030 (1-20)
 Qy 176 LeuArgArgIleLeu 180
 Db 1 CTGCGCGAATCCTG 15
 RESULT 285
 AAV14584
 ID AAV14584 standard; DNA; 20 BP.
 XX
 AC AAV14584;
 XX
 XX 27-AUG-2003 (revised)
 DT
 XX 21-MAY-1998 (first entry)
 DE
 XX Sequence used in construction of SELEX template for T4 polymerase.
 KW High affinity RNA ligand motif; polymer binding; cell sorting; inhibitor;
 KW systematic evolution of ligands by exponential enrichment; SELEX;
 KW sequestering agent; bacteriophage T4 DNA polymerase; ss.
 XX
 XX Synthetic.
 OS
 XX Enterobacteria phage T4.
 PN
 XX US5696249-A.
 XX
 XX 09-DEC-1997.
 PD

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XX 24-MAR-1995; 95US-00409442.
XX
XX 11-JUN-1990; 90US-00536428.
XX
PR 10-JUN-1991; 91US-00714131.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Tuerk C, Gold L;
XX
XX WPI; 1998-041356/04.
XX
XX Synthetic nucleic acid ligands - that bind to target molecules other than
XX nucleic acids.
XX
XX Example 1; Col 54; 137pp; English.
XX
XX This sequence represents a sequence used to prepare the template for a
XX systematic evolution of ligands by exponential enrichment (SELEX)
XX reaction to isolate ligands specific for the bacteriophage T4 DNA
XX polymerase. The identified sequences are examples of the ligands of the
XX invention. The ligands are non-naturally occurring nucleic acid ligand
XX with specific binding affinity for a target molecule, where: the target
XX molecule is not a polynucleotide that binds to the ligand by Watson-Crick
XX base pairing or triple helix binding; the ligand is not a nucleic acid
XX having the known physiological function of being bound by the target
XX molecule; and the ligand is obtained by: (a) contacting the target
XX molecule with a candidate mixture of nucleic acids, each having a region
XX of randomised sequence; (b) separating the nucleic acids having the
XX highest affinity for the target; and (c) amplifying the separated nucleic
XX acids. Ligands as above that bind to natural or synthetic polymers, e.g.
XX proteins, polysaccharides, glycoproteins, hormones, receptors, cell
XX surfaces, drugs, metabolites, cofactors, transition-state analogues or
XX toxins, may be useful in assays, diagnostic procedures or cell sorting,
XX as inhibitors of target molecule function, as probes, as sequestering
XX agents, etc.; or may have catalytic activity. (Updated on 27-AUG-2003 to
XX correct OS field.)
XX
XX Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV14584 (1-20)

QY 32 ValVallyLysArgArg 36
DB 4 GTTGTAAACGACGG 18

RESULT 286
AAV28063
ID AAV28063 standard; DNA; 20 BP.
XX
XX AAV28063;
AC
XX
XX 25-SEP-1998 (first entry)
DT
XX
XX Ataxia telangiectasia exon 53 primer 2.
DE
XX
XX ss; PCR; primer; amplification; ataxia telangiectasia; diagnosis; human;
XX radiation; breast cancer.
KW
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO9822621-A1.
XX
XX 28-MAY-1998.
XX

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XX 17-NOV-1997; 97WO-US020953.
XX
XX 20-NOV-1996; 96US-00753147.
XX
XX (VIRG-) VIRGINIA MASON RES CENT.
XX
XX Concannon P;
PI
XX
XX WPI; 1998-312503/27.
XX
XX Method of detecting ataxia telangiectasia - comprises use of primers
XX based on intron-exon boundaries, useful for diagnosing disease in
XX heterozygotes.
XX
XX Claim 6; Page 8; 47pp; English.
XX
XX The primers AAV27964-V28086 are used to amplify ataxia telangiectasia
XX (ATM) exons and their adjacent splice junction sites. These can be used
XX as a method of detecting a mutation in the ATM gene by comparing the PCR
XX products of amplification from a sample from a patient suspected of
XX having an ATM mutation with a sample from a non-mutated ATM patient. This
XX method is especially useful for diagnosing ataxia telangiectasia in
XX heterozygotes and can be used to locate the positions of the mutation.
XX The diagnosis of ataxia telangiectasia in patients needing therapeutic
XX radiation will prevent fatal radiation burns and the development of
XX breast cancer which can occur
XX
XX Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV28063 (1-20)

QY 97 PheLeuArgGlyAsn 101
DB 4 TTCTTAGAGGGAAT 18

RESULT 287
AAZ09818
ID AAZ09818 standard; DNA; 20 BP.
XX
XX AAZ09818;
AC
XX
XX 26-NOV-1999 (first entry)
DT
XX
XX Phytophthora citricola PCR primer CITR1.
DE
XX
XX PCR primer; detection; pathogenic; oak; beech; tree; probe; screening;
XX natural forest; infection; nursery; disease-resistant genotype;
XX asymptomatic tissue; ss.
XX
XX Phytophthora citricola.
OS
XX
XX EP949337-A2.
XX
XX 13-OCT-1999.
XX
XX 01-APR-1999; 99EP-00105198.
XX
XX 03-APR-1998; 98DE-01015138.
XX
XX (GSFS-) GSF GES STRAHLEN & UMWELTFORSCH GMBH.
XX
XX Bahnweg G, Schubert R, Sandermann H, Mueller-Starck G;
XX
XX WPI; 1999-553461/47.
XX

```

XX Primers for species-specific detection of Phytophthora species,
PT especially in oak and beech trees.
XX
PS Claim 1; Page 11; 19pp; German.
XX
CC This invention describes novel PCR primers for species-specific detection
CC of Phytophthora spp. The primers can be used to detect, quantify or
CC distinguish between Phytophthora spp. that are pathogenic to oak and
CC beech trees, either (a) in pairs as primers per se in a conventional
CC polymerase chain reaction or (b) individually as probes in conventional
CC hybridization assays. The assays can be used for mass screening of
CC natural forest trees to prevent spread of infection to nursery material,
CC and in the development of disease-resistant genotypes. The primers do not
CC cross-react with DNA from other species and can be used in assays capable
CC of detecting pathogenic Phytophthora spp. in asymptomatic tissues of oak
CC and beech trees. AAZ09816-409825 represent the PCR primers and probes
CC used in the method of the invention
XX
SQ Sequence 20 BP; 1 A; 5 C; 4 G; 10 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ09818 (1-20)

QY 59 LeuLeuPheLeuArg 63
DB 3 TTGCTTTTTCGA 17

RESULT 288
AAZ77443/C
ID AAX77443 standard; DNA; 20 BP.
XX
AC AAX77443;
XX
XX 05-AUG-1999 (first entry)
XX
XX JP11127897 primer 5.
XX
XX Detection; primer; hybridisation; target; probe; interaction;
XX electron current; double helix; ss.
XX
XX Synthetic.
XX
XX JP11127897-A.
XX
XX 18-MAY-1999.
XX
XX 31-OCT-1997; 97JP-00300944.
XX
XX 31-OCT-1997; 97JP-00300944.
XX
XX (CANO) CANON KK.
XX
XX WPI; 1999-350344/30.
XX
XX Detection of a target nucleic acid - using substances capable of
XX interaction with a phenomenon which allow electron current in the double
XX helix structure bound via a linker.
XX
XX Example 3; Page 6; 7pp; Japanese.
XX
CC This invention describes a novel method for the detection of a target
CC nucleic acid and a probe nucleic acid hybrid in a sample, comprising (1)
CC substances capable of interaction with a phenomenon which allow electron
CC current in the double helix structure bound via a linker (2)
CC immobilisation of the base sequence of target nucleic acid and the probe

CC nucleic acid having complementary base sequence of the target nucleic
CC acid on a predetermined site of a carrier (3) contact of the probe
CC nucleic acid and the sample under a condition capable of forming a hybrid
CC of the target nucleic acid and the probe nucleic acid (4) supply of the
CC labelled unit on the predetermined site of the carrier presumed to form
CC the hybrid (5) detection of change of 1st and/or 2nd labelled
CC substance(s) in the labelled unit supplied to the predetermined site and
CC (6) detection of the presence of the hybrid in the sample. This sequence
CC represents a primer used in the method of the invention
XX
SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX77443 (1-20)

QY 32 ValVallysArgArg 36
DB 20 GTTGTAACGACGG 6

RESULT 289
AAZ77439
ID AAX77439 standard; DNA; 20 BP.
XX
AC AAX77439;
XX
XX 05-AUG-1999 (first entry)
XX
XX JP11127897 primer 1.
XX
XX Detection; primer; hybridisation; target; probe; interaction;
XX electron current; double helix; ss.
XX
XX Synthetic.
XX
XX JP11127897-A.
XX
XX 18-MAY-1999.
XX
XX 31-OCT-1997; 97JP-00300944.
XX
XX 31-OCT-1997; 97JP-00300944.
XX
XX (CANO) CANON KK.
XX
XX WPI; 1999-350344/30.
XX
XX Detection of a target nucleic acid - using substances capable of
XX interaction with a phenomenon which allow electron current in the double
XX helix structure bound via a linker.
XX
XX Example 1; Page 6; 7pp; Japanese.
XX
CC This invention describes a novel method for the detection of a target
CC nucleic acid and a probe nucleic acid hybrid in a sample, comprising (1)
CC substances capable of interaction with a phenomenon which allow electron
CC current in the double helix structure bound via a linker (2)
CC immobilisation of the base sequence of target nucleic acid and the probe
CC nucleic acid having complementary base sequence of the target nucleic
CC acid on a predetermined site of a carrier (3) contact of the probe
CC nucleic acid and the sample under a condition capable of forming a hybrid
CC of the target nucleic acid and the probe nucleic acid (4) supply of the
CC labelled unit on the predetermined site of the carrier presumed to form
CC the hybrid (5) detection of change of 1st and/or 2nd labelled
CC substance(s) in the labelled unit supplied to the predetermined site and
CC (6) detection of the presence of the hybrid in the sample. This sequence
CC represents a primer used in the method of the invention

AAK15307
ID AAK15307 standard; DNA; 20 BP.
XX
AC AAK15307;
XX
DT 29-APR-1999 (first entry)
XX
DE PCR primer F5S1 for DNA encoding a DNA polymerase binding factor F5.
XX
KW Thermostable polypeptide factor; DNA synthesis activity; DNA polymerase;
KW in vitro DNA synthesis; PCR primer; ss.
XX
OS Synthetic.
OS Pyrococcus furiosus.
XX
PN WO9900506-A1.
XX
PD 07-JAN-1999.
XX
PF 24-JUN-1998; 98WO-JP002845.
XX
PR 26-JUN-1997; 97JP-00187496.
PR 21-NOV-1997; 97JP-00320692.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
PI Uemori T, Sato Y, Fujita T, Miyake K, Mukai H, Asada K, Kato I;
XX
DR WPI; 1999-095751/08.
XX
PT Thermostable polypeptide factors promoting the activity of DNA polymerase
PT - for improvement of DNA synthesis and amplification in vitro.
XX
PS Example 12; Page 138; 177pp; Japanese.
XX
CC PCR primers AAK15307-08 were used to amplify Pyrococcus furiosus DNA
CC encoding a thermostable polypeptide factor. This factor binds to, and
CC promotes the DNA synthesis activity of DNA polymerase. The polymerase
CC related factors can be used to provide more efficient in vitro DNA
CC synthesis and amplification systems (e.g. for polymerase chain reaction)
CC by using the factors in conjunction with a DNA polymerase
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAK15307 (1-20)

QY 156 GLUArgThrPheLys 160
Db 3 GAGAGAACTTCAAG 17

RESULT 293
AAK81307/C
ID AAK81307 standard; DNA; 20 BP.
XX
AC AAK81307;
XX
DT 20-AUG-1999 (first entry)
XX
DE 3' ribonucleoside oligonucleotide probe AT-A5.
XX
KW Microelectronic device; multi-step reaction; microscopic format;
KW ion-permeable permeation layer; electrode; electrical control; transport;
KW attachment; binding; DNA/RNA hybrid; probe; ss.
XX
OS Synthetic.

XX Key Location/Qualifiers
FH misc_RNA 20
FT /*tag= a
XX
PN WO9929711-A1.
XX
PD 17-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US025475.
XX
PR 05-DEC-1997; 97US-00986065.
XX
PA (NANO-) NANOGEN INC.
XX
PI Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;
XX
DR WPI; 1999-385567/32.
XX
PT New microelectronic device designed to carry out and control multi-step
XX and multiplex molecular biological reactions in microscopic format.
XX
PS Example 1; Page 89; 179pp; English.
XX
CC The specification describes a self-addressable, self-assembling
CC microelectronic device which is designed to actively carry out and
CC control multi-step and multiplex molecular biological reactions in
CC microscopic formats. A key aspect of this invention is played by the ion
CC -permeable permeation layer which overlies the electrode. This permeation
CC layer allows attachment of nucleic acids to permit immobilization but
CC also separates the attached oligonucleotides and hybridized target DNA
CC sequences from the highly reactive electrochemical environment generated
CC immediately at the electrode surface. The microelectronic device is
CC designed and fabricated to actively carry out and control reactions such
CC as nucleic acid hybridizations, antibody/antigen reactions, sample
CC preparation, diagnostics and biopolymer synthesis. The device can
CC electronically control the transport and attachment of specific binding
CC entities, such as nucleic acids and polypeptides, to specific micro-
CC locations. The device can subsequently control the transport and reaction
CC of analytes or reactants at the addressed specific micro-locations. The
CC device is able to concentrate analytes and reactants, remove non-
CC specifically bound molecules, provide stringency control for DNA
CC hybridization reactions and improve the detection of analytes. The
CC present sequence represents a probe used to exemplify the invention
XX
SQ Sequence 20 BP; 4 A; 3 C; 7 G; 5 T; 1 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAK81307 (1-20)

QY 56 HisValGluLeuLeu 60
Db 18 CAGTAGAACTGCTC 4

RESULT 294
AAK76912
ID AAK76912 standard; DNA; 20 BP.
XX
AC AAK76912;
XX
DT 05-AUG-1999 (first entry)
XX
DE Probe used to test nucleic acid detection method.
XX
KW Nucleic acid detection; probe; ss.
XX

OS Synthetic.
 XX JP11127862-A.
 PN
 XX
 PD 18-MAY-1999.
 XX
 XX 31-OCT-1997; 97JP-00300943.
 XX
 XX 31-OCT-1997; 97JP-00300943.
 XX
 XX (CANO) CANON KK.
 PA
 XX
 DR WPI; 1999-350323/30.
 XX
 XX Detection of a target nucleic acid - using a labelled unit with labels
 PT capable of interactive action in a phenomenon of electron flow in double
 PT helix structure.
 XX
 XX Example 1; Page 4; 9pp; Japanese.
 PS
 CC This sequence is a probe used to test the method of the invention. The
 CC method is for the detection of a hybrid of a target nucleic acid and a
 CC probe nucleic acid in a sample comprises: (1) preparation of a labelled
 CC unit composed of 1st and 2nd labelled substances capable of interactive
 CC action in a phenomenon of electron flow in double helix structure in the
 CC presence of a hybrid via a linker; (2) addition of a probe nucleic acid
 CC having a complementary base sequence to the base sequence of target
 CC nucleic acid; (3) placing the sample under conditions capable of forming
 CC the target nucleic acid and the probe nucleic acid to give a hybrid; (4)
 CC mixing the sample capable of forming the hybrid and the labelled unit;
 CC (5) detection of the change in the 1st and/or 2nd labelled substances
 CC caused by their interaction; and (6) detection of the presence of a
 CC hybrid in the sample. The method can be used for the detection of a
 CC target nucleic acid having a specified base sequence. The method allows
 CC for the simple and easily operable detection of labelled nucleic acids
 CC without complicated synthesis of labelled probe nucleic acids for
 CC respective base sequence
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAX76912 (1-20)
 QY 32 ValVallysArgArg 36
 Db 1 GTTGTAAACGACGG 15
 RESULT 295
 AAV64129
 ID AAV64129 standard; DNA; 20 BP.
 XX
 AC AAV64129;
 XX
 XX 25-JAN-1999 (first entry)
 DT
 XX
 DE Bovine beta-mannosidase PCR sense primer MJ-124.
 XX
 XX Bovine; beta-mannosidase; beta-mannosidosis; diagnosis; goat; cattle;
 KW pathogenic; antigen; excretory; secretory; modified cell; vaccine;
 KW differential; diagnosis; detection; antibody; screening;
 KW antisense therapy; lambda clone; PCR; primer; ss.
 XX
 XX Synthetic.
 OS
 OS Bos taurus.
 XX
 XX US5837836-A.
 PN
 XX
 PD

PD 17-NOV-1998.
 XX
 XX 19-SEP-1995; 95US-00530524.
 XX
 PR 15-SEP-1994; 94US-00306546.
 XX
 XX (UNMS) UNIV MICHIGAN STATE.
 PA
 XX
 XX Chen H, Cavanagh KT, Friderici K, Jones MZ;
 PI WPI; 1999-023539/02.
 XX
 DR
 XX
 XX Bovine beta-mannosidase nucleic acid sequence and mutation(s) - useful
 PT for diagnosis of the disease beta-mannosidosis and its carriers.
 XX
 XX Example 2; Col 18; 39pp; English.
 PS
 XX
 CC The present sequence represents a PCR primer for bovine beta-mannosidase.
 CC The present invention also describes a nucleic acid molecule encoding
 CC bovine beta-mannosidase, but where the adenine at position 2648 is
 CC replaced by guanine. The nucleic acid is useful for the detection of the
 CC disease beta-mannosidosis. This is an autosomal recessive inherited
 CC disorder affecting mainly goats and cattle, caused a defect in the enzyme
 CC beta-mannosidase. This mutation renders the inflicted animals incapable
 CC of correctly processing primary storage products, resulting in tremors,
 CC deafness and dysmyelination amongst other symptoms. The nucleic acid is
 CC used in hybridisation assays, or other nucleic acid based assays (e.g.
 CC PCR or restriction mapping) to detect beta-mannosidase, especially where
 CC nucleic acid encoding bovine beta-mannosidase contains the adenine to
 CC guanine mutation at position 2648, for specific detection of the disease.
 CC The nucleic acid allows specific detection of presence or absence of the
 CC disease. Previous detection methods relied on enzyme activity assays
 CC which can be inaccurate as the range of activities greatly varies from
 CC one individual to another, especially when tested for in cross-breeds
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x AAV64129 (1-20)
 QY 179 IleleuleuProleu 183
 Db 6 ATTCTTTTACCCTG 20
 RESULT 296
 AAZ32733
 ID AAZ32733 standard; DNA; 20 BP.
 XX
 AC AAZ32733;
 XX
 XX 31-JAN-2000 (first entry)
 DT
 XX
 DE Neospora caninum GRA1 PCR primer bd219.
 XX
 XX GRA1; GRA2; SAG1; MIC1; MAG1; protozoan; parasite; neosporosis; abortion;
 KW neonatal death; congenital infection; encephalitic disease; paralysis;
 KW pathogenic; antigen; excretory; secretory; modified cell; vaccine;
 KW differential; diagnosis; detection; antibody; screening;
 KW antisense therapy; lambda clone; PCR; primer; ss.
 XX
 XX Synthetic.
 OS
 OS Neospora caninum.
 XX
 XX EP953641-A2.
 PN
 XX
 XX 03-NOV-1999.
 PD

XX 09-MAR-1999; 99BP-00301746.
 XX 26-MAR-1998; 98US-0079389P.
 PR 15-DEC-1998; 98US-0112282P.
 XX (PFIZ) PFIZER PROD INC.
 XX
 XX Brake DA, Madura RA, Durtschi BA, Krishnan BR, Yoder SC;
 XX WPI; 1999-621834/54.
 XX Polypeptides encoding Neospora caninum proteins, useful for vaccines
 PT against neosporosis and as diagnostic reagents.
 XX
 XX Example; Page 23; 59pp; English.
 XX This sequence represents Neospora caninum GRA1 PCR primer bd219, used
 CC with primer bd220 (AA232734) in the amplification of a fragment of cDNA
 CC encoding the Neospora caninum cytoplasmic excretory/secretory antigen
 CC GRA1 (AAV50130), subsequently used as a probe for secondary screening of
 CC GRA1 lambda clones. Neospora is a pathogenic protozoan parasite of
 CC mammals that is a major cause of abortion, neonatal death, congenital
 CC infection, and encephalitic disease. Neospora caninum infects dogs, and
 CC congenitally infects pups, often leading to paralysis. Neospora-related
 CC disease has also been reported in goats, sheep and horses. The invention
 CC relates to novel isolated Neospora caninum proteins GRA1, GRA2
 CC (AAV50131), SAG1 (AAV50132), MIC1 (AAV50133) and MAG1 (AAV50134) and the
 CC nucleotides which encode them. Genetic constructs comprising mutated or
 CC otherwise modified GRA1, GRA2, SAG1, MIC1 and/or MAG1 nucleotides can be
 CC used to disable or mutate the genes encoding these proteins. This method
 CC can be used to create a modified Neospora cell expressing GRA1, GRA2,
 CC SAG1, MIC1 and/or MAG1 proteins with altered function. The recombinant
 CC proteins, nucleotides encoding them or the modified Neospora cell may be
 CC used to prepare vaccines against neosporosis. Such vaccines can be used
 CC to prevent abortion, neonatal death, congenital infection and
 CC encephalitic disease in mammals. The proteins or derived peptides can be
 CC used as diagnostic reagents to screen for Neospora specific antibodies in
 CC blood or serum samples, or as antigens to raise polyclonal or monoclonal
 CC antibodies used to screen for Neospora proteins in cell or tissue samples
 CC from mammals. GRA1, GRA2, SAG1, MIC1 and MAG1 nucleotides may be used in
 CC differential disease diagnosis or as antisense molecules
 XX
 SQ Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AA232733 (1-20)

QY 39 AlaThrSerPheSer 43
 Db 4 QCGACATCTTTTCT 18
 RESULT 297
 AAV63539
 ID AAV63539 standard; DNA; 20 BP.
 XX
 AC AAV63539;
 XX
 XX 29-JAN-1999 (first entry)
 DT
 XX Antisense oligonucleotide AS2 directed against human Napi-2 cDNA.
 DE
 XX Phosphorothioate; antisense; human; kidney disease;
 KW renal sodium/phosphate cotransporter protein; Napi-2; hyperphosphataemia;
 KW renal disease; cystic fibrosis; polycystic kidney disease; hypertension;
 KW ss.

XX Synthetic.
 OS Homo sapiens.
 XX US5840875-A.
 XX 24-NOV-1998.
 XX
 XX 06-JUN-1995; 95US-00467007.
 PF
 XX 06-JUN-1995; 95US-00467007.
 PR
 XX (THER-) THERAPEUTICS CV.
 PA
 XX Oberbauer R, Schreiner GF, Meyer TW;
 PI WPI; 1999-034128/03.
 XX
 DR Antisense oligonucleotide to renal sodium/phosphate cotransporter mRNA -
 PT useful for treating kidney diseases.
 PT
 XX Example 2; Col 10; 19pp; English.
 FS
 XX The present sequence represents a phosphorothioate antisense
 CC oligonucleotide which is directed against human Napi-2. The antisense
 CC molecule blocks the expression of a renal sodium/phosphate cotransporter
 CC protein (Napi-2), which is useful for treating kidney diseases associated
 CC with hyperphosphataemia. The antisense oligonucleotide can be used
 CC against a variety of systemic or renal diseases e.g. cystic fibrosis,
 CC polycystic kidney disease and various forms of hypertension
 XX
 SQ Sequence 20 BP; 2 A; 10 C; 2 G; 6 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9.44e+03 Length: 20
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV63539 (1-20)

QY 102 ProAsnLeuSerLeu 106
 Db 5 CCCAATCTCTCGCTG 19
 RESULT 298
 AAV79659
 ID AAV79659 standard; DNA; 20 BP.
 XX
 AC AAV79659;
 XX
 XX 24-FEB-1999 (first entry)
 DT
 XX HIV RT DNA template constructing oligo.
 DE
 XX Target molecule; detection; measuring; high-affinity; ligand; SELEX;
 KW systemic evolution of ligands by exponential enrichment; assay;
 KW diagnostic; cell sorting; metabolite; reverse transcriptase; HIV;
 KW RNA ligand; ss.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus 1.
 XX
 XX US5843653-A.
 XX
 XX 01-DEC-1998.
 PD
 XX 06-JUN-1995; 95US-00469609.
 PF
 XX 11-JUN-1990; 90US-00536428.
 KW
 PR 10-JUN-1991; 91US-00714131.

PT Genome sequence of Chlamydia trachomatis.
XX
PS Disclosure; Page 1619; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAZ06754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
SQ Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ03591 (1-20)

QY 179 IleLeuLeuProLeu 183
Db 15 ATACTATTGCCACTC 1
|||||

Search completed: March 5, 2004, 00:35:09
Job time : 412 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:50:45 ; Search time 2268.59 Seconds
(without alignments)
9552.848 Million cell updates/sec

Title: US-09-966-880A-35_COPY_1_500

Perfect score: 500

Sequence: 1 aggttcagagagactgtggg.....gagactgcaggaggaag 500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	500	100.0	5514	6	BD016834	BD016834 Novel cyt
2	500	100.0	11204	6	BD016860	BD016860 Novel cyt
3	500	100.0	11204	9	AB040430	AB040430 Homo sapi
4	498.4	99.7	71132	9	AC092184	AC092184 Homo sapi
5	145.6	29.1	178130	2	AC119975	AC119975 Mus muscu
6	144	28.8	1767	10	AB091291	AB091291 Mus muscu
7	128.4	25.7	241757	2	AC094826	AC094826 Rattus no
8	128.4	25.7	259506	2	AC109119	AC109119 Rattus no
9	128.4	25.7	345098	2	AC120617	AC120617 Rattus no
10	59	11.8	87	6	BD016836	BD016836 Novel cyt
11	59	11.8	2818	9	BC006296	BC006296 Homo sapi
12	56	11.2	1828	9	BC006296	BC006296 Homo sapi
13	56	11.2	2791	9	AB040431	AB040431 Homo sapi
14	49	9.8	181060	5	EX119907	EX119907 Zebrafish
15	46.6	9.3	275142	2	AC103174	AC103174 Rattus no
16	45.8	9.2	92464	5	AL606705	AL606705 Zebrafish
17	45	9.0	160280	2	AL953909	AL953909 Danio rer
18	44.4	8.9	234545	5	EX470214	EX470214 Zebrafish
19	44.2	8.8	153687	5	EX119987	EX119987 Zebrafish
20	44.2	8.8	230614	10	AC138320	AC138320 Mus muscu
21	44.2	8.8	232304	2	AC111030	AC111030 Mus muscu
22	43.8	8.8	158639	2	EX072539	EX072539 Danio rer
23	43.8	8.8	214628	2	AC101947	AC101947 Mus muscu
24	43.8	8.8	333321	3	AC116986	AC116986 Dictyoste
25	43.6	8.7	154160	2	EX571709	EX571709 Danio rer
26	43.6	8.7	207737	2	EX640470	EX640470 Danio rer
27	43.4	8.7	173096	2	EX511094	EX511094 Danio rer
28	43.4	8.7	198645	2	EX469885	EX469885 Danio rer
29	43	8.6	158904	10	AC135807	AC135807 Mus muscu
30	43	8.6	204737	2	AC147107	AC147107 Mus muscu
31	43	8.6	211345	2	EX004890	EX004890 Danio rer
32	43	8.6	221552	2	AC112328	AC112328 Rattus no
33	43	8.6	243739	2	AC109679	AC109679 Rattus no
34	42.8	8.6	131355	2	AC139655	AC139655 Rattus no
35	42.8	8.6	243735	2	AC106614	AC106614 Rattus no
36	42.6	8.5	212722	2	AC087158	AC087158 Mus muscu
37	42.6	8.5	331039	3	AC116988	AC116988 Dictyoste
38	42.4	8.5	28670	9	AC104621	AC104621 Homo sapi
39	42.4	8.5	154930	2	EX571944	EX571944 Danio rer
40	42.4	8.5	167409	2	AC073374	AC073374 Homo sapi
41	42.4	8.5	179510	2	AC013820	AC013820 Homo sapi
42	42.2	8.4	278	8	AY023421	AY023421 Oryza sat
43	42.2	8.4	2767	3	AB039883	AB039883 Dictyoste
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45	42.2	8.4	175081	2	EX085194	EX085194 Danio rer

ALIGNMENTS

RESULT 1	BD016834	Novel cytidine deaminase.	5514 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD016834	Novel cytidine deaminase.				
DEFINITION	BD016834	Novel cytidine deaminase.				
ACCESSION	BD016834	Novel cytidine deaminase.				
VERSION	BD016834.1	GI:22558010				
KEYWORDS	JP 2001245669-A/7.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 5514)					
AUTHORS	Honjo, T. and Muramatsu, M.					
TITLE	Novel cytidine deaminase					
JOURNAL	Patent: JP 2001245669-A 7 11-SEP-2001;					

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COMMENT
JAPAN TOBACCO INC,TASUKU HONJO
OS Homo sapiens (human)
PN JP 2001245669-A/7
PD 11-SEP-2001
PF 28-MAR-2000 JP 2000092981
PI TASUKU HONJO,MASAMICHI MURAMATSU
PC C12N15/00,A61K39/395,A61P1/00,A61P11/06,A61P13/12,
PC A61P17/00,
PC A61P27/02,A61P27/16,A61P37/02,A61P37/08,C07K16/18,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12N9/78,C12P21/02,C12P21/08//((C12N1/21,C12R1:19), PC
(C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC
FH Key Location/Qualifiers
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FT exon (1119)..(5514).
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Best Local Similarity 100.0%; Pred. No. 4.2e-114;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 591 AGTTTCAGAGAGACTGTGGGAATATGGGGAAATTAGAGGCTATCTGAGGCTCTTCAACAC 650
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Db 1071 GAGACTTGAGGGAGGCAAG 1090
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LOCUS BD016860 11204 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel cytidine deaminase.
ACCESSION BD016860
VERSION BD016860.1 GI:22558036
KEYWORDS JP 2001245669-A/33.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 11204)
AUTHORS Honjo,T. and Muramatsu,M.
TITLE Novel cytidine deaminase
JOURNAL Patent: JP 2001245669-A 33 11-SEP-2001;
JAPAN TOBACCO INC,TASUKU HONJO
COMMENT
OS Homo sapiens (human)
PN JP 2001245669-A/33
PD 11-SEP-2001
PF 28-MAR-2000 JP 2000092981
PI TASUKU HONJO,MASAMICHI MURAMATSU
PC C12N15/00,A61K39/395,A61P1/00,A61P11/06,A61P13/12,
PC A61P17/00,
PC A61P27/02,A61P27/16,A61P37/02,A61P37/08,C07K16/18,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12N9/78,C12P21/02,C12P21/08//((C12N1/21,C12R1:19), PC
(C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC
FH Key Location/Qualifiers
FT intron (1032)..(1118)
FT exon (1119)..(5514).
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 500; DB 6; Length 11204;
Best Local Similarity 100.0%; Pred. No. 4.1e-114;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTTTCAGAGAGACTGTGGGAATATGGGGAAATTAGAGGCTATCTGAGGCTCTTCAACAC 60
Db 1 AGTTTCAGAGAGACTGTGGGAATATGGGGAAATTAGAGGCTATCTGAGGCTCTTCAACAC 60
QY 61 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAATATTACTATTCTC 120
Db 61 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAATATTACTATTCTC 120
QY 121 ATTGTGCTTTTATTTTGTGTATCATGATTATTAATGAGTGTCTACTGTCTCTCC 180
Db 121 ATTGTGCTTTTATTTTGTGTATCATGATTATTAATGAGTGTCTACTGTCTCTCC 180
QY 181 TGATCTTTGCTAGCTATGGAGCATGGAGCTGGGCTTTTAGAGCAGCAGCCCAAGGAACC 240
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QY 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTGTGCTATGACAGC 300
Db 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTGTGCTATGACAGC 300
QY 301 CCCACCCACCATCTTCTACTGTGATCCAAATCAGAGCAAGGCCGTTGGGGTACCTGGTGG 360
Db 301 CCCACCCACCATCTTCTACTGTGATCCAAATCAGAGCAAGGCCGTTGGGGTACCTGGTGG 360
QY 361 GGGTGATGCTGTGAGGGAGAGGCCCAAGGGCAAGCTCAAAATTTGAATGTGAAGGGCC 420
Db 361 GGGTGATGCTGTGAGGGAGAGGCCCAAGGGCAAGCTCAAAATTTGAATGTGAAGGGCC 420
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Db 421 AATGCACTGTGAGAGCAGAGAACCATATTAAATTTGAATGTGAAGGGCC 480
QY 481 GAGACTTGAGGGAGGCAAG 500
Db 481 GAGACTTGAGGGAGGCAAG 500
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AB040430
LOCUS AB040430 11204 bp DNA linear PRI 03-OCT-2000
DEFINITION Homo sapiens AID gene for activation-induced cytidine deaminase,
complete cds.
ACCESSION AB040430
```



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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Direct Submission
Unpublished
2 (bases 1 to 71132)
Worley,K.C.
Direct Submission
Submitted (25-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 71132)
Worley,K.C.
Direct Submission
Submitted (18-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 71132)
Worley,K.C.
Direct Submission
Submitted (12-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 71132)
Worley,K.C.
Direct Submission
Submitted (12-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 25, 2002 this sequence version replaced gi:20901754.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

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Query Match 99.7%; Score 498.4; DB 9; Length 71132;
Best Local Similarity 99.8%; Pred. No. 9.2e-114;
Matches 499; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 191 TGAATCTTGTAGCTATGGACATGGACTGGCTTTTAGAGCAGACGCCCAAGGAACC 240

DB TGAATCTTGTAGCTATGGACATGGACTGGCTTTTAGAGCAGACGCCCAAGGAACC 34788

QY 241 TAAACATTAAAGCAGAGTGCCTCAATGTTTAACTGTGTGACTCTGCTATGACAGC 300

DB TAAACATTAAAGCAGAGTGCCTCAATGTTTAACTGTGTGACTCTGCTATGACAGC 34848

QY 301 CCCACCCACCATCTTCTACTGTATCCAAATCAGAGCAGGCCCTTGGGTACTGTGG 360

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QY 361 GGGTGATCTGTCTGAGGGGAGAGGCCCAAGGCAAGCTCAAAATTTGAATGTGAAGGCC 420

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QY 421 AATGCACTGTGAGCTGAGACAGAGACCATCATTAATGAAGTGAGATTTTCTGCGCT 480

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DB GAGACTTCGAGGGGCAAG 35048

RESULT 5
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LOCUS 178130 bp DNA linear HTG 14-MAR-2003
DEFINITION Mus musculus clone RP24-483K3, WORKING DRAFT SEQUENCE, 8 unordered pieces.
AC119975
VERSION AC119975.3 GI:28951252
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 178130)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-483K3
Unpublished

2 (bases 1 to 178130)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collumore, A.,
Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R.,
Lander, E., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,

Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, N.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strass, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 178130)
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collumore, A., Cooke, P., Corum, B., DeArrellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (14-MAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 14, 2003 this sequence version replaced gi:28195895.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information
Center project name: L25744
Center clone name: 483_K_3

----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 176301 bases at least Q40
Consensus quality: 176937 bases at least Q30
Consensus quality: 177194 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 177430; sum-of-ctngs
Quality coverage: 9.0 in Q20 bases; agarose-fp
Quality coverage: 8.9 in Q20 bases; sum-of-ctngs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 11982: contig of 11982 bp in length
* 11983 12082: gap of 100 bp
* 12083 13278: contig of 1196 bp in length
* 13278 13378: gap of 100 bp
* 13379 15640: contig of 2262 bp in length

* 15641 15740: gap of 100 bp
 * 15741 22800: contig of 7060 bp in length
 * 22900: gap of 100 bp
 * 22901 101338: contig of 78438 bp in length
 * 101339 101439: gap of 100 bp
 * 101439 133612: contig of 32174 bp in length
 * 133613 133713: gap of 100 bp
 * 133713 173588: contig of 39876 bp in length
 * 173589 173689: gap of 100 bp
 * 173689 173800: contig of 4442 bp in length.

FEATURES

source

1..178130
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="RP24-483K3"
 /clone_lib="RPCI-24 Male Mouse BAC"
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misc_feature

/note="assembly_fragment"

clone_end:SP6

vector_side:left

misc_feature

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/note="assembly_fragment"

misc_feature

22901..101338

/note="assembly_fragment"

misc_feature

101439..133612

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misc_feature

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/note="assembly_fragment"

misc_feature

173689..178130

/note="assembly_fragment"

misc_feature

clone_end:T7

vector_side:right

ORIGIN

Query Match 29.1%; Score 145.6; DB 2; Length 178130;
 Best Local Similarity 69.6%; Pred. No. 8.7e-26;
 Matches 263; Conservative 0; Mismatches 94; Indels 21; Gaps 4;
 QY 138 TGTATCATGATTATAATTGAAGTGTCTACTGTCTACTGCTCCTGATCTTTGCTAGCTAT 197
 Db 138982 TATCATGATACCAATGTGAAAGTGTCCAGTGTCTATTTCTCTGATCTTTGTTACCTGT 138923
 QY 198 GGAGCATGACTGGGCTTTTAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 257
 Db 138922 GGTACTGGCTGGCTTTTATAGAGCAACAGCCTCGAAGGAAGTTGGACATTAAGCATGAG 138863
 QY 258 CTG-----CCCTCAATGGTTTAACTGTGTGACTCTGCTATGACATGACAGCCCA 304
 Db 138862 CAGAACTGCCCGCCCGCCCAATCATTTATCCGTGTGGCTCTGCCACACACAGC----- 138807
 QY 305 CCCACCCATCTTCACTGGATCCAAATCAGGAGCAGGCGCGTGGGGTACCTGGTGGGGGT 364
 Db 138806 CCGGCCATCTTTACTGGACCAACCCAGAGGCAG--ATGTTGGATACCTGGTGGTAGT 138749
 QY 365 GATGCTGTC--AGGGAGAGGCCCAAAAGGCAAGCTCAATTTGAATGTGAAGGCCAA 422
 Db 138748 GATGCTGTCTGGGGGAGAGGCCCAAGAGCAAGCTCAGATTGAATGCCAGGGGCCAG 138689
 QY 423 TGCACTGTCTGAGACTGAGACAGAGCAACCATTAATTGAAGTGAAGTGTGAGATTTTCTGSCCTGA 482
 Db 138688 TGCTCTGTCTACACACAGCACTGAGCAGCCTTGTGTAAGCAAGCTTCCCTTTGSCCTAA 138629
 QY 483 GACTTCAGGGAGGCAAG 500
 Db 138628 GACTTTGAGGAGTCAAG 138611

RESULT 6

AB091291

LOCUS

DEFINITION

Mus musculus AID gene for activation-induced cytidine deaminase, 5'

flanking region and partial cds.

ACCESSION

AB091291

VERSION

AB091291.1

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Gonda,H., Sugai,M., Nambu,Y., Katakai,T., Agata,Y., Yokota,Y. and

Shimizu,A.

Id2: Inhibitor of Pax5 and E2A in B cell activation

2 (bases 1 to 1767)

Unpublished

REFERENCE

AUTHORS

TITLE

JOURNAL

SUBMITTED (04-SEP-2002) Hiroyuki Gonda, Center for Molecular

Biology and Genetics; 53 Shogoin-Kawahara-cho, Sakyo-ku, Kyoto

606-8507, Japan [E-mail:hgonda@virus.kyoto-u.ac.jp].

Tel:81-75-751-4189, Fax:81-75-751-4190)

Location/Qualifiers

1..1767

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="6"

<1..1759

/note="5' flanking region"

1760..1767

/gene="AID"

1760..1767

/gene="AID"

/codon_start=1

/product="activation-induced cytidine deaminase"

/protein_id="BAC84974.1"

/db_xref="GI:34447116"

/db_xref="LocusID:11628"

/translation="MD"

source

misc_feature

gene

CDS

ORIGIN

Query Match 28.8%; Score 144; DB 10; Length 1767;
 Best Local Similarity 69.3%; Pred. No. 2.8e-25;
 Matches 262; Conservative 0; Mismatches 95; Indels 21; Gaps 4;
 QY 138 TGTATCATGATTATAATTGAAGTGTCTACTGTCTACTGCTCCTGATCTTTGCTAGCTAT 197
 Db 1367 TATCATGATACCAATGTGAAGTGTCCAGTGTCTATTGTCCTGATCTTTGTACCTGT 1426
 QY 198 GGAGCATGACTGGGCTTTTAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 257
 Db 1427 GATACCTGGCTGGCTTTTAGAGGACAGCCTCGAGGAAGTTGGACATTAAGCATGAG 1486
 QY 258 CTG-----CCCTCAATGGTTTAACTGTGTGACTCTGCTATGACATGACAGCCCA 304
 Db 1487 CAGAACTGGCCCCCCCCCAATCATTTAATCCGTGTGGCTTTGCCACACACAGC----- 1542
 QY 305 CCCACCCATCTTCACTGGATCCAAATCAGGAGCAGGCGCTTTGGGGTACCTGGTGGGGGT 364
 Db 1543 CCGGCCATCTTTACTTGGACCCCAACCCAGAGGCAG--ATGTTGGATACCTGGTGGTAGT 1600
 QY 365 GATGCTGTC--AGGGAGAGGCCCAAAAGGCAAGCTCAAAATTTGAATGTGAAGGCCAA 422
 Db 1601 GATGCTGTCTGGGGGAGAGGCCCAAGAGCAAGCTCAGATTGTAATCCAGGGGCCAG 1660
 QY 423 TGCACTGTCTGAGACTGAGACAGAGCAACCATCATTTAATTGAAGTGAAGTGTGAGATTTTCTGGCCTGA 482
 Db 1661 TGCTCTGTCTACACAAAGCACTGAGCAGCCTTGTCTTGAAGCAAGCTTCTCTTGGCTAA 1720
 QY 483 GACTTGCAGGGAGGCAAG 500

Db 119027 CCTGGCTGGGCTAGCTTTTATGAGGAGCAGCAGCCCTCAAGGAAGCTGGCCATTGACGATAA 118968

Qy 257 GCTG -CCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGAGCCACCCACCCATC 314

Db 118967 GCAGAACTGTCAATCATTTTATCTAATGTGCTCTGGCCACCATGCGC-----CCGCGCCCTC 118912

Qy 315 TTCACTGGATCCAAATCAGGAGCAAGCCCGT-TGGGGTACCTGGTGGGGGTGATGCTGTC 373

Db 118911 CTTACTGGAGCCCAACCCAGGAGGAGGAGATGTTGGATATCTGCTGGCGAGTGATGCTATC 118852

Qy 374 A---GGGGAGGAGCCCAAGGCAAGCTCAAAATTTGAATGTGAAGGCGCAATGCACTCT 430

Db 118851 ATTGGGGAGGAGACCTCAAGAGCAAGCTCAAAATTTGAATGCCAGGGCCAGTCTCTCT 118792

Qy 431 CAGACTGAGACAGAGCAACCATCATTAATGAAGTGAGATTTTCTGGCTGAGACTTGCA 490

Db 118791 CACACAAGGCACTGAAGCAGCCTTGCTTGAAGCAGCTCCCTTTGACCTAAGACTTTGA 118732

Qy 491 GGGAGGCAAG 500

Db 118731 GGGAAACAAG 118722

RESULT 8

AC109119/c

LOCUS AC109119 259506 bp DNA linear HTG 08-OCT-2002

DEFINITION Rattus norvegicus clone CH230-98A4, *** SEQUENCING IN PROGRESS ***

ACCESSION AC109119

VERSION AC109119.5 GI:22856767

KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 259506)

AUTHORS Muzny,D.,Marie, Metzker,M.,Lee, S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalto,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuwa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mathew,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwackemeleh,O., Okwono,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,

Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneid,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,K., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,C., Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,P., Williams,G., Willson,R., Wlezyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,X., Zhao,S., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission

Unpublished

2 (bases 1 to 259506)

Worley,K.C.

Direct Submission

Submitted (03-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 259506)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 14, 2002 this sequence version replaced gi:22538869.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center of Medicine

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GRFZ

Center clone name: CH230-98A4

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 225337 bases at least Q40

Consensus quality: 220008 bases at least Q30

Consensus quality: 230948 bases at least Q20

Estimated insert size: 248565; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 259506: contig of 259506 bp in length.

Location/Qualifiers

1..259506

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-98A4"

FEATURES

source

KEYWORDS JP 2001245669-A/9.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 87)
AUTHORS Honjo,T. and Muramatsu,M.
TITLE Novel cytidine deaminase
JOURNAL Patent: JP 2001245669-A 9 11-SEP-2001;
COMMENT JAPAN TOBACCO INC,TASUKU HONJO
OS Homo sapiens (human)
PN JP 2001245669-A/9
PD 11-SEP-2001
PF 28-MAR-2000 JP 2000092981
PI TASUKU HONJO,NASAMICHI MURAMATSU
PC C12N15/09,A61K39/395,A61P17/00,
PC A61P17/00,
PC A61P27/02,A61P27/16,A61P37/02,A61P37/08,C07K16/18,C12N1/19,C12N1/21,
PC C12N5/10,C12N9/78,C12P21/02,C12P21/08//C12N1/21,C12R1/19),
PC (C12N5/10,C12R1/91),C12N15/00,C12N5/00,C12N5/00,C12R1/91) CC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred.No.0.00051;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 442 AGAGAACCATCATTAATTGAAGTGAGATTTTCGGCCCTGCAGACTTCGAGGAGGCAAG 500
Db 1 AGAGAACCATCATTAATTGAAGTGAGATTTTCGGCCCTGCAGACTTCGAGGAGGCAAG 59

RESULT 11
BD016833 2818 bp DNA linear PAT 27-AUG-2002
LOCUS Novel cytidine deaminase.
DEFINITION BD016833
ACCESSION BD016833.1 GI:22558009
VERSION BD016833.1
KEYWORDS JP 2001245669-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2818)
AUTHORS Honjo,T. and Muramatsu,M.
TITLE Novel cytidine deaminase
JOURNAL Patent: JP 2001245669-A 6 11-SEP-2001;
COMMENT JAPAN TOBACCO INC,TASUKU HONJO
OS Homo sapiens (human)
PN JP 2001245669-A/6
PD 11-SEP-2001
PF 28-MAR-2000 JP 2000092981
PI TASUKU HONJO,NASAMICHI MURAMATSU
PC C12N15/09,A61K39/395,A61K39/395,A61P17/00,A61P17/06,A61P13/12,
PC A61P17/00,
PC A61P27/02,A61P27/16,A61P37/02,A61P37/08,C07K16/18,C12N1/19,C12N1/21,
PC C12N5/10,C12N9/78,C12P21/02,C12P21/08//C12N1/21,C12R1/19),
PC (C12N5/10,C12R1/91),C12N15/00,C12N5/00,C12N5/00,C12R1/91) CC
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1..(79)
5'UTR (80)..(676)
CDs (677)..(2818).
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/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 11.8%; Score 59; DB 6; Length 2818;
 Best Local Similarity 100.0%; Pred. No. 0.00043;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 442 AGAGAACCATCAATTAATGAAGTGAAGATTTTCTGGCCTGAGACTTGCGAGGAGGCAAG 500
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 Db 1 AGAGAACCATCAATTAATGAAGTGAAGATTTTCTGGCCTGAGACTTGCGAGGAGGCAAG 59

RESULT 12

BC006296 1828 bp mRNA linear PRI 03-OCT-2003
 LOCUS
 DEFINITION Homo sapiens activation-induced cytidine deaminase, mRNA (cdna
 clone MGC:12911 IMAGE:4054915), complete cds.

ACCESSION BC006296

VERSION BC006296.2 GI:33871601

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1828)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Schwee, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)

2388257

12477932

2 (bases 1 to 1828)

Strausberg, R.

Direct Submission

Submitted (09-APR-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

On Aug 19, 2003 this sequence version replaced gi:13623400.

Contact: MGC help desk

Email: cgaps-remail.nih.gov

Tissue Procurement: Louis Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>Contact: nisc_mgc@nhgri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantirip, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 17 Row: a Column: 1
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 10190699.

FEATURES

source

1. 1828

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="MGC:12911 IMAGE:4054915"

/tissue_type="Primary B-Cells from Tonsils"

/clone_lib="NIH MGC 48"

/lab_host="DH10B-R"

/note="Vector: pOTB7"

gene

1. 1828

/gene="AICDA"

/note="synonyms: AID, HIGM2, CDA2, ARP2"

/db_xref="LocusID:57379"

/db_xref="MIM:605257"

77. 673

/product="activation-induced cytidine deaminase"

/protein_id="AA06296.1"

/db_xref="GI:13623401"

/db_xref="LocusID:57379"

/translation="MDSLMMNRKFLYQKXNRWAKGRRTYLCVVKRRDSATPSFL

DFGIRKNGCHVLELRYSIDLDLPGRCYRVFTWSVPCDCAHVADFLRGNP

NLSRIFTARLYFCDEKAPGEGRLRHRAGVQIAIMTKDYFCWMTFVENHETFK

AWGLHNSVLSQLRILLPLVEVDLDRDPAFTGL"

ORIGIN

Query Match 11.2%; Score 56; DB 9; Length 1828;

Best Local Similarity 100.0%; Pred. No. 0.0024;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

445 GAACCATCATTAATTAAGTGAAGATTTTTCGGCTGAGACTTGCGAGGAGGCAAG 500

Db

1 GAACCATCATTAATTAAGTGAAGATTTTTCGGCTGAGACTTGCGAGGAGGCAAG 56

RESULT 13

LOCUS

AB040431 2791 bp mRNA linear PRI 03-OCT-2000

Homo sapiens AID mRNA for activation-induced cytidine deaminase,

Complete CDS.

ACCESSION

AB040431

VERSION

AB040431.1 GI:9988409

KEYWORDS

AID; activation-induced cytidine deaminase; Human AID.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (sites)

Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.

Isolation, tissue distribution, and chromosomal localization of the

human activation-induced cytidine deaminase (AID) gene

Genomics 68 (1), 85-88 (2000)

20408890

MEDLINE

10950930

REFERENCE

2 (sites)

Revy, P., Muto, T., Levy, Y., Geissmann, F., Plebani, A., Sanal, O.,

Catalan, N., Forveille, M., Dufourcq-Lagelouse, R., Gennery, A.,

Tezcan, I., Ersoy, F., Kayserili, H., Ugazio, A.G., Brousse, N.,

Muramatsu, M., Notarangelo, L.D., Kinoshita, K., Honjo, T., Fischer, A.

and Durandy, A.

Activation-induced cytidine deaminase (AID) deficiency causes the

autosomal recessive form of the Hyper-IgM syndrome (HIGM2)

Cell 102 (5), 565-575 (2000)

20460541

JOURNAL

MEDLINE

11007475
 3 (bases 1 to 2791)
 Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.
 Direct Submission
 Submitted (18-MAR-2000) Tsukuba Honjo, Kyoto University, Department
 of Medical Chemistry, Faculty of Medicine, Yoshida, Sakyo-Ku,
 Kyoto, Kyoto 606-8501, Japan (E-mail:honjo@four.med.kyoto-u.ac.jp,
 Tel:81-75-753-4371(ex.4371), Fax:81-75-753-4388)
 Location/Qualifiers
 1..2791
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 1..2791
 /gene="18S"
 77..673
 /gene="18S"
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 /protein_id="BAB12721.1"
 /db_xref="GI:9988410"
 /translation="MDSLMMRKLFLVQKRVKAKGRRETYLVVVRDSDATPSGL
 DFGYRNKGCHVLLFLRYISDWDLPGRCYRVTFWTSKPCYDCARHVAFLRGNP
 NLSIRIFARLYFCEDKAEPEGLRLHRAVGQIAIMTFKDYFCWNTFVENHRTFK
 AWEGHLSNLSRLRLPLLYEVDLDLDAFRTGL"

Query Match 11.2%; Score 56; DB 9; Length 2791;
 Best Local Similarity 100.0%; Pred. No. 0.0024;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 GAACCATCAATTAATGAAGTGGAGATTTTCTGGCTGAGACTGCGAGGAGCAAG 500
 |||||
 Db 1 GAACCATCAATTAATGAAGTGGAGATTTTCTGGCTGAGACTGCGAGGAGCAAG 56

RESULT 14
 BX119907
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 SOURCE
 ORGANISM

BX119907 181060 bp DNA linear VRT 30-NOV-2003
 Zebrafish DNA sequence from clone CH211-208D14 in linkage group 6,
 complete sequence.
 BX119907
 BX119907.8 GI:38568093
 HTG.
 Danio rerio (zebrafish)
 Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 181060)
 Smith,M.
 Direct Submission
 Submitted (29-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Nov 30 2003 this sequence version replaced gi:38201264.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e. phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclones; and the
 assembly was confirmed by restriction digest, except on the rare
 occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em.; EMBL; SW.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information

on the WORMPEP database can be found at
<http://www.sanger.ac.uk/Projects/Celegans/wormpep>
 Zebrafish pUC subclones occasionally display inconsistency over the
 length of mononucleotide A/T runs and conserved TA repeats. Where
 this is found the longest good quality representation will be
 submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat
 discovery system (Zhirong Bao and Sean Eddy, submitted), and those
 beginning 'drr' were identified by Rick Waterman (Stephen Johnson
 lab, WashU). For further information see

http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml

CH211-208D14 is from a CHORI-211 BAC library

VECTOR: pTARBAC2.1.

FEATURES
 Location/Qualifiers
 source
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 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="CH211-208D14"
 /clone_lib="CHORI-211"

ORIGIN

Query Match 9.8%; Score 49; DB 5; Length 181060;
 Best Local Similarity 56.5%; Pred. No. 0.11;
 Matches 91; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 39 GGTATCTGAGGCTCTCAACACATAACCAAGAGCTATTAAATGCTCTTTAAGGAT 98
 |||||

Db 2100 GCGACCTCGATTATAAAGGACTAGCCAAAGAAATTAAGAATGAATTT 2159
 |||||

QY 99 TTACATAAATATCTATCTCTGCTTCTGCTTTTATTTTGTTCATCATGATATATGA 158
 |||||

Db 2160 TATCAT 2219
 |||||

QY 159 AGTGCTACTGTTACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 199
 |||||

Db 2220 TATTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 2260
 |||||

RESULT 15
 AC103174
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 SOURCE
 ORGANISM

AC103174 275142 bp DNA linear HTG 22-SEP-2002
 Rattus norvegicus clone CH230-95N13, *** SEQUENCING IN PROGRESS
 *** 4 unordered pieces.
 AC103174
 AC103174.4 GI:23268241
 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 AUTHORS
 1 (bases 1 to 275142)
 Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
 Anyalebechi,V., Ayodeji,A., Ayodeji,M., Baca,E., Baden,H.,
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
 Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
 Bryant,N., Bukay,C., Burch,P., Burrell,K., Calderon,E.,
 Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Chen,R.,
 Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
 Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
 Davila,M., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
 Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
 Draper,H., Duan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
 Egan,A., Escoto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
 Fernandez,S., Finley,M., Flagg,N., Forbes,I., Foster,M., Foster,P.,

Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hoques, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Tdebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Mareshuwa, L., Loulseghe, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangin, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, S., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasckelmech, O., Okwou, G., Olarnpunsagoon, A., Pal, S., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L., Puzos, M., Qulroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shivartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steamle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmari, K., Valas, R., Vega, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 275142)
Worley, K.C.

Direct Submission
Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 275142)

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (22-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 22, 2002 this sequence version replaced gi:2731125.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GJUZ
Center clone name: CH230-95N13
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 242490 bases at least Q40
Consensus quality: 246431 bases at least Q30
Consensus quality: 248443 bases at least Q20
Estimated insert size: 282574; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 11:56:09 ; Search time 285.857 Seconds
(without alignments)
7430.646 Million cell updates/sec

Title: US-09-966-880A-35_COPY_1_500
Perfect score: 500
Sequence: 1 aggttcagagacgtggg.....gagacttcaggaggcaag 500

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	100.0	5514	3 AAC55313	Aac55313 Human act
2	500	100.0	11204	3 AAC55339	Aac55339 Human act
3	500	100.0	11204	6 ABS73286	Abs73286 DNA encod
4	118	23.6	772	5 AAS81193	Aas81193 DNA encod
5	59	11.8	87	3 AAC55315	Aac55315 Human act
6	59	11.8	2818	3 AAC55312	Aac55312 Human act
7	56	11.2	1543	7 ABX05468	Abx05468 Human nov
8	56	11.2	2791	6 ABS73287	Abs73287 DNA encod
9	56	11.2	2791	6 ABS73288	Abs73288 DNA encod
10	43.8	8.8	983	7 ABZ24315	Abz24315 Sclerotin
11	39.6	7.9	346	5 ABV57342	Abv57342 Human pro
12	38.4	7.7	11143	4 ABL12834	Ab112834 Drosophil
13	38.4	7.7	12024	6 AAD38807	Aad38807 CODR3 ORF
14	38.2	7.6	328	6 ABQ97746	Abq97746 Mouse ES
15	38.2	7.6	4363	4 ABL08198	Ab108198 Drosophil
16	38.2	7.6	4386	4 ABL08180	Ab108180 Drosophil
17	38	7.6	7131	6 ABK31450	Abk31450 Signal tr
18	38	7.6	7131	6 ABL70427	Ab170427 Chemical tr
19	38	7.6	7131	6 AAS61360	Aas61360 Human gen
20	37.8	7.6	529	7 ABZ24320	Abz24320 Sclerotin
21	37.8	7.6	5454	3 AA70236	Aa70236 Plasmodiu
22	37.4	7.5	8578	4 ABL06880	Ab106880 Drosophil
23	37.2	7.4	520	5 AAS21880	Aas21880 Human col

c 24	37.2	7.4	2787	2	AAx15661	Aax15661 Protein p
c 25	37.2	7.4	2886	7	ACC59886	Acc59886 Saccharom
c 26	37.2	7.4	3300	3	Aaz55699	Aaz55699 DNA encod
27	37.2	7.4	24183	5	AAS21771	Aas21771 Human gen
28	37.2	7.4	53585	28	AAX20251	Aax20251 Borrelia
29	37.2	7.4	91552	6	AAD38803	Aad38803 BAC clone
c 30	37	7.4	758	6	AAS95261	Aas95261 Long term
31	37	7.4	26997	4	AAS46747	Aas46747 Tumour su
32	36.8	7.4	6325	6	ABN80070	Abn80070 Human che
33	36.8	7.4	9832	6	ABL32656	Ab132656 Human imm
34	36.8	7.4	14552	4	ABL03818	Ab103818 Drosophil
35	36.8	7.4	28066	9	ADC87584	Adc87584 Human GPC
c 36	36.6	7.3	110000	2	AAT42063_07	ContInuation (8 of
37	36.4	7.3	1859	6	AD42874	Ad42874 Human DNA
38	36.4	7.3	2111	4	AAH17042	Aah17042 Human CDN
c 39	36.4	7.3	4023	6	ABN79892	Abn79892 Fungal ZB
c 40	36.4	7.3	4985	4	ABN01906	Ab101906 Drosophil
41	36.4	7.3	8413	6	ABL34497	Ab134497 Human met
42	36.4	7.3	8413	6	ABL70520	Ab170520 Chemicall
43	36.4	7.3	19380	6	AAS61426	Aas61426 Human gen
c 44	36.4	7.3	82952	6	ABN85766	Abn85766 Arabidops
c 45	36.2	7.2	412	5	ABV56553	Abv56553 Human pro

ALIGNMENTS

RESULT 1
ID AAC55313 standard; DNA; 5514 BP.
XX
AC AAC55313;
DT 05-FEB-2001 (first entry)
XX
DE Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:9.
XX
KW Activation-induced cytidine deaminase; AID; cytidine deaminase;
KW immune related disease; allergy; allergic disease; antiallergic;
KW antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;
KW gene therapy; B cell associated immune system disorder; food allergy;
KW immunodeficiency disease; immunoglobulin A deficiency disease; asthma;
KW IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;
KW drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;
KW ataxia telangiectasia; common variable immunodeficiency disorder;
KW major histocompatibility class II deficiency disease;
KW auto immunodeficiency syndrome; IgG subclass selection disorder; ds.

OS Homo sapiens.

XX WO200058480-A1.

XX 05-OCT-2000.

XX 28-MAR-2000; 2000WO-JP001918.

XX 29-MAR-1999; 99JP-00087192.

XX 24-JUN-1999; 99JP-00178999.

XX 27-DEC-1999; 99JP-00371382.

XX (NIBS) JAPAN TOBACCO INC.

XX (HONJ/) HONJO T.

XX Honjo T, Muramatsu M;

XX WPI; 2000-611715/58.

XX Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies.

XX Claim 17; Page 142-145; 174pp; Japanese.

QY 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGC 300
 Db 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGC 300
 QY 301 CCCACCCACCCATCTTCACTGATCCAAATCAGAGGAGGCGCTGGGTACCTGGTGG 360
 Db 301 CCCACCCACCCATCTTCACTGATCCAAATCAGAGGAGGCGCTGGGTACCTGGTGG 360
 QY 361 GGGTGATGTGTTCAGGGGAGGAGCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCC 420
 Db 361 GGGTGATGTGTTCAGGGGAGGAGCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCC 420
 QY 421 AATGCACTGTGACGTGACAGAGACCAATCAATTAATGAAGTGAAGTCTGGCT 480
 Db 421 AATGCACTGTGACGTGACAGAGACCAATCAATTAATGAAGTGAAGTCTGGCT 480
 QY 481 GAGACTTGCAGGGAGGCAAG 500
 Db 481 GAGACTTGCAGGGAGGCAAG 500

RESULT 3
 ABS73286
 ID ABS73286 standard; DNA; 11204 BP.
 XX
 AC ABS73286;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE DNA encoding human translocation del(12p) protein #1.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200269900-A2.
 XX
 XX 12-SEP-2002.
 XX
 XX 01-MAR-2002; 2002WO-US006518.
 XX
 XX 01-MAR-2001; 2001US-0272751P.
 XX
 XX (CONF-) CONFORMA THERAPEUTICS CORP.
 XX
 XX Fritz LC, Burrows FU;
 XX
 XX WPI; 2002-698710/75.
 XX
 XX P-FSDB; ABG95082.
 XX
 XX Treating genetically-defined disease associated with chromosomal
 XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 XX diseases, involves administering an inhibitor of heat shock protein 90.
 XX
 XX Disclosure; Page 242-245; 389pp; English.
 XX
 XX The invention describes a method of treating genetically-defined disease
 XX associated with chromosomal aberrations yielding oncogenic fusion
 XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
 XX cell population, treating proliferative diseases associated with mutant
 XX protein or cellular protein isoforms (II) dependent on heat shock protein
 XX (HSP)-90, or selectively treating cells expressing (II) involving
 XX administering HSP90-inhibitor. The method is useful for treating
 XX genetically-defined disease with chromosomal aberration yielding
 XX oncogenic fusion protein, treating cancerous cells containing fusion

CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This represents the DNA sequence of a chromosome aberration
 XX
 SQ Sequence 11204 BP; 3305 A; 2273 C; 2373 G; 3253 T; 0 U; 0 Other;
 Query Match 100.0%; Score 500; DB 6; Length 11204;
 Best Local Similarity 100.0%; Pred. No. 2.4e-136; Indels 0; Gaps 0;
 Matches 500; Conservative 0; Mismatches 0;
 QY 1 AGGTTTCAGAGAGAGCTGTGGGAATATGGGGGAATTAGAGGCTATCTGAGGCTCTTCAACAC 60
 Db 1 AGGTTTCAGAGAGAGCTGTGGGAATATGGGGGAATTAGAGGCTATCTGAGGCTCTTCAACAC 60
 QY 61 AATAACCCCAAGAGCTATTAAATGCTCTTTAAGGTATTACATAAATATTACTATTCTC 120
 Db 61 AATAACCCCAAGAGCTATTAAATGCTCTTTAAGGTATTACATAAATATTACTATTCTC 120
 QY 121 ATTGTGCTTTTATTGTTGTTATCATGATTATAATTGAAGTGTCTACTGTACTGCTCTC 180
 Db 121 ATTGTGCTTTTATTGTTGTTATCATGATTATAATTGAAGTGTCTACTGTACTGCTCTC 180
 QY 181 TGATCTTTGTAGCTATGGAGCATGAGCTGGGCTTTTAGAGCAGCAGCCCCAAGGAACC 240
 Db 181 TGATCTTTGTAGCTATGGAGCATGAGCTGGGCTTTTAGAGCAGCAGCCCCAAGGAACC 240
 QY 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGC 300
 Db 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGC 300
 QY 301 CCCACCCACCCATCTTCACTGATCCAAATCAGAGGAGGCGCTGGGTACCTGGTGG 360
 Db 301 CCCACCCACCCATCTTCACTGATCCAAATCAGAGGAGGCGCTGGGTACCTGGTGG 360
 QY 361 GGGTGATGTGTTCAGGGGAGGAGCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCC 420
 Db 361 GGGTGATGTGTTCAGGGGAGGAGCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCC 420
 QY 421 AATGCACTGTGACAGCTGACAGAGAACCATCAATTAATGAAGTGAAGTCTGGCT 480
 Db 421 AATGCACTGTGACAGCTGACAGAGAACCATCAATTAATGAAGTGAAGTCTGGCT 480
 QY 481 GAGACTTGCAGGGAGGCAAG 500
 Db 481 GAGACTTGCAGGGAGGCAAG 500

RESULT 4
 AAS81193/C
 ID AAS81193 standard; cDNA; 772 BP.
 XX
 AC AAS81193;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #16997.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200175067-A2.
 XX
 XX 11-OCT-2001.

immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IGA subclass selection disorder; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

FN CDS 80..676

FT /*tag= a

FT /*product= "activation-induced cytidine deaminase"

XX WO200058480-A1.

XX PD 05-OCT-2000.

XX PF 28-MAR-2000; 2000WO-JF001918.

XX PR 29-MAR-1999; 99JP-00087192.

XX PR 24-JUN-1999; 99JP-00178999.

XX PR 27-DEC-1999; 99JP-00371382.

XX PA (NISR) JAPAN TOBACCO INC.

XX PA (HONJ/) HONJO T.

XX PI Honjo T, Muramatsu M;

XX WPI; 2000-611715/58.

XX P-PSDB; AAS24198.

XX Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies.

XX Claim 3; Page 135-139; 174pp; Japanese.

XX The present sequence encodes human activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has anti-allergic, antianaemic, antitastmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IGA) deficiency disease, IGA nephritis, gamma-globulinemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disorder, MHC (major histocompatibility class) class II deficiency disease, AIDS (auto immunodeficiency syndrome), elevated Ige disorder, and IGA subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders

XX Sequence 2818 BP; 868 A; 548 C; 626 G; 776 T; 0 U; 0 Other;

Query Match 11.8%; Score 59; DB 3; Length 2818;

Best Local Similarity 100.0%; Pred. No. 1.3e-06;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 AGAGAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCAGGGAGGCAAG 500

DB 1 AGAGAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCAGGGAGGCAAG 59

RESULT 7

ABX05468

ID ABX05468 standard; cDNA; 1543 BP.

XX AC ABX05468;

XX 17-JAN-2003 (first entry)

Human novel polynucleotide #483.

XX Human; gene; ss; genetic disorder; gene mapping; medical imaging; cancer; neurodegenerative disorder; lymphoid cell disorder; osteoporosis; Parkinson's disease; Alzheimer's disease; bone degenerative disorder; osteoarthritis; periodontal disease; liver fibrosis; viral infection; fungal infection; bacterial infection; autoimmune disease; diabetes; atopic dermatitis.

XX Homo sapiens.

OS WO200274961-A1.

FN 26-SEP-2002.

XX PD 14-MAR-2002; 2002WO-US005109.

XX PF 15-MAR-2001; 2001US-00810173.

XX PR (HYSE-) HYSEQ INC.

XX PI Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;

XX PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;

XX PI Wehrman T, Wang J, Wang D, Drmanac RT;

XX WPI; 2003-040556/03.

XX P-PSDB; ABU00390.

XX New isolated polypeptides and polynucleotides, useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders, lymphoid cell disorders, bone degenerative disorders, and infections.

XX Claim 1; SEQ ID NO 483; 235pp; English.

XX The invention relates to human polynucleotides and the polypeptides they encode. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, medical imaging, identification of mutations, responsible for genetic disorders or other traits, assessing biodiversity and producing many other types of data and products dependent on DNA and amino acid sequences. They are also useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell disorders, osteoporosis, osteoarthritis, bone degenerative disorders, periodontal disease, liver fibrosis, infections (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis). Sequences ABX04986-ABX05511 represent human polynucleotides of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office

XX Sequence 1543 BP; 428 A; 334 C; 352 G; 429 T; 0 U; 0 Other;

Query Match 11.2%; Score 56; DB 7; Length 1543;

Best Local Similarity 100.0%; Pred. No. 7.3e-06;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 GAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCAGGGAGGCAAG 500

DB 2 GAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCAGGGAGGCAAG 57

RESULT 8

ABX73287

ID ABX73287 standard; DNA; 2791 BP.

XX AC ABX73287;

XX 04-DEC-2002 (first entry)

XX DNA encoding human translocation del(12p) protein #2.

KW Chromosome aberration; oncogenic fusion protein; cancer;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200269900-A2.
 PN
 XX
 PD 12-SEP-2002.
 XX
 XX
 PF 01-MAR-2002; 2002WO-US006518.
 XX
 XX
 PR 01-MAR-2001; 2001US-0272751P.
 XX
 XX (CONF-) CONFORMA THERAPEUTICS CORP.
 PA
 XX Fritz LC, Burrows FU;
 PI
 XX WPI: 2002-698710/75.
 DR
 DR P-PSDB; ABG95083.
 XX
 XX Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90.
 PT
 XX
 XX Disclosure; Page 246-247; 389pp; English.
 PS
 XX The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock protein
 CC (HSP)-90, or selectively treating cells expressing (II) involving
 CC administering HSP90-inhibitor. The method is useful for treating
 CC genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This represents the DNA sequence of a chromosome aberration
 XX
 XX Sequence 2791 BP; 842 A; 548 C; 625 G; 776 T; 0 U; 0 Other;
 SQ
 Query Match 11.2%; Score 56; DB 6; Length 2791;
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 445 GAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCGAGGAGGCAAG 500
 DB 1 GAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCGAGGAGGCAAG 56
 RESULT 9
 ABS73288
 ID ABS73288 standard; DNA; 2791 BP.
 XX
 XX ABS73288;
 AC
 XX 04-DEC-2002 (first entry)
 DT
 XX DNA encoding human translocation del(12p) protein #3.
 DE

XX Chromosome aberration; oncogenic fusion protein; cancer;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200269900-A2.
 PN
 XX
 PD 12-SEP-2002.
 XX
 XX
 PF 01-MAR-2002; 2002WO-US006518.
 XX
 XX
 PR 01-MAR-2001; 2001US-0272751P.
 XX
 XX (CONF-) CONFORMA THERAPEUTICS CORP.
 PA
 XX Fritz LC, Burrows FU;
 PI
 XX WPI: 2002-698710/75.
 DR
 DR P-PSDB; ABG95084.
 XX
 XX Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90.
 PT
 XX
 XX Disclosure; Page 248-249; 389pp; English.
 PS
 XX The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock protein
 CC (HSP)-90, or selectively treating cells expressing (II) involving
 CC administering HSP90-inhibitor. The method is useful for treating
 CC genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This represents the DNA sequence of a chromosome aberration
 XX
 XX Sequence 2791 BP; 842 A; 548 C; 625 G; 776 T; 0 U; 0 Other;
 SQ
 Query Match 11.2%; Score 56; DB 6; Length 2791;
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 445 GAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCGAGGAGGCAAG 500
 DB 1 GAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCGAGGAGGCAAG 56
 RESULT 10
 ABS24315
 ID ABS24315 standard; DNA; 983 BP.
 XX
 XX ABS24315;
 AC
 XX 18-MAR-2003 (first entry)
 DT
 XX

DE Sclerotinia stem rot resistance quantitative trait locus Satt329.
 XX
 KW Sclerotinia; stem rot; disease resistance; transgenic plant; plant;
 KW soybean; quantitative trait locus; QTL; marker; ds.
 XX
 OS Glycine max.
 XX
 PN WO200299385-A2.
 XX
 PD 12-DEC-2002.
 XX
 PF 07-JUN-2002; 2002WO-US018173.
 XX
 PR 07-JUN-2001; 2001US-0297044P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Han F, Katt M, Schuh W, Webb DW;
 XX
 XX WPI; 2003-148684/14.
 XX
 XX Identifying a Sclerotinia stem rot or white mold resistant or susceptible
 PT dicot plants e.g. soybean, by identifying a quantitative trait loci or
 PT markers associated with Sclerotinia stem rot resistance.
 XX
 PS Disclosure; Page 63; 65pp; English.
 XX
 XX The present sequence is the nucleotide sequence of soybean quantitative
 CC trait locus (QTL) Satt329, a marker for Sclerotinia stem rot resistance.
 CC The invention relates to the identification of genetic markers correlated
 CC with Sclerotinia stem rot resistance. The markers are used to identify
 CC plants, especially soybean, that are resistant or exhibit improved
 CC resistance to Sclerotinia stem rot, or white mold. A claimed method
 CC involves the identification of a nucleic acid that is flanked by the
 CC marker pair Satt329 and Sat 129 (see AB224314). The markers are useful
 CC for marker-assisted selection and breeding of Sclerotinia stem rot
 CC resistant plants, and for the identification of susceptible plants. The
 CC markers are also used to identify and define chromosome intervals
 CC corresponding to, or including, QTL associated with Sclerotinia stem rot
 CC resistance. The QTL can be isolated by positional cloning e.g. of genetic
 CC intervals defined by a pair of markers. The QTL can be used to produce
 CC transgenic cells and plants exhibiting improved resistance to
 CC Sclerotinia. QTL nucleic acids isolated from e.g. soybean can be used to
 CC identify homologues of QTLs for Sclerotinia stem rot resistance from
 CC other susceptible plants, including canola, alfalfa and sunflower
 XX
 SQ Sequence 983 BP; 325 A; 129 C; 118 G; 402 T; 0 U; 9 Other;
 Query Match 8.8%; Score 43.8; DB 7; Length 983;
 Best Local Similarity 54.5%; Pred. No. 0.023; Mismatches 0; Gaps 0;
 Matches 78; Conservative 0; Indels 65; Indels 0; Gaps 0;
 QY 30 GAATTAGAGGCTATCTGAGGCTCTTCAACACAAATACCCAAAGCTATTTAAATGCTCT 89
 DB 361 GAATCAATCTTATCTATCTTCTTCAACCAATGATTTTNGGGTGNANTCACATATTTT 420
 QY 90 TTAAGTATTTCATATAATATCTATCTCTCTGCTTTTATTTTCTGTTATCATGAT 149
 DB 421 TATNTGCTTANAT 480
 QY 150 TATAATTGAAGTCTCTACTGTGA 172
 DB 481 TATTATTATTATATATATATATAT 503

RESULT 11
 ABV57342/c
 ID ABV57342 standard; cDNA; 346 BP.
 XX
 AC ABV57342;
 XX
 DT 17-SEP-2002 (first entry)
 XX

DE Human prostate expression marker cDNA 57333.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 23-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 XX WPI; 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 11032; 11750pp; English.
 XX
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
 CC of progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 346 BP; 194 A; 66 C; 47 G; 39 T; 0 U; 0 Other;
 Query Match 7.9%; Score 39.6; DB 5; Length 346;
 Best Local Similarity 54.0%; Pred. No. 0.25; Mismatches 0; Gaps 0;
 Matches 81; Conservative 0; Indels 69; Indels 0; Gaps 0;
 QY 76 TATTTAAATGCTCTTTAAGGTATTTACATAAATATTAATCTATCTATGCTTTATTT 135
 DB 232 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 173
 QY 136 TGTGTTATCATGATTAATTAATGAAGTCTCTACTGTTCTCTGCTCTCTGCTCTAGCT 195
 DB 172 TTTTCTTTTCTTTGAGTTTGAATGTTTAACTCTCTCTCTCTCTCTCTCTCTCTCT 113
 QY 196 ATGAGCATGAGCTGGGCTTTTAGACGAC 225
 DB 112 CTCGTGCTGCACAGCTATTGATGACACC 83

RESULT 12
 ABL12834/c
 ID ABL12834 standard; cDNA; 11143 BP.
 XX
 AC ABL12834;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32984.


```

XX (FRIE/) FRIEDRICH G.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
XX
XX Friedrich G, Zambrowicz B, Sands AT;
XX WPI; 2002-626541/67.
XX
XX Novel murine polynucleotides that individually identify novel genes into
PT which a retroviral gene trap vector has been integrated, useful in
PT genomic analysis and in discovery, development of therapeutic and
PT diagnostic agents.
XX
XX Claim 2; SEQ ID NO 1014; 29pp + Sequence Listing; English.
XX
XX The invention relates to isolated murine polynucleotides (I) comprising a
CC contiguous stretch of at least about 60 nucleotides of a sequence
CC (ABQ96733-ABQ98191) chosen from 1461 OMIBANK gene trapped sequences
CC (GTSs). The novel genes can be used in a process to identify novel
CC polynucleotide sequences by comparing them to the novel gene sequences.
CC The novel genes and cells are useful in functional genomic analysis and
CC in the discovery and development of new therapeutic and diagnostic agents
CC and methods. (I) is useful for identifying the coding regions of the
CC murine genome, to isolate cDNAs, genomic clones or full-length
CC genes/polynucleotides or homologues, heterologues, paralogues or
CC orthologues that are capable of hybridising to one or more of the GTSs
CC under stringent conditions. (I) can be incorporated into a phage display
CC system that can be used to screen for proteins or other ligands, that are
CC capable of binding an amino acid sequence encoded by an oligonucleotide
CC or polynucleotide sequence in at least one of the GTS sequences. (I) is
CC useful in arrays, such as gene chips, to identify and characterise
CC temporal and tissue specific gene expression, to identify the gene of
CC interest from many sources and for genetic manipulations such as
CC antisense inhibition and gene targeting. Decreasing the level of
CC expression of (I) and/or down regulating the activity of peptides or
CC proteins encoded by (I) is useful for treating development and cell
CC differentiation disorders. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20020081668
XX
XX Sequence 328 BP; 97 A; 74 C; 99 G; 56 T; 0 U; 2 Other;
SQ
Query Match 7.6%; Score 38.2; DB 6; Length 328;
Best Local Similarity 56.3%; Pred. No. 0.62; Mismatches 0; Gaps 0;
Matches 55; Conservative 0; Indels 28;
QY 418 GCCAATGCACTGTTCAGACTGAGACAGAGAACCATTAATTAAGTGCAGATTTTCG 477
Db 79 GACACAGGGGCTGGGACAGAGACAGAGAACCAACAGGACTTGGAGGAGAGAGATCCGA 138
QY 478 CCTGACACTTGCAGGAGGAGCAAG 500
Db 139 TGTCAGAGCTGCAGGAAGAAAG 161
XX
RESULT 15
ABL08198/C
ID ABL08198 standard; cDNA; 4363 BP.
XX
XX ABL08198;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 19076.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN

```

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XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656960/75.
XX
XX P-PSDB; ABB64095.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Claim 1; SEQ ID NO 19076; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at fip.wipo.int/pub/published_pct_sequences
XX
XX Sequence 4363 BP; 1461 A; 939 C; 974 G; 989 T; 0 U; 0 Other;
SQ
Query Match 7.6%; Score 38.2; DB 4; Length 4363;
Best Local Similarity 55.7%; Pred. No. 2.1;
Matches 73; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 87 TCTTTAAGCTATTACATAAATATTACTATTCTCATTTGCTTTTATTTTGTTCATCAT 146
Db 3656 TATTTGTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 3597
QY 147 GATTATAATTTGAAGTGTCTACTGTCTTACTGCTCTCTGATCTTTGCTAGCTATGAGCATGG 206
Db 3596 ATTTTGTAGTGTATTATGATAGAGTTCTTGTGTACTGCTGTACATTTGTTATGATCTGCG 3537
QY 207 ACTGGGCTTTT 217
Db 3536 CCTATGCTTTT 3526
XX
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Job time : 288.857 secs

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 13:06:29 ; Search time 55.4449 Seconds
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Total number of hits satisfying chosen parameters: 1365418

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	37.2	7.4	520	3	US-08-943-731-112
3	37.2	7.4	24183	3	US-08-943-731-3
C 4	36.6	7.3	1830121	4	US-09-557-884-1
C 5	36.6	7.3	1830121	4	US-09-643-990A-1
6	36.2	7.2	3155	2	US-08-591-629-7
C 7	36	7.2	7605	3	US-09-417-455-8
C 8	36	7.2	7605	4	US-09-348-942-8
C 9	36	7.2	7605	4	US-09-457-626-8
C 10	36	7.2	7605	4	US-09-576-008-8
11	35.6	7.1	3836	4	US-09-976-594-59
12	35.2	7.0	832	4	US-09-621-976-2813
13	35	7.0	2540	4	US-09-684-708A-4
14	35	7.0	1664976	4	US-08-916-421B-1
C 15	34.4	6.9	13124	2	US-08-487-826B-13
16	34.2	6.8	246240	2	US-08-724-394A-20
17	34.2	6.8	246240	2	US-08-724-394A-21
18	34.2	6.8	246240	2	US-08-724-394A-22
19	33.8	6.8	3707	3	US-09-276-531-42
20	33.8	6.8	5714	4	US-09-620-312D-393
21	33.8	6.8	6709	3	US-09-285-601-3
22	33.8	6.8	19233	4	US-10-204-708-46
23	33.8	6.8	640681	4	US-09-790-988-1
24	33.4	6.7	12571	4	US-09-322-478-20
C 25	33.4	6.7	640681	4	US-09-790-988-1
26	33.4	6.7	1230025	4	US-09-198-452A-1
C 27	33.2	6.6	1631	3	US-09-118-319-1

28	33.2	6.6	3156	4	US-09-134-001C-2168	Sequence 2168, Ap
C 29	33.2	6.6	4000	2	US-08-861-464-5	Sequence 5, Appli
C 30	33.2	6.6	4000	2	US-08-395-001-5	Sequence 5, Appli
C 31	33.2	6.6	4000	3	US-09-323-433A-5	Sequence 5, Appli
32	33.2	6.6	786431	4	US-09-751-389-3	Sequence 3, Appli
33	33	6.6	975	4	US-09-601-198-32	Sequence 32, Appli
34	33	6.6	2075	1	US-08-238-163-3	Sequence 3, Appli
C 35	32.8	6.6	789	4	US-09-134-001C-2581	Sequence 2581, Ap
C 36	32.8	6.6	4185	4	US-09-417-485D-7	Sequence 7, Appli
C 37	32.8	6.6	5340	4	US-09-627-122-21	Sequence 21, Appli
C 38	32.8	6.6	6070	4	US-10-204-708-9	Sequence 9, Appli
39	32.8	6.6	6669	4	US-10-204-708-6	Sequence 6, Appli
40	32.8	6.6	9347	4	US-10-204-708-35	Sequence 35, Appli
C 41	32.8	6.6	10640	4	US-09-417-485D-5	Sequence 5, Appli
42	32.6	6.5	63000	4	US-09-780-172-18	Sequence 18, Appli
C 43	32.4	6.5	972	3	US-09-286-690-1	Sequence 1, Appli
C 44	32.4	6.5	11485	4	US-09-410-464-9	Sequence 9, Appli
45	32.2	6.4	1173	3	US-09-285-601-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-914-999-7/c
; Sequence 7, Application US/08914999
; Patent No. 6346406
; GENERAL INFORMATION:
; APPLICANT: Ryazanov, Alexey G.
; APPLICANT: Hait, William N.
; APPLICANT: Pavur, Karen S.
; TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
; TITLE OF INVENTION: AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,999
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 601-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2237 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Dictyostelium discoideum
; US-08-914-999-7

Query Match 8.4%; Score 41.8; DB 4; Length 2237;
Best Local Similarity 59.8%; Pred. No. 0.0065;
Matches 70; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
Query Match 7.3%; Score 36.6; DB 4; Length 1830121;
Best Local Similarity 48.3%; Pred. No. 9;
Matches 102; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
QY 40 CTATCTGAGGCTCTTCAACACAAATACCCAGAGCTATTATAATGCTCTTTAAGGTATT 99
DB 710070 CTATTAAATGACCTGAACTATAAATCCAAAGGAATTTTCCCGACATTTTCTCT 710011
QY 100 TACATAAATATTACTTCTCATTTGCTGCTTTTATTTTGTATCATGATTATAATTGAA 159
DB 710010 AACAAAAAATCGCACCTTTAACAGTGCATTTTCTTATTAATTAAATTAGGACATTCG 709951
QY 160 GTGCTACTGTTACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 219
DB 709950 CGTTTTCATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 709891
QY 220 AGCAGCAGCCCCAAAGGAACCTAAACATTAA 250
DB 709890 AGAATAATCAATTTTTCAGCTTTCACATTGA 709860
RESULT 5
US-09-643-990A-1/c
Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
Hamilton O. Smith

J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1
Query Match 7.3%; Score 36.6; DB 4; Length 1830121;
Best Local Similarity 48.3%; Pred. No. 9;
Matches 102; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
QY 40 CTATCTGAGGCTCTTCAACACAAATACCCAGAGCTATTATAATGCTCTTTAAGGTATT 99
DB 710070 CTATTAAATGACCTGAACTATAAATCCAAAGGAATTTTCCCGACATTTTCTCT 710011
QY 100 TACATAAATATTACTTCTCATTTGCTGCTTTTATTTTGTATCATGATTATAATTGAA 159
DB 710010 AACAAAAAATCGCACCTTTAACAGTGCATTTTCTTATTAATTAAATTAGGACATTCG 709951
QY 160 GTGCTACTGTTACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 219
DB 709950 CGTTTTCATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 709891
QY 220 AGCAGCAGCCCCAAAGGAACCTAAACATTAA 250
DB 709890 AGAATAATCAATTTTTCAGCTTTCACATTGA 709860
RESULT 6
US-08-591-629-7
Sequence 7, Application US/08591629
Patent No. 5993808
GENERAL INFORMATION:
APPLICANT: MELCHERS, Leo Sjoerd
APPLICANT: APOTHEKER-DE GROOT, Marion
APPLICANT: BOL, John Ferdinand
APPLICANT: CORNELISSEN, Bernardus Johannes Clemens
APPLICANT: LINTHORST, Hubertus Josephus Maria

APPLICANT: PONSTEIN, Anne Silene
 APPLICANT: SELA-BURLAGE, Marianne Beatrix
 TITLE OF INVENTION: Plant chitinases, DNA coding therefor and
 TITLE OF INVENTION: Plants containing same
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ladas & Parry
 STREET: 26 West 61st Street
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10023-7604
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 COMPUTER: IBM PC 4.86 SX 50 Mhz
 OPERATING SYSTEM: DOS 6.20
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/591,629
 FILING DATE: 15-FEB-96
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP94/02761
 FILING DATE: 17-AUG-94
 PRIOR APPLICATION NUMBER: EP 93202425.0
 FILING DATE: 17-AUG-93
 ATTORNEY/AGENT INFORMATION:
 NAME: MASS, CLIFFORD J.
 REGISTRATION NUMBER: 30,086
 REFERENCE/DOCKET NUMBER: U-010627-0
 TELEPHONE: (212) 708-1800
 TELEFAX: (212) 246-8959
 TELEX: 233288

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 3155 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORGANISM: Nicotiana tabacum

STRAIN: Samsun NN

FEATURE:

NAME/KEY: exon

LOCATION: 454..907

FEATURE:

NAME/KEY: exon

LOCATION: 1859..2497

FEATURE:

NAME/KEY: exon

LOCATION: 2847..2884

FEATURE:

NAME/KEY: intron

LOCATION: 908..1858

FEATURE:

NAME/KEY: intron

LOCATION: 2498..2846

FEATURE:

NAME/KEY: CDS

LOCATION: Join(454..907, 1859..2497, 2847..2884)

US-08-591-629-7

Query Match

Best Local Similarity 7.2%; Score 36.2; DB 2; Length 3155;

Matches 83; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 77 AATTAAATGCTTTTAAGGTATTACATAAATATTACTTCTCATTTGCTTTTATTTT 136

DB 2731 AATTAAATGCTTTTAAGGTATTACATAAATATTACTTCTCATTTGCTTTTATTTT 2790

QY 137 GTGTTATCATGATTATTAATGAAGTGTCTACTGTCTACTGCTCTCTGATCTTTGTAGCTA 196
 DB 2791 TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 2850
 QY 197 TGGAGCATGGACTGGGCTTTTAGACAGCAGCAGCCCAAGGA 237
 DB 2851 ACAACATGGGAGTGTCAATTTCAAGAGATGAAGTGATGGA 2891

RESULT 7

US-09-417-455-8/c

; Sequence 8, Application US/09417455

; Patent No. 6294655

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Page, Ann

; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF

; FILE REFERENCE: 28110/36328

; CURRENT APPLICATION NUMBER: US/09/417,455

; CURRENT FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: US 09/348,942

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: PCT/US99/04291

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: US 09/287,210

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: US 09/251,370

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: US 09/229,591

; PRIOR FILING DATE: 1999-01-13

; PRIOR APPLICATION NUMBER: US 09/127,698

; PRIOR FILING DATE: 1998-07-31

; PRIOR APPLICATION NUMBER: US 09/099,818

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 09/082,364

; PRIOR FILING DATE: 1998-05-20

; PRIOR APPLICATION NUMBER: US 09/079,909

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: US 09/055,010

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 7605

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-417-455-8

Query Match

Best Local Similarity 7.2%; Score 36; DB 3; Length 7605;

Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 80 TAAATGCTTTTAAGGTATTACATAAATATTACTTCTCATTTGCTTTTATTTG 139

DB 632 TAATTATTGTTAAAGCATACACTTTATTTTAAAGTTTATTTTCTTTTCTTTT 573

QY 140 TTATCATGATTATTAATGAAGTGT 163

DB 572 TTATTATTATTACTTTAAGTTT 549

RESULT 8

US-09-348-942-8/c

; Sequence 8, Application US/09348942

; Patent No. 6337072

; GENERAL INFORMATION:

; APPLICANT: John Ford

; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF

; FILE REFERENCE: 28110/35801

; CURRENT APPLICATION NUMBER: US/09/348,942

; CURRENT FILING DATE: 1999-07-07

; EARLIER APPLICATION NUMBER: PCT/US99/04291

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; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7605
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-348-942-8

Query Match      7.2%; Score 36; DB 4; Length 7605;
Best Local Similarity 64.3%; Pred. No. 0.77;
Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 80 TAAATGCTCTTTAAAGGTATTACATAAATATTACTTCTCATTTGCTTTTATTG 139
Db 632 TAAATTTGTTAAAGCATACACTTTATTTTAAAGTTTATTTTCTTTTCTTTTA 573

QY 140 TTATCATGATTATAATTGAAGTGT 163
Db 572 TTATTATTATTACTTTAAGTTT 549

RESULT 9
US-09-457-626-8/c
; Sequence 8, Application US/09457626
; Patent No. 6426191
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US 09/457,626
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7605
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-348-942-8

Query Match      7.2%; Score 36; DB 4; Length 7605;
Best Local Similarity 64.3%; Pred. No. 0.77;
Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 80 TAAATGCTCTTTAAAGGTATTACATAAATATTACTTCTCATTTGCTTTTATTG 139
Db 632 TAAATTTGTTAAAGCATACACTTTATTTTAAAGTTTATTTTCTTTTCTTTTA 573

QY 140 TTATCATGATTATAATTGAAGTGT 163
Db 572 TTATTATTATTACTTTAAGTTT 549

RESULT 9
US-09-457-626-8/c
; Sequence 8, Application US/09457626
; Patent No. 6426191
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US 09/457,626
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7605
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-348-942-8

Query Match      7.2%; Score 36; DB 4; Length 7605;
Best Local Similarity 64.3%; Pred. No. 0.77;
Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 80 TAAATGCTCTTTAAAGGTATTACATAAATATTACTTCTCATTTGCTTTTATTG 139
Db 632 TAAATTTGTTAAAGCATACACTTTATTTTAAAGTTTATTTTCTTTTCTTTTA 573

QY 140 TTATCATGATTATAATTGAAGTGT 163
Db 572 TTATTATTATTACTTTAAGTTT 549

RESULT 10
US-09-576-008-8/c
; Sequence 8, Application US/09576008
; Patent No. 6541623
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice Suk-Yue
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36456
; CURRENT APPLICATION NUMBER: US 09/576,008
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/523,552
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/457,626
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7605
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-576-008-8

Query Match      7.2%; Score 36; DB 4; Length 7605;
Best Local Similarity 64.3%; Pred. No. 0.77;
Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 80 TAAATGCTCTTTAAAGGTATTACATAAATATTACTTCTCATTTGCTTTTATTG 139
Db 632 TAAATTTGTTAAAGCATACACTTTATTTTAAAGTTTATTTTCTTTTCTTTTA 573

QY 140 TTATCATGATTATAATTGAAGTGT 163
Db 572 TTATTATTATTACTTTAAGTTT 549
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; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349491)..(1349491)
;
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (871619)..(871619)
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; NAME/KEY: misc feature
; LOCATION: (1084830)..(1084830)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1096846)..(1096846)
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; NAME/KEY: misc feature
; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349491)..(1349491)

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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1664855)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

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	Query Match	7.0%;	Score 35;	DB 4;	Length 1664976;
	Best Local Similarity	50.9%;	Pred. No. 26;		
	Matches 83;	Conservative 0;	Mismatches 80;	Indels 0;	Gaps 0;
Qy	1	AGTTTCAGAGAGACTGTGGGAATATGGGGGAATTAGAGGCTATCTGAGGCTCTTTCACAC	60		
Dd	482394	AGTTAGAGAGAGAAATTGAAAACCTTAGAAGAGATGAGAAATGCGCCGCAAAATTAG	482453		
Qy	61	AATAACCCAGAGCTATTTTAAATCTCTTTAAAGTATTTACATPAAATATTACTATCTC	120		
Dd	482454	AAAAGCTTAAGGAGAAGTTTGAAGAAGTTTAACTGTAATAGAGAAATAATTAATTTTC	482513		
Qy	121	ATTGTGCTTTTATTTTGGTGTTATCATGATTAATAATTGAAGTGT	163		
Dd	482514	ATTCTATTTTATTTTGGCTTTTATTTTATTTTATTTTATCAATTTTT	482556		

RESULT 15
US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 15:00:30 ; Search time 243.692 Seconds
(without alignments)

7504.213 Million cell updates/sec

Title: US-09-966-880A-35_COPY_1_500

Perfect score: 500

Sequence: 1 aggttcagagactgtggg.....gagacttcgaggaggaag 500

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	100.0	5514	9	US-09-966-880A-9
2	500	100.0	11204	9	US-09-966-880A-35
3	59	11.8	87	9	US-09-966-880A-11
4	59	11.8	2818	9	US-09-966-880A-7
5	43.8	8.8	983	14	US-10-165-617B-26
6	41.8	8.4	2237	9	US-09-994-485-7
7	41.8	8.4	2237	9	US-09-832-292-11
8	39.2	7.8	3673778	14	US-10-312-841-1
9	38.6	7.7	2001	9	US-09-801-368-35
10	38.2	7.6	328	9	US-09-728-448-1014
11	38	7.6	7131	12	US-10-221-613-323
12	37.8	7.6	529	14	US-10-165-617B-31
13	37.6	7.5	3673778	14	US-10-312-841-1
14	37.2	7.4	2787	9	US-09-801-368-281
15	37.2	7.4	2787	15	US-10-369-493-25437

c	16	37.2	7.4	2886	9	US-09-801-368-131	Sequence 131, Appl
	17	37	7.4	380	9	US-09-969-373-85	Sequence 85, Appl
	18	37	7.4	380	9	US-09-969-373-86	Sequence 86, Appl
	19	36.8	7.4	9832	14	US-10-311-455-829	Sequence 628, Appl
	20	36.8	7.4	28066	14	US-10-017-161-3395	Sequence 2395, Ap
	21	36.8	7.4	28066	15	US-10-292-798-2037	Sequence 2037, Ap
c	22	36.8	7.4	3673778	14	US-10-312-841-1	Sequence 1, Appl1
	23	36.6	7.3	572	15	US-10-027-632-244183	Sequence 244183,
	24	36.6	7.3	572	15	US-10-027-632-244184	Sequence 244184,
c	25	36.6	7.3	714	12	US-10-424-599-65277	Sequence 65277, A
c	26	36.6	7.3	1830121	14	US-10-329-960-1	Sequence 1, Appl1
c	27	36.6	7.3	1830121	15	US-10-329-960-1	Sequence 1, Appl1
c	28	36.4	7.3	1859	9	US-09-880-192-33	Sequence 33, Appl
	29	36.4	7.3	1859	14	US-10-427-348-33	Sequence 33, Appl
	30	36.4	7.3	8413	14	US-10-240-485-50	Sequence 50, Appl
	31	36.4	7.3	19380	12	US-10-221-613-389	Sequence 389, Appl
c	32	36.2	7.2	748	15	US-10-027-632-15365	Sequence 15365, A
	33	36.2	7.2	6827	14	US-10-311-455-1154	Sequence 1154, Ap
	34	36.2	7.2	8346	14	US-10-240-433-401	Sequence 201, Appl
	35	36.2	7.2	4985	14	US-10-094-240-10	Sequence 10, Appl
	36	36	7.2	4985	14	US-10-056-405-10	Sequence 10, Appl
	37	36	7.2	6861	14	US-10-311-455-1201	Sequence 1201, Ap
c	38	36	7.2	7605	14	US-10-205-821-6	Sequence 6, Appl1
c	39	35.8	7.2	774	15	US-10-027-632-150736	Sequence 150736,
c	40	35.8	7.2	774	15	US-10-027-632-150737	Sequence 150737,
	41	35.8	7.2	7560	14	US-10-311-455-1195	Sequence 1195, Ap
c	42	35.6	7.1	254	9	US-09-969-373-1027	Sequence 1027, Ap
	43	35.6	7.1	693	15	US-10-027-632-268730	Sequence 268730,
	44	35.6	7.1	5273	14	US-10-311-455-847	Sequence 847, Appl
c	45	35.6	7.1	5328	14	US-10-311-455-534	Sequence 534, Appl

ALIGNMENTS

RESULT 1

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US-09-966-880A-9
; Sequence 9, Application US/09966880A
; Patent No. US20020164743A1
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Muramatsu, Masamichi
; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
; FILE REFERENCE: 06501-088001
; CURRENT APPLICATION NUMBER: US/09/966,880A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: PCT/JP00/01918
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: JP 11-371382
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: JP 11-178999
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: JP 11-87192
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 5514
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1)...(1031)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1032)...(1118)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1119)...(5514)
; US-09-966-880A-9
; Query Match 100.0%; Score 500; DB 9; Length 5514;
; Best Local Similarity 100.0%; Pred. No. 4.2e-131;
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Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGTTTCAGAGAGCTGGGATATGGGGATTTAGAGCTATCTGAGGCTCTTCAACAC 60
 Db 591 AGGTTTCAGAGAGCTGGGATATGGGGATTTAGAGCTATCTGAGGCTCTTCAACAC 650

QY 61 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAAATTTACTATTCTC 120
 Db 651 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAAATTTACTATTCTC 710

QY 121 ATTGTGCTTTTATTTTGTATCATGATTAATTAAGTATTTACATAAAATTTACTATTCTC 180
 Db 711 ATTGTGCTTTTATTTTGTATCATGATTAATTAAGTATTTACATAAAATTTACTATTCTC 770

QY 181 TGATCTTTTCTAGCTATGAGCATGGAGTGGGCTTTTATAGACAGCAGCCCCCAAGGAACC 240
 Db 771 TGATCTTTTCTAGCTATGAGCATGGAGTGGGCTTTTATAGACAGCAGCCCCCAAGGAACC 830

QY 241 TAAACATTTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCCCTATGACAGC 300
 Db 831 TAAACATTTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCCCTATGACAGC 890

QY 301 CCCACCCACCCATCTTCACTGGATCCAAATCAGGAGCAAGCCGTTGGGGTACCTGGTGG 360
 Db 891 CCCACCCACCCATCTTCACTGGATCCAAATCAGGAGCAAGCCGTTGGGGTACCTGGTGG 950

QY 361 GGGTGATGCTGTGAGGGAGGAGCCCAAAAGGCGAAGCTCAAAATTTGAATGTGAAGGCC 420
 Db 951 GGGTGATGCTGTGAGGGAGGAGCCCAAAAGGCGAAGCTCAAAATTTGAATGTGAAGGCC 1010

QY 421 AATGCACTCTCAGACTGACAGAGAGCAACCATCAATTAATTTGAAGTGAAGTATTTCTGGCCT 480
 Db 1011 AATGCACTCTCAGACTGACAGAGAGCAACCATCAATTAATTTGAAGTGAAGTATTTCTGGCCT 1070

QY 481 GAGACTTGCAGGAGGCAAG 500
 Db 1071 GAGACTTGCAGGAGGCAAG 1090

RESULT 2

US-09-966-880A-35
 ; Sequence 35, Application US/09966880A
 ; Patent No. US20020164743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Honjo, Tasuku
 ; APPLICANT: Muramatsu, Masamichi
 ; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
 ; FILE REFERENCE: 06501-088001
 ; CURRENT APPLICATION NUMBER: US/09/966,880A
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: PCT/JP00/01918
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: JP 11-371382
 ; PRIOR FILING DATE: 1999-12-27
 ; PRIOR APPLICATION NUMBER: JP 11-178999
 ; PRIOR FILING DATE: 1999-06-24
 ; PRIOR APPLICATION NUMBER: JP 11-87192
 ; PRIOR FILING DATE: 1999-03-29
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 35
 ; LENGTH: 11204
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-966-880A-35

Query Match 100.0%; Score 500; DB 9; Length 11204;
 Best Local Similarity 100.0%; Pred. No. 6.2e-131;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGTTTCAGAGAGCTGGGATATGGGGATTTAGAGCTATCTGAGGCTCTTCAACAC 60
 Db 1 AGGTTTCAGAGAGCTGGGATATGGGGATTTAGAGCTATCTGAGGCTCTTCAACAC 60

QY 61 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAAATTTACTATTCTC 120
 Db 61 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAAATTTACTATTCTC 120

QY 121 ATTGTGCTTTTATTTTGTATCATGATTAATTAAGTATTTACTGTGTTACTGCTCTCC 180
 Db 121 ATTGTGCTTTTATTTTGTATCATGATTAATTAAGTATTTACTGTGTTACTGCTCTCC 180

QY 181 TGATCTTTTCTAGCTATGAGCATGGAGTGGGCTTTTATAGACAGCAGCCCCCAAGGAACC 240
 Db 181 TGATCTTTTCTAGCTATGAGCATGGAGTGGGCTTTTATAGACAGCAGCCCCCAAGGAACC 240

QY 241 TAAACATTTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCCCTATGACAGC 300
 Db 241 TAAACATTTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCCCTATGACAGC 300

QY 301 CCCACCCACCCATCTTCACTGGATCCAAATCAGGAGCAAGCCGTTGGGGTACCTGGTGG 360
 Db 301 CCCACCCACCCATCTTCACTGGATCCAAATCAGGAGCAAGCCGTTGGGGTACCTGGTGG 360

QY 361 GGGTGATGCTGTGAGGGAGGAGCCCAAAAGGCGAAGCTCAAAATTTGAATGTGAAGGCC 420
 Db 361 GGGTGATGCTGTGAGGGAGGAGCCCAAAAGGCGAAGCTCAAAATTTGAATGTGAAGGCC 420

QY 421 AATGCACTCTCAGACTGACAGAGAGCAACCATCAATTAATTTGAAGTGAAGTATTTCTGGCCT 480
 Db 421 AATGCACTCTCAGACTGACAGAGAGCAACCATCAATTAATTTGAAGTGAAGTATTTCTGGCCT 480

QY 481 GAGACTTGCAGGAGGCAAG 500
 Db 481 GAGACTTGCAGGAGGCAAG 500

RESULT 3

US-09-966-880A-11
 ; Sequence 11, Application US/09966880A
 ; Patent No. US20020164743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Honjo, Tasuku
 ; APPLICANT: Muramatsu, Masamichi
 ; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
 ; FILE REFERENCE: 06501-088001
 ; CURRENT APPLICATION NUMBER: US/09/966,880A
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: PCT/JP00/01918
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: JP 11-371382
 ; PRIOR FILING DATE: 1999-12-27
 ; PRIOR APPLICATION NUMBER: JP 11-178999
 ; PRIOR FILING DATE: 1999-06-24
 ; PRIOR APPLICATION NUMBER: JP 11-87192
 ; PRIOR FILING DATE: 1999-03-29
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 87
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-966-880A-11

Query Match 11.8%; Score 59; DB 9; Length 87;
 Best Local Similarity 100.0%; Pred. No. 8.7e-07;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 AGAGAACCATCATTAATTAAGTGAAGTATTTCTGCGCTGAGACTTGCAGGAGGCAAG 500
 Db 1 AGAGAACCATCATTAATTAAGTGAAGTGAAGTATTTCTGCGCTGAGACTTGCAGGAGGCAAG 59

RESULT 4

US-09-966-880A-7
 ; Sequence 7, Application US/09966880A

		82	AATGTCCTTTAAAGGTATTACATAAATTAATTAATCTCATTTGCGTNTTAATTTTGCTT	141
Qy				
		1128	ATTAGTATTGCATTTATTAATTTATTAATTAATTTATTTATTTATTTATTTATTTATTT	1069
Db				
		142	ATCATGATTAAATGAAGTCTCACTGTTACT	174
Qy				
		1068	ATTATTATTATTATTATTTGGTACTATTATTACT	1036
Db				

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RESULT 10
US-09-728-446-1014
; Sequence 1014, Application US/09728446
; Patent No. US2002081668A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T
; TITLE OF INVENTION: No. US2002081668A1el
; TITLE OF INVENTION: and Mutant Cells and
; FILE REFERENCE: LEX-0101-USA
; CURRENT APPLICATION NUMBER: US/09/728,446
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,270
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 1461
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1014
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(328)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-446-1014

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	Query Match	7.6%	Score 38.2	DB 9	Length 328
	Best Local Similarity	66.3%	Fred.No. 1.5		
	Matches 55	Conservative	0	Mismatches 28	Indels 0
QY	418	GCCAAATGCACCTGTGACACTGAGACACAGAGAACCATTCATTAAATTGAAGTCGAGATTTTCTCGG	477		
DB	79	GACACAGCGCTGGGAGACAGACACAGAGAAACCCACGAGCACTTGGAGGACGAGAGATCCGA	138		

RESULT 11
US-10-221-613-323
; Sequence 323, Application US/10221613
; Publication No. US20040029123A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
; FILE REFERENCE: 5013.1004
; CURRENT APPLICATION NUMBER: US/10/221.613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/EP01/02945
; DE 10013847.00
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-03-15
; 2000-03-15
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01

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: NUMBER OF SEQ ID NOS: 428
:
: SEQ ID NO 323
:
: LENGTH: 7131
:
: TYPE: DNA
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-613-323

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Query Match 7.6%; Score 38; DB 12; Length 7131;
Best Local Similarity 54.2%; Pred. No. 8.9;
Matches 77; Conservative 0; Mismatches 65; Indels

Qy	1	AGCTTCAGAGAGACTGCGGAATATCGGGAAATTAGAGGCTATCTGAGGCTCTTCAACAC	60
Db	2029	AGGTTTAGATTATTTGGTAAATATGCAATCTGGGTGTTATGTTAATTATATGTTT	2088
Qy	61	AATAACCCAGAGAGCTATTTAAATGCTCTTTAAGTATTTACATAAATATACTATCTC	120
Db	2089	GATATTATAAGAAATTTGTTAAATGTTTTTTTAGAGGCTTGTTATTATTAATAGTATATA	2148
Qy	121	ATTGTCGCTTTTATTTTGTGTTA	142
Db	2149	AGAGAGTTTTTAAGTTGTTTTAA	2170

RESULT 12

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US/10-165-617B-31/C
Sequence 31, Application US/10165617B
Publication No. US20030150016A1
GENERAL INFORMATION:
APPLICANT: Pioneer Hi-Bred International, Inc
APPLICANT: Han, Feng
APPLICANT: Katt, Maria
APPLICANT: Schuh, Wolfgang
APPLICANT: Webb, David M
TITLE OF INVENTION: QTL Controlling Sclerotinia
FILE REFERENCE: 04-010210US
CURRENT APPLICATION NUMBER: US/10/165,617B
CURRENT FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 529

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Query Match      7.6%; Score 37.8; DB 14; Length 529;
Best Local Similarity 51.5%; Pred. No. 2.5;
Matches 87; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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Qy	78	TTTTAAATGCTCTTTAAAGTATTACATATAATATTACTATTCTCATTTGGCTTTATTATTG	13
Db	212	TAT	153
Qy	138	TGTTATCATGATTAATAATTGAAGTGTCTACGTGTTACTGGCCTCCGATCTTTGGCTAGCTAT	197
Db	152	TATTATTATTATTATTATTATTATTATTATTATTATTATTAAAGTGCATTATTCTCAATTTCTTAA	93
Qy	198	GAGATCATGGACTGGGCTTTTATAGACGACGAGCCGCCCAAGGAACCTTAAACA	246

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Db 92 TAAAAAATACACCCAGGTTTCACAGCAGAAATAGGATCAGAAAA 44
|||||
|
RESULT 13
US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: EpiGenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match
Best Local Similarity 7.5%; Score 37.6; DB 14; Length 3673778;
Matches 70; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 51 TCTTCACACATACCCACAGAGCTATTAAATGCTCTTACGCTATTACATAAATAT 110
Db 968725 TTTTAAAAAAGGTTTATTTGATTTTAAAGGTTTAGAGTTTGTAT 968784

Qy 111 TACTATTCCTAATGCTTTTATTTGTTATCATGATTATTAATGAAGTGTCTACTGT 170
Db 968785 TAAAGTTATAGGCTTTTATAGTATTTTATTTTGTGTTTTTGTGTTTTTTT 968844

Qy 171 TACT 174
Db 968845 TATT 968848

RESULT 14
US-09-801-368-281/c
; Sequence 281, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 281
; LENGTH: 2787
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; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-281

Query Match
Best Local Similarity 7.4%; Score 37.2; DB 9; Length 2787;
Matches 54; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 95 GTATTACATAAATATTACTATTCTCATTTGCTTTTATTTTGTGTTATCATGATTATAA 154
Db 2159 GCAGTAACAGGAATATTACTATTGTTATTGTTATTATTATTGTTGTTGTTATCA 2100

Qy 155 TTGAAGTGTCTACTGTTACTGC 176
Db 2099 TTATCAGTACTATAGTTACTAC 2078

RESULT 15
US-10-369-493-25437/c
; Sequence 25437, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 25437
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-25437

Query Match
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Matches 54; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 95 GTATTACATAAATATTACTATTCTCATTTGCTTTTATTTTGTGTTATCATGATTATAA 154
Db 2159 GCAGTAACAGGAATATTACTATTGTTATTGTTATTATTATTGTTGTTGTTATCA 2100

Qy 155 TTGAAGTGTCTACTGTTACTGC 176
Db 2099 TTATCAGTACTATAGTTACTAC 2078

Search completed: March 4, 2004, 19:00:13
Job time : 257.025 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:54:45 ; Search time 1955.18 Seconds
(without alignments)
7636.686 Million cell updates/sec

Title: US-09-966-880A-35_COPY_1_500

Perfect score: 500

Sequence: 1 aggttcagagactgtggg.....gagactgcaggagggaag 500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estci:*

9: gb_est2:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_estfun:*

15: em_estcom:*

16: em_esthum:*

17: em_estinv:*

18: em_estpln:*

19: em_estvrt:*

20: em_estfun:*

21: em_estmam:*

22: em_estmus:*

23: em_estpro:*

24: em_estrod:*

25: em_estphg:*

26: em_estvrl:*

27: gb_est1:*

28: gb_est2:*

29: gb_est2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	106.8	21.4	765	29	CG915486 t087k19ba
2	71	14.6	1201	13	BX402063 BX402063
3	71	14.2	535	14	CD707143
4	62.4	12.5	820	12	BG757089 602715124

ALIGNMENTS

RESULT 1
CG915486/c
LOCUS
DEFINITION t087k19ba.r1 TAMBT Bos taurus genomic clone t087k19ba, genomic survey sequence.
ACCESSION CG915486
VERSION CG915486.1 GI:33542955
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
1 (bases 1 to 765)
Lin, S., Najjar, F.Z., Adelson, D., Gill, C.A. and Roe, B.A.
Bovine BAC End Sequences from Library TAMBT
Unpublished (2003)
Contact: Bruce A. Roe
Advanced Center for Genome Technology
University of Oklahoma Department of Chemistry and Biochemistry
620 Parrington Oval, Room 208, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Class: BAC ends
High quality sequence start: 12
High quality sequence stop: 461.

5 59 11.8 693 12 BG757392
6 56 11.2 541 10 BF238155
7 56 11.2 743 12 BG68133
8 56 11.2 942 10 BF75166
9 46.4 9.3 1201 13 BX403812
C 10 44.4 8.9 429 9 AU270161
C 11 43.8 8.7 983 28 BH126520
C 12 43.4 8.7 560 12 BJ328375
C 13 43 8.6 410 28 BH126608
C 14 43 8.6 512 28 BH841403
C 15 43 8.6 953 13 EQ065440
C 16 43 8.6 1052 13 EQ055935
C 17 42.8 8.6 464 28 BH126691
C 18 42.4 8.5 872 12 BG758510
C 19 42.2 8.4 663 12 BM164461
C 20 42 8.4 505 9 AI668763
C 21 41.8 8.4 321 28 BZ713536
C 22 41.8 8.4 609 12 BJ415548
C 23 41.8 8.4 694 28 BZ013305
C 24 41.8 8.4 728 28 BH728612
C 25 41.6 8.3 458 28 BZ386931
C 26 41.6 8.3 459 12 BM276124
C 27 41.6 8.3 705 28 AZ962863
C 28 41.4 8.3 607 13 BQ739557
C 29 41.2 8.2 276 9 AU051814
C 30 41.2 8.2 555 28 BZ678338
C 31 41.2 8.2 770 29 CC726004
C 32 41.2 8.2 776 29 CE071267
C 33 41.2 8.2 908 28 CC454033
C 34 41.2 8.2 937 29 CC726011
C 35 41 8.2 269 12 BJ439114
C 36 41 8.2 362 12 BJ351256
C 37 41 8.2 554 28 A2159643
C 38 41 8.2 785 28 AQ739211
C 39 41 8.2 868 28 BH126559
C 40 40.8 8.2 500 29 CE727726
C 41 40.8 8.2 625 12 BJ396037
C 42 40.8 8.2 690 28 BZ389657
C 43 40.8 8.2 801 28 CC363214
C 44 40.8 8.2 821 29 CG059191
C 45 40.8 8.2 827 29 CG370251

765 bp DNA linear GSS 08-AUG-2003
t087k19ba, genomic clone t087k19ba, genomic survey sequence.

CG915486

CG915486.1 GI:33542955

GSS.

Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 765)

Lin, S., Najjar, F.Z., Adelson, D., Gill, C.A. and Roe, B.A.

Bovine BAC End Sequences from Library TAMBT

Unpublished (2003)

Contact: Bruce A. Roe

Advanced Center for Genome Technology

University of Oklahoma Department of Chemistry and Biochemistry

620 Parrington Oval, Room 208, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Class: BAC ends

High quality sequence start: 12

High quality sequence stop: 461.

FEATURES

source
Location/Qualifiers
1..765
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Angus bull T A M U Shoshone Y6 11519666"
/db_xref="taxon:9913"
/clone="t087k19ba"
/sex="Male"
/cell_type="Blood"
/clone_lib="TAMBT"
/note="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; TAMBT Bovine BAC library (Male) produced by Texas A&M University, Department of Animal Science."
ORIGIN
Query Match 21.4%; Score 106.8; DB 29; Length 765;
Best Local Similarity 65.8%; Pred. No. 7.4e-16;
Matches 217; Conservative 0; Mismatches 107; Indels 6; Gaps 4;
QY 123 TGTGCTTTTATTTGTTATCATGATTATTAATGAAGTGTCTACTGTACTGTCTCTG 182
DB 341 TATCTTTTTTTTTTACCAGGATTACAATATACAACTGTCTACTCTCTCTCTCTG 282
QY 183 ATCTTGTAGTATGGAGTGGCTGGCTTTTAGAGCAGCAGCCCAAGAACTTA 242
DB 281 ATCTTTACTACTGTGGAGGTAGACTGCATTTTAAAGACGAACTAAAGAACTTA 222
QY 243 AACATTAAAGCAGAGTGCCTCAATGGTTTAACTGTGTGA--CTCTGCCTATGACAGC 300
DB 221 TACATT-AGGCAGAGTGGCCGCGAGTCATTTCTCTGTGATTTTTCCTATGAAGAAC 163
QY 301 CCCACCCAC--CCATCTTCACTGGATCCAAATCAGAGCAAGCGGTGGGTACCTGGT 358
DB 162 CCCACCCACCTCCAGTGGACCCAAACAGAGGAAGCCCTGTGGGTATGGGTACCTGGT 103
QY 359 GGGGGTGATGTGTG--TCAGGGGAGGAGCCCAAGGCAAGCTCAAAATTTGAATGTGAAG 417
DB 102 GGTGTGTGTGTGCTGCTGGGGGAGGAGCCTAAAGGCTGAGTCAAAATTTGAATGTGTGAG 43
QY 418 GCAATGCACTGTCACTGACATGACACAGAGNA 447
DB 42 ACCGGTGCCTGTGTCAGCCAGTCAGCAGAGAA 13

RESULT 2

EX402063
LOCUS BX402063 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DL012YD18 5-PRIME, mRNA sequence.
ACCESSION BX402063
VERSION BX402063.1 GI:30626645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6672.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DL012YD1809QPI&cluster=6672.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DL012YD1809QPI.
Location/Qualifiers

FEATURES

source

1..1201
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DL012YD18"
/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/clone_lib="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 14.2%; Score 73; DB 13; Length 1201;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 428 TGTCACTGACAGACAGAACCATCATTAATTAAGTGAAGTATTTCTGGCCTGAGACTT 487
DB 59 TGTCACTGACAGACAGAACCATCATTAATTAAGTGAAGTATTTCTGGCCTGAGACTT 118
QY 488 GCAGGGAGGCAAG 500
DB 119 GCAGGGAGGCAAG 131
RESULT 3
CD707143
LOCUS CD707143 535 bp mRNA linear EST 25-JUN-2003
DEFINITION EST23670 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD707143
VERSION CD707143.1 GI:32237773
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 535)
AUTHORS Zeng, Y.-X., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Liu, X.-Q.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
1..535
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"
ORIGIN
Query Match 14.2%; Score 71; DB 14; Length 535;
Best Local Similarity 93.7%; Pred. No. 5.3e-07;
Matches 74; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 422 ATGCACCTGTCACTGACAGACAGAACCATCATTAATTAAGTGAAGTATTTCTGGCCTG 481
DB 22 ATGCCCGGGAGACTGACAGACAGAACCATCATTAATTAAGTGAAGTATTTCTGGCCTG 81
QY 482 AGACTTCACGGAGGCAAG 500
DB 82 AGACTTCACGGAGGCAAG 100

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 693)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1694 row: k column: 05
High quality sequence stop: 693.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4851580"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

Query Match 11.8%; Score 59; DB 12; Length 693;
Best Local Similarity 100.0%; Pred. NO. 0.00051;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 AGAGAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTTCGACGGAGGCAAG 500
|||||
Db 2 AGAGAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTTCGACGGAGGCAAG 60
|||||

RESULT 6
BF238155 541 bp mRNA linear EST 14-NOV-2000
LOCUS 601811880F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054915 5',
DEFINITION mRNA sequence.
ACCESSION BF238155
VERSION BF238155.1 GI:11152074
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 541)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1695 row: p column: 20
High quality sequence stop: 541.
Location/Qualifiers

FEATURES
source

source

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1. 541
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4054915"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/organism="Homo sapiens"
/site="EcORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

```

ORIGIN

```

Query Match 11.2%; Score 56; DB 10; Length 541;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 445 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 500
Db 2 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 57

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RESULT 7
BG686133 743 bp mRNA linear EST 01-MAY-2001
LOCUS 602538412F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766234 5',
DEFINITION mRNA sequence.
ACCESSION BG686133
VERSION BG686133.1 GI:13917530
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 743)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1626 row: g column: 03
High quality sequence stop: 740.

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FEATURES

source

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1. 743
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/organism="Homo sapiens"
/site="EcORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

```

ORIGIN

```

Query Match 11.2%; Score 56; DB 12; Length 743;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 445 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 500
Db 2 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 57

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RESULT 8
BF975166 942 bp mRNA linear EST 22-JAN-2001
LOCUS 602244657F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335639 5',
DEFINITION mRNA sequence.
ACCESSION BF975166
VERSION BF975166.1 GI:12342381
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 942)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1207 row: a column: 16
High quality sequence stop: 707.

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FEATURES

source

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1. 942
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/organism="Homo sapiens"
/site="EcORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

```

ORIGIN

```

Query Match 11.2%; Score 56; DB 10; Length 942;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 445 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 500
Db 2 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 57

```

```

RESULT 9
EX403812 1201 bp mRNA linear EST 13-MAY-2003
LOCUS EX403812 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION CLOB80022C04 5-PRIME, mRNA sequence.
ACCESSION EX403812

```


ORIGIN

Query Match
Best Local Similarity 8.8%; Score 43.8; DB 28; Length 983;
Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 30 GAATTAGAGGCTATCGAGGCTTTCACACACAATAACCAAGAGCTATTAAATGCTCT 89
|||||
Db 361 GAATCAAAATCTATCTAAATCTTTCNCAANCCATNGATTTTNGGGTGNANTCACATATTT 420
|||||

QY 90 TTAAGGTATTACATAAATATTACTATCTCTCATCTGCTTTTATTGTTGATCATGAT 149
|||||

Db 421 TATNTGTCAT 480
|||||

QY 150 TATAATTGAAGTCTACTGTTA 172
|||||

Db 481 TATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 503
|||||

RESULT 12

BJ328375/c

LOCUS

DEFINITION

BJ328375 Dictyostelium discoidium cDNA library, AF Dictyostelium discoidium cDNA clone dda23023 5', mRNA sequence.

ACCESSION

BJ328375

VERSION

1 (bases 1 to 560)

KEYWORDS

EST.

SOURCE

Dictyostelium discoidium

ORGANISM

Dictyostelium discoidium

REFERENCE

1 (bases 1 to 560)

AUTHORS

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

TITLE

Full length cDNA of Dictyostelium discoidium at the aggregation stage

JOURNAL

Unpublished (2002)

COMMENT

Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source

1..560

/organism="Dictyostelium discoidium"

/mol_type="mRNA"

/strain="AX4"

/db_xref="taxon:44689"

/clone="dda23023"

/sex="mat A"

/dev_stage="Aggregation stage"

/clone_lib="Dictyostelium discoidium cDNA library, AF"

ORIGIN

Query Match
Best Local Similarity 8.7%; Score 43.4; DB 12; Length 560;
Matches 71; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 72 AAGCTATTAAATGCTTTTAAAGGATTATTAACATAATATTACTATCTCATGCTGCTTT 131
|||||

Db 217 ATGATATTGAATACTACTATTGTTTATTATTATTATTATTATTATTATTATTATTATTAT 158
|||||

QY 132 ATTCTGTGATCATGATTAATTAATGAAGTGTCTACTGCTTACTGCTCTCATCTTT 188
|||||

Db 157 TATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 101
|||||

RESULT 13

BJ126608

LOCUS

DEFINITION

BARC-Satt429 Size-selected soybean genomic Glycine max genomic, genomic survey sequence.

ACCESSION

BJ126608

VERSION

BH126608.1 GI:14970111

KEYWORDS

GSS.

SOURCE

Glycine max (soybean)

ORGANISM

Glycine max

REFERENCE

1 (bases 1 to 410)

AUTHORS

Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G., Kahler, A.L., Kaya, N., VanToai, T.T., Lohnes, D.G., Chung, J. and Specht, J.E.

TITLE

An Integrated Genetic Linkage Map of the Soybean Genome

JOURNAL

Crop Sci. 39, 1464-1490 (1999)

COMMENT

Contact: Cregan PB
Soybean Genomics and Improvement Lab
USDA-ARS
BARC-West, Bldg. 006, Beltsville, MD 20705, USA
Tel: 301-504-5070
Fax: 301-504-5728
Email: cregan@ba.ars.usda.gov
Single pass sequence. See the SoyBase home page (http://soybase.agron.iastate.edu) for PCR primer sequences and amplification conditions.
Class: SSR-containing genome clone.

FEATURES

source

1..410

/organism="Glycine max"

/mol_type="genomic DNA"

/db_xref="taxon:3847"

/clone_lib="Size-selected soybean genomic"

/note="Simple sequence repeat containing clones from genomic DNA of the cultivar 'Williams', as described by Cregan, P.B., Bhagwat, A.A., Akkaya, M.S. and Rongwen, J. (1994). Methods Cell. Mol. Biol. 5:49-61"

ORIGIN

Query Match
Best Local Similarity 8.6%; Score 43; DB 28; Length 410;
Matches 76; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 44 CTGAGCTCTTCAACACATATACCAAGAGCTATTAAATGCTCTTTAAGGTATTACA 103
|||||

Db 39 CTGTTGATTTTATATAATAATCTTTAAAGTTATATAAATGATTTGTGATGAATT 98
|||||

QY 104 TAAATATTACTATCTCATTTGCTTTTATTGTTTATCATGATTATTAATGAAGTGT 163
|||||

Db 99 TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTAT 158
|||||

QY 164 CTAATCTTACT 174
|||||

Db 159 TTATTATTATT 169
|||||

RESULT 14

BH841403

LOCUS

DEFINITION

TC3-55G15-TV TC3 Trypanosoma cruzi genomic clone TC3-55G15, genomic survey sequence.

ACCESSION

BH841403

VERSION

BH841403.1 GI:21408618

KEYWORDS

GSS.

SOURCE

Trypanosoma cruzi

ORGANISM

Trypanosoma cruzi

REFERENCE

1 (bases 1 to 512)

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma; Schizotrypanum.

Query Match
Best Local Similarity 58.0%; Pred. No. 4.5;
Matches 76; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 44 CTGAGCTCTTCAACACATATACCAAGAGCTATTAAATGCTCTTTAAGGTATTACA 103
|||||

Db 39 CTGTTGATTTTATATAATAATCTTTAAAGTTATATAAATGATTTGTGATGAATT 98
|||||

QY 104 TAAATATTACTATCTCATTTGCTTTTATTGTTTATCATGATTATTAATGAAGTGT 163
|||||

Db 99 TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTAT 158
|||||

QY 164 CTAATCTTACT 174
|||||

Db 159 TTATTATTATT 169
|||||

AUTHORS

Myler, P.J., Aggarwal, G., Fazelinia, G., Mack, J., Marty, A.,
Munden, H., Nelson, S., Pentony, M., Rinta, J., Robertson, L.,
Seyler, A., Slak, B., Stuart, K., Vogt, C., Worthey, E., El-Sayed, N.M.,
Chedin, E., and Anderson, B.
Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing
Other GSSs: TC3-55G15.TP
Unpublished (2001)
Contact: Peter Myler
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109, USA
Tel: 206 284 8846
Fax: 206 284 0313
Email: mylerp@bri.org

Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seq primer: 77
Class: BAC ends.

FEATURES

Location/Qualifiers
1..512

/organism="Trypanosoma cruzi"
/mol_type="genomic DNA"
/strain="CL Brener"
/db_xref="taxon:5693"
/clone="TC3-55G15"
/clone_lib="TC3"

/note="Vector: pBelosAC11; Site 1: Hin dIII; Constructed
for Uppsala University by Marie-Christine Le Paslier in
the laboratory of Denis Le Paslier at the Centre d'Etude
du Polymorphisme Humain (CEPH), Paris, France. Briefly,
Trypanosoma cruzi CL-Brener agarose embedded DNA (obtained
from Dr. Franco da Silveira) was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBelosAC11 digested with Hin dIII. The average insert
size is 100 kb. Total clone coverage: approx. 33 X the
haploid genome."

ORIGIN

Query Match 8.6%; Score 43; DB 28; Length 512;
Best Local Similarity 62.6%; Pred. No. 4.6;
Matches 67; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 59 ACAATAACCCAGAGCTATTAAATGCTCTTTAAGGTATTACATAAATTAATCTATTC 118
Db 181 ACAACCAACATGCATACATTATATGCGCTTTATTATTATTATTATTATTATTATTA 240
QY 119 TCATGTGCTTTTATTGTTGTTATCATGATTAATGAAGTCTCT 165
Db 241 TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTGCGGTGT 287

RESULT 15

BQ065440

LOCUS

DEFINITION BQ065440 953 bp mRNA linear EST 02-APR-2002
AGENCOURT_6955061 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929977

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/

1 (bases 1 to 953)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lou Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLCM2108 row: p column: 10

High quality sequence stop: 634.

FEATURES

Location/Qualifiers

1..953
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5929977"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 99"

/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 8.6%; Score 43; DB 13; Length 953;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 TTGAAGTGAGATTTTCTGGCCTGAGACTTGCAGGAGGCAAG 500

Db 1 TTGAAGTGAGATTTTCTGGCCTGAGACTTGCAGGAGGCAAG 43

Search completed: March 4, 2004, 16:38:33
Job time: 1959.18 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:50:45 ; Search time 2273.13 Seconds
(without alignments)
9552.848 Million cell updates/sec

Title: US-09-966-880A-35_COPY_5000_5500

Perfect score: 501

Sequence: 1 atacattaaaacacaggtgt.....ggtcttcagcatgggaatgg 501

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.tod.*

36: em.htg.nam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	100.0	11204	6	BD016860 Novel cyt
2	501	100.0	11204	9	AB040430 Homo sapi
3	501	100.0	71132	9	AC092184 Homo sapi
4	283.4	56.6	6564	6	BD016835 Novel cyt
5	220.2	44.0	47177	9	AL157391 Human DNA
6	216.8	43.3	79528	9	BD176843 A method
7	216.8	43.3	79528	9	BD176843 A method
8	216.8	43.3	79528	9	BD176843 A method
9	212.8	42.5	81278	9	AL606477 Human DNA
10	210.8	42.1	125304	9	AC091062 Homo sapi
11	207.4	41.4	65489	9	AC080044 Homo sapi
12	207.4	41.4	65489	9	AF108083 Homo sapi
13	207.2	41.4	157075	9	AC005486 Homo sapi
14	207	41.3	182558	9	CNS01DXI Human chr
15	206.2	41.2	50125	9	AC088531 Homo sapi
16	206	41.1	161090	9	AL353708 Human DNA
17	205	40.9	67524	2	AC117415 Homo sapi
18	205	40.9	92472	9	AC134649 Homo sapi
19	205	40.9	107480	9	HS181C9 Human DNA s
20	205	40.9	144878	2	AL596094 Human DNA
21	205	40.9	208024	9	AC145422 Homo sapi
22	205	40.9	208145	2	AC010900 Homo sapi
23	204.6	40.8	164168	9	AC033504 Homo sapi
24	204.4	40.8	3010	6	AX834001 Sequence
25	204.4	40.8	173052	9	AK096194 Homo sapi
26	204.2	40.8	96625	9	AP001885 Homo sapi
27	204.2	40.8	96625	9	AC000118 Homo sapi
28	203.6	40.6	185847	9	AC121334 Homo sapi
29	203.2	40.6	93582	9	AC090681 Homo sapi
30	203.2	40.6	146017	2	AC027473 Homo sapi
31	203.2	40.6	154608	2	AC073620 Homo sapi
32	203	40.5	85311	2	AL354912 Homo sapi
33	203	40.5	146120	2	AL138794 Homo sapi
34	203	40.5	164179	9	AC007227 Homo sapi
35	203	40.5	192462	9	CNS01RHC Human chr
36	202.6	40.4	73041	9	AL356155 Human DNA
37	202.4	40.4	169089	9	AC055725 Homo sapi
38	202	40.3	110000	2	AP002753_1 Continuation (2 of
39	202	40.3	110000	2	AP002753_2 Continuation (3 of
40	201.8	40.3	112366	9	AL591804 Human DNA
41	201.8	40.3	179947	2	AL591853 Homo sapi
42	201.8	40.3	182897	2	AL158202 Homo sapi
43	201.8	40.3	204679	9	AC099676 Homo sapi
44	201.6	40.2	2762	9	AK125252 Homo sapi
45	201.6	40.2	23301	9	AC137633 Homo sapi

ALIGNMENTS

RESULT 1	BD016860	BD016860	11204 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	Novel cytidine deaminase.					
DEFINITION	BD016860					
ACCESSION	BD016860					
VERSION	BD016860.1	GI:22558036				
KEYWORDS	JP 2001245669-A/33.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
REFERENCE	1 (bases 1 to 11204)					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
TITLE	Honjo, T. and Muramatsu, M.					
JOURNAL	Novel cytidine deaminase					
	Patent: JP 2001245669-A 33 11-SEP-2001;					

COMMENT	JAPAN TOBACCO INC, TASUKU HONJO
OS	Homo sapiens (human)
PN	JP 2001245669-A/33
PD	11-SEP-2001
PF	28-NAR-2000 JP 2000092981
PI	TASUKU HONJO, MASAMICHI MURAMATSU
PC	C12N15/09, A61K39/395, A61P11/00, A61P13/12, A61P17/00, A61P27/02, A61P37/08, C07K16/18, C12N1/19, PC C12N1/21, PC C12N5/10, C12N5/78, C12P21/02, C12P21/08, C12N1/21, C12R1/19, PC C12N5/10, C12R1/91, C12N5/00, C12N5/00, C12N5/00, C12R1/91
CC	CC
FEATURES	Location/Qualifiers.
FH	Key Location/Qualifiers
source	1. 11204
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
ORIGIN	
Query Match	100.0%; Score 501; DB 6; Length 11204;
Best Local Similarity	100.0%; Pred. No. 1.7e-117;
Matches 501;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATACATTAAAAAAGCGTGTGAGCCACTCGCGCCAGCCAGGTATTGCTTTACATTAA 60
Db	5000 ATACATTAAAAAAGCGTGTGAGCCACTCGCGCCAGCCAGGTATTGCTTTACATTAA 5059
Qy	61 AAAATAGCCGGTCAGTGCTCAGCGCTGTATATCCAGCACATTTGGGAAGCCAGGCGG 120
Db	5060 AAAATAGCCGGTCAGTGCTCAGCGCTGTATATCCAGCACATTTGGGAAGCCAGGCGG 5119
Qy	121 GCAGAACACCCGAGGTGAGGAGTCCAAAGGCCAGCGCTGGCCAAAGATGGTGAACCCCGTCT 180
Db	5120 GCAGAACACCCGAGGTGAGGAGTCCAAAGGCCAGCGCTGGCCAAAGATGGTGAACCCCGTCT 5179
Qy	181 CTATTAAAAATACAAACATTACCTGGGCATGATGGTGGGCGCTGTATATCCAGCTACTC 240
Db	5180 CTATTAAAAATACAAACATTACCTGGGCATGATGGTGGGCGCTGTATATCCAGCTACTC 5239
Qy	241 AGGAGGCTGAGGCAGGAGGATCCGCGAGCGCTGCAGATCTGCCTGAGCCTGGGAGGTTG 300
Db	5240 AGGAGGCTGAGGCAGGAGGATCCGCGAGCGCTGCAGATCTGCCTGAGCCTGGGAGGTTG 5299
Qy	301 AGGCTACAGTAAGCCAAAGATCATGCCAGTATCTTCAGCCTGGGCGCAAGGTGAGACCG 360
Db	5300 AGGCTACAGTAAGCCAAAGATCATGCCAGTATCTTCAGCCTGGGCGCAAGGTGAGACCG 5359
Qy	361 TAACAAAAAAGAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAATGTGAAAAAGTG 420
Db	5360 TAACAAAAAAGAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAATGTGAAAAAGTG 5419
Qy	421 GCCTTAAACACCATTAAGAGTTTGAGTTTATTTCTGCGAGGCAGGAAGAACCATCAGG 480
Db	5420 GCCTTAAACACCATTAAGAGTTTGAGTTTATTTCTGCGAGGCAGGAAGAACCATCAGG 5479
Qy	481 GGGTCTTTGAGCATGGGAATGG 501
Db	5480 GGGTCTTTGAGCATGGGAATGG 5500

RESULT 2	AB040430	11204 bp	DNA	linear	PRI 03-OCT-2000
LOCUS	AB040430				
DEFINITION	Homo sapiens AID gene for activation-induced cytidine deaminase, complete cds.				
ACCESSION	AB040430				
VERSION	AB040430.1	GI-9988407			
KEYWORDS	AID; activation-induced cytidine deaminase.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

```

1 (sites)
Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.
Isolation, tissue distribution, and chromosomal localization of the
human activation-induced cytidine deaminase (AID) gene
Genomics 68 (1), 85-88 (2000)
20408890
JOURNAL
MEDLINE
PUBMED
10950930
REFERENCE
AUTHORS
Revy,F., Muto,T., Levy,Y., Geissmann,F., Plebani,A., Sanal,O.,
Catalan,N., Forveille,M., Dufourcq-Iagelouse,R., Gennery,A.,
Tezcan,I., Ersoy,F., Kayseril,H., Ugazio,A.G., Brousse,N.,
Muramatsu,M., Notarangelo,L.D., Kinoshita,K., Honjo,T., Fischer,A.
and Durandy,A.
Activation-induced cytidine deaminase (AID) deficiency causes the
autosomal recessive form of the Hyper-IgM syndrome (HIGM2)
Cell 102 (5), 565-575 (2000)
20460541
JOURNAL
MEDLINE
PUBMED
11007475
REFERENCE
AUTHORS
Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.
Direct Submission
Submitted (18-MAR-2000) Tasuku Honjo, Kyoto University, Department
of Medical Chemistry, Faculty of Medicine; Yoshida, Sakyo-ku,
Kyoto, Kyoto 606-8501, Japan [E-mail:honjo@four.med.kyoto-u.ac.jp,
Tel:81-75-753-4371(ex.4371), Fax:81-75-753-4388]
JOURNAL
FEATURES
Location/Qualifiers
1..11204
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
join(521..528,6280..6427,7807..8077,8371..8486,8956..9009)
/gene="AID"
join(521..528,6280..6427,7807..8077,8371..8486,8956..9009)
/gene="AID"
/codon_start=1
/product="activation-induced cytidine deaminase"
/protein_id="BAB12720.1"
/db_xref="GI:9988408"
/translation="MDSLLMNRKFLQFKXNRWAKGRRETYLCYVVKRSDSATSPSL
NGLYLRNGKCHVELFLRYISDLDLPGRYCTWFTSPCYDCARHVADFLRGNP
DFSLRIFARYFLCEDRAKEPEGLHRAQGVQIAIMTFDFYCWNTFVENHRTFK
AMEWELHNSVRLSRQLRIPLLEYVDLDRDAPFTGL"
gene
CDS.
ORIGIN

```

ORIGIN	Query Match	100.0%;	Score 501;	DB 9;	Length 11204;
	Best Local Similarity	100.0%;	Pred. No. 1.7e-117;		
	Matches 501;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATACATTAAAAACAGGTGTGAGCGCACTGGCCCGCAGCGAGGTATTGCTCTTATACATTAA	60		
Db	5000	ATACATTAAAAAACAGGTGTGAGCCACTGGCCCGCAGCGAGGTATTGCTCTTATACATTAA	5059		
Qy	61	AAAATAGGCGGGTGCACTGGCTCAGCGCTGTAAATCCAGCACATTTGGGAAGCCAAAGCGG	120		
Db	5060	AAAATAGGCGGGTGCACTGGCTCAGCGCTGTAAATCCAGCACATTTGGGAAGCCAAAGCGG	5119		
Qy	121	GCAGAACACCCGAGGTGCAGAGTCCAAGGCCAGCCTGGGCCAAGATGGTGAACCCCGTCT	180		
Db	5120	GCAGAACACCCGAGGTGCAGAGTCCAAGGCCAGCCTGGGCCAAGATGGTGAACCCCGTCT	5179		
Qy	181	CTATTAAAAATACAAACATTCTACCTGGGCATGATGGTGGGCGCTGTAAATCCCAAGCTACTC	240		
Db	5180	CTATTAAAAATACAAACATTCTACCTGGGCATGATGGTGGGCGCTGTAAATCCCAAGCTACTC	5339		
Qy	241	AGGAGGCTGAGGCAGGAGGATCCGCGAGCCTGGCAGATCTGCCTGAGCTGTGGAGGTG	300		
Db	5240	AGGAGGCTGAGGCAGGAGGATCCGCGAGCCTGGCAGATCTGCCTGAGCTGTGGAGGTG	5299		
Qy	301	AGGCTACAGTAAGCCACAGATCATGCCAGTATACCTTCAGGCTGGCGACAAAGTGAACCG	360		
Db	5300	AGGCTACAGTAAGCCACAGATCATGCCAGTATACCTTCAGGCTGGCGACAAAGTGAACCG	5359		
Qy	361	TAAACAAAAAATAAATTTTAAAAAAGAAATTTAGATCAAGATCCAACCTGTAAAAAGTG	420		

```

Db      5360  TAACAAAAAATTTTAAAAAAGAAATTTAGATCAATCAATGAAAAAGTG 5419
QY      421   GCTTAAACCAACATTAAGAGTTTGGAGTTTATTTCTGCAGGCAGAGAACCATCAGG 480
Db      5420  GCCTAAACCAACATTAAGAGTTTGGAGTTTATTTCTGCAGGCAGAGAACCATCAGG 5479
QY      481   GGGTCTTCAGCAGGGAATGG 501
Db      5480  GGGTCTTCAGCAGGGAATGG 5500

RESULT 3
AC092184
LOCUS   71132 bp      DNA      linear      PRI 12-JUN-2002
DEFINITION Homo sapiens 12 BAC RP11-438L7 (Roswell Park Cancer Institute Human
AC092184 AC013443
VERSION AC092184.7 GI:21206067
KEYWORDS HTG.
SOURCE  Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Anaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S.,
Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P.,
Francz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N.,
Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P.,
Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M.,
Holloway,C., Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S.,
Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y.,
Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U.,
King,L., Korval,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N.,
Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O.,
Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X.,
Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P.,
Marandel,I., Martin,R., Martindale,A., Martinez,E., Massey,E.,
Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S.,
Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,I.,
Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M.,
Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokoko,S., Ogih,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shim,C., Shookhari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,K.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansley,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczkyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R.,
Weinstock,G., and Gibbs,R.
Unpublished
Direct Submission
TITLE 2 (bases 1 to 71132)
REFERENCE
AUTHORS Worley,K.C.
Direct Submission
JOURNAL Submitted (25-JUN-2001) Human Genome Sequencing Center, Department

```

```

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 71132)
Worley,K.C.
Direct Submission
JOURNAL Submitted (18-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 71132)
Worley,K.C.
Direct Submission
JOURNAL Submitted (25-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 71132)
Worley,K.C.
Direct Submission
JOURNAL Submitted (12-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 25, 2002 this sequence version replaced gi:20901754.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu

```

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.

Genes and region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT.

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FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-438L7"
/complement(1..1448)
/notes="overlaps bases 1..1448 of clone AC092490"
/function="clone overlap"
187..408
/standard_name="57233"
439..560
/standard_name="92005"

misc_feature
complement(1..1448)
/notes="overlaps bases 1..1448 of clone AC092490"
187..408
/standard_name="57233"
439..560
/standard_name="92005"

STS
STS

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Best Local Similarity 99.6%; Pred. No. 7.4e-62;
Matches 284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 217 GGGGGCTGTAAATCCAGCTACTCAGGAGGCTGAGCAGGAGATCCGGGAGCTGGCA 276
Db 1 GGGGGCTGTAAATCCAGCTACTCAGGAGGCTGAGCAGGAGATCCGGGAGCTGGCA 60
QY 277 GATCTGCTGAGCTGGGAGTTGAGCTACAGTAAAGCAAGATGATGATATCTTC 336
Db 61 GATCTGCTGAGCTGGGAGTTGAGCTACAGTAAAGCAAGATGATGATATCTTC 120
QY 337 AGCTGGGACAAAGTGAACCGTAAACAAAATAAAATAAAATAAAATAAAATAAA 396
Db 121 AGCTGGGACAAAGTGAACCGTAAACAAAATAAAATAAAATAAAATAAAATAAA 180
QY 397 ATCAAGATCAACTGTAAAGTGGCTTAACACCACTTAAGAGTTTGGAGTTTATTC 456
Db 181 ATCAAGATCAACTGTAAAGTGGCTTAACACCACTTAAGAGTTTGGAGTTTATTC 240
QY 457 TGCAGGACAGAGACCACTCAGGGGCTTTCAGCATGGATGG 501
Db 241 TGCAGGACAGAGACCACTCAGGGGCTTTCAGCATGGATGG 285

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RESULT 5
AL157391/C
LOCUS Human DNA sequence from clone RP11-271M1 on chromosome 10, complete
DEFINITION
ACCESSION AL157391
VERSION AL157391.11 GI:15149560
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 47177)
Direct Submission
Submitted (10-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonesrequest@sanger.ac.uk
On Aug 13, 2001 this sequence version replaced gi:15021290.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Swi:
SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/projects/c_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr10
RP11-271M1 is from the library RP11-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-271M1. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP11-271M1 is at 1 in this sequence. The

true left end of clone RP11-455B2 is at 45178 in this sequence.

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     source            1..47177
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /clone="RP11-271M1"
                     /clone_lib="RPC1-11.1"
                     1..2296
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                     2313..2628
     repeat_region     /note="4 copies 79 mer 67% conserved"
                     2726..2883
     repeat_region     /note="2 copies 79 mer 82% conserved"
                     2797..3100
     repeat_region     /note="4 copies 76 mer 70% conserved"
                     3348..3581
     repeat_region     /note="3 copies 78 mer 79% conserved"
                     3371..3895
     misc_feature      /note="CpG island"
                     /evidence=not_experimental
                     3499..3806
     repeat_region     /note="4 copies 77 mer 75% conserved"
                     3616..3843
     repeat_region     /note="3 copies 76 mer 78% conserved"
                     3734..3889
     repeat_region     /note="2 copies 78 mer 82% conserved"
                     3949..4134
     repeat_region     /note="3 copies 62 mer 75% conserved"
                     4101..4352
     repeat_region     /note="4 copies 63 mer 77% conserved"
                     4290..4413
     repeat_region     /note="2 copies 62 mer 83% conserved"
                     4525..4902
     repeat_region     /note="6 copies 63 mer 77% conserved"
                     4813..5122
     repeat_region     /note="5 copies 62 mer 68% conserved"
                     4947..5072
     repeat_region     /note="2 copies 63 mer 85% conserved"
                     5164..5415
     repeat_region     /note="4 copies 63 mer 75% conserved"
                     5501..5815
     repeat_region     /note="5 copies 63 mer 75% conserved"
                     5772..6005
     repeat_region     /note="3 copies 78 mer 85% conserved"
                     6094..6245
     repeat_region     /note="2 copies 76 mer 85% conserved"
                     6294..6445
     repeat_region     /note="2 copies 76 mer 86% conserved"
                     complement(6834..7148)
     misc_feature      /note="match: STS: Em:HSPH09B8"
                     8157..8457
     repeat_region     /note="AluSq repeat: matches 1..299 of consensus"
                     8524..8636
     repeat_region     /note="L2 repeat: matches 2596..2710 of consensus"
                     9039..9348
     repeat_region     /note="AluSg repeat: matches 1..308 of consensus"
                     9743..9955
     repeat_region     /note="MIR repeat: matches 32..252 of consensus"
                     10799..11045
     repeat_region     /note="L1MB3 repeat: matches 5896..6151 of consensus"
                     11046..11335
     repeat_region     /note="AluXs repeat: matches 12..304 of consensus"
                     11336..11461
     repeat_region     /note="L1MB3 repeat: matches 5766..5896 of consensus"
                     11462..11771
     repeat_region     /note="AluXs repeat: matches 6..312 of consensus"
                     11772..12766
     repeat_region     /note="L1MB3 repeat: matches 4818..5766 of consensus"
                     12812..13119
     repeat_region     /note="AluSg repeat: matches 1..308 of consensus"
                     13200..13406

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repeat_region	/note="Alusp repeat: matches 1. .312 of consensus" 14547. .14692
repeat_region	/note="MER5B repeat: matches 25. .172 of consensus" 14798. .14995
misc_feature	/note="MER6B repeat: matches 5. .210 of consensus" complement(15721. .16199)
repeat_region	/note="match: STS: Em:G55345" 16895. .17117
repeat_region	/note="Alusg repeat: matches 1. .222 of consensus" 17114. .17365
repeat_region	/note="4 copies 63 mer 86% conserved" 17293. .17444
repeat_region	/note="2 copies 76 mer 83% conserved" 17389. .17514
repeat_region	/note="2 copies 63 mer 83% conserved" 17446. .17597
repeat_region	/note="2 copies 76 mer 87% conserved" 17528. .17716
repeat_region	/note="3 copies 63 mer 89% conserved" 17645. .17796
repeat_region	/note="2 copies 76 mer 89% conserved" 17721. .17972
repeat_region	/note="4 copies 63 mer 88% conserved" 17913. .18444
repeat_region	/note="7 copies 76 mer 82% conserved" 19048. .19883
repeat_region	/note="11 copies 76 mer 63% conserved" 19355. .19654
repeat_region	/note="2 copies 150 mer 86% conserved" 19645. .19800
repeat_region	/note="2 copies 78 mer 82% conserved" 20048. .20351
repeat_region	/note="4 copies 76 mer 79% conserved" 20414. .20641
repeat_region	/note="3 copies 76 mer 71% conserved" 20697. .22765
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repeat_region	/note="Alusx repeat: matches 1. .309 of consensus" 23984. .24293
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repeat_region	/note="Alusx repeat: matches 4. .296 of consensus" 25132. .25437
repeat_region	/note="Alusx repeat: matches 1. .307 of consensus" 25926. .26093
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repeat_region	32274..32578
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Best Local Similarity	80.4%; Pred.No.1.1e-45;
Matches 258; Conservative	0; Mismatches 63; Indels 0; Gaps 0;
Qy	71 GGTCAGTGGCTCACGCGTTAATCCACGACTTTGGGAAGCAAGCGGGCAGAACC 130
Dd	41836 GGTGCAGTGGCTTACTTCCTGTAATCCACGACTCTGGGAGGCCGAGGTGGCAGATCACC 41777
Qy	131 CGAGGTCAGAGTGCCAGGCCAGCGCTGGCCAGATGGTGAAACCCCGCTCTATTAAAAA 190
Dd	41776 TGAGGTCAGAGTTCAGAGTTCAGAGTGGGCAACATGGCGAAAACCCCGCTCTTACTAAAAA 47177
Qy	191 TACAACATTACCTGGGCATGATGGTGGCGGCTGTAAATCCCAGCTACTCTCAGAGGCTGA 250
Dd	41716 TACAAAANTTAGCAGGCATGGTGGGAGCGCTGTAATCCAGCTACTTGGGAAGGCTGA 41657
Qy	251 GCAGGAGGATCGGAGGAGCTTGGCAGATCTGCCTAGCTCGGAGGTTGAGGCTACAGT 310
Dd	41656 GGCAGGAGATCTCTTTGAACCCAGGAGATTTGCTTGAACCTGGGAGGCGAGTTGCGAGT 41597
Qy	311 AAGCCAAGATCATGCCAGGTATACTTCAGCTGGCGCAAAAGTGAGACCGTAACAAAAA 370
Dd	41596 GAGCCAGATCTTGCATTGCACTCCAGCTGGGTGACAGCGAGAGTCCGCTCANAAA 41537
Qy	371 AAAAAAATTAAAAAAGAAA 391
Dd	41536 AAAAAAAAAAAGAAAAAAA 41516
RESULT 6	
Bd176843/c	
LOCUS	Bd176843 79528 bp DNA linear PAT 18-MAR-2003
DEFINITION	A method of predicting cancer condition.
ACCESSION	Bd176843
VERSION	Bd176843.1 GI:29122555
KEYWORDS	WO 02072828-A/6.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 79528) Kato,K., Iwao,K., Noguchi,S. and Matoba,R. A method of predicting cancer condition Patent: WO 02072828-A 6 19-SEP-2002; DNA CHIP RESEARCH INC,HITACHI SOFTWARE ENGINEERING CO LTD, KIKUYA KATO, KYOKO IWAO, SHINZABURO NOGUCHI, RYO MATOBA OS Homo sapiens (human) PN WO 02072828-A/6 PD 19-SEP-2002 PF 07-MAR-2002 WO 2002JP002153 PR 14-MAR-2001 JP 01P 073063,06-APR-2001 JP 01P 108503 PR PI KIKUYA KATO,KYOKO IWAO,SHINZABURO NOGUCHI,RYO MATOBA PC C2N15/12,C12Q1/68,G06F19/00 Cc A method of predicting cancer condition FH Key Location/Qualifiers FT source 1..79528 /organism='Homo sapiens (human)'. Location/Qualifiers 1..79528 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
COMMENT	
FEATURES	
source	
ORIGIN	

Query Match 43.3%; Score 216.8; DB 6; Length 79528;
Best Local Similarity 77.4%; Pred. No. 8e-45;
Matches 263; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 71 GGTGAGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAAGCAAGCGGGGAGACACC 130
DB 64240 GGTGCGGTGCTCATCCCTATATCTAGACATTTGGGAGGCTGAGGTGGGGAATCACC 64181

QY 131 CGAGGTGAGGAGTCCAGGCGAGCCCTGGCCAGAGATGTTGAAACCCCGCTCTCTATTAAAAA 190
DB 64180 TGACGTGAGCAGTTCGAGACCAAGCCCTGGCCAGCGTGAACCCCGCTCTCTACTAAAAA 64121

QY 191 TACAACATTAACCTGGGCGATGATGGTGGGCGCTGTAATCCAGCACTACTCAGAGGCTGA 250
DB 64120 TACAAAATTAAGTGTGGCGGTGGTGGCGGCGCTGTAATCCAGCACTACCGGAGGCTGA 64061

QY 251 GGCAGGAGGATCGCGGAGCGCTGGCAGATCTGCTGAGCCTGGGAGGTTGAGGCTACAGT 310
DB 64060 GGTAGGAGAAATTCCTTGAACCTAGGAGATCGCTTGAACCTGGGAGGCGAGGTTGCAGT 64001

QY 311 AAGCCAGATCATGCGAGTATATCTTCAAGCTGGGCGACAAAGTGAGACCGTTAAACAAAAA 370
DB 64000 GAGCCAGATGTTGCCACTGTACTTCAGCCTGGGAGACAGACGAGCTCCATCTCAAAA 63941

QY 371 AAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAACT 410
DB 63940 AATATATAATAATAATAATAATAATAATAATAATAATAAT 63901

RESULT 7
HS466N1/c
LOCUS
DEFINITION
79528 bp DNA linear PRI 05-JUN-2003
Human DNA sequence from clone Rp3-466N1 on chromosome 22q12-13
Contains the H1FO gene for H1 histone family member 0, the GCAT
gene for glycine C-acetyltransferase (2-amino-3-ketobutyrate
coenzyme A ligase), the GALR3 gene for galanin receptor, the gene
for a novel protein similar to ANK3 (ankyrin 3, node of Ranvier
(ankyrin G)), the 5' end of the gene for proteins HSPC025 and
HSPC021 (similar to C. elegans FAT-3 alcohol dehydrogenase), ESTs,
STSs, GSSs and eight putative CpG islands, complete sequence.
257630
257630.11 GI:458128
H1G; alcohol dehydrogenase; ANK3; ankyrin; CpG island; FAT-3;
galanin receptor; GALR3; GCAT; H1FO; histone; HSPC021; HSPC025.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 79528)
Pearce, A.
Direct Submission
Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 13, 1999 this sequence version replaced gi:4581359.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Enr., EMBL; Swi., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep -----
Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the rare assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr22

RP3-466N1 is from the library RP3-3 constructed by the group of

Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pCYFAC2

IMPORTANT: This sequence is not the entire insert of clone

RP3-466N1. It may be shorter because we sequence overlapping

sections only once, except for a short overlap.

The true left end of clone RP3-1014D13 is at 79429 in this

sequence. The true right end of clone RP1-37E16 is at 100 in this

sequence.

FEATURES

source

Location/Qualifiers

1. 79528

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="22"

/map="q12-13"

/clone="RP3-466N1"

/clone_lib="RPCI-3"

8. 17

/note="2.0 copies 5 mer AGCTC 20% conserved"

39. 174

/note="Alusq/x repeat: matches 1. 136 of consensus"

175. 492

/note="Alusx repeat: matches 1. 312 of consensus"

494. 505

/note="3.0 copies 4 mer GAAA 24% conserved"

850. 1133

/note="AluJo repeat: matches 22. 312 of consensus"

1134. 1446

/note="Alusq repeat: matches 1. 313 of consensus"

1514. 1597

/note="MIR repeat: matches 180. 262 of consensus"

1837. 2110

/note="AluJo repeat: matches 13. 294 of consensus"

2113. 2253

/note="FLAM_C repeat: matches 1. 133 of consensus"

2261. 2280

/note="3.3 copies 6 mer AACAC 26% conserved"

2299. 2319

/note="2.3 copies 9 mer TTAGATCAG 33% conserved"

2537. 2555

/note="3.8 copies 5 mer TTGT 38% conserved"

complement(2556. 2759)

/note="Alusx repeat: matches 146. 311 of consensus"

complement(2760. 3070)

/note="AluY2 repeat: matches 1. 310 of consensus"

complement(3071. 3202)

/note="Alusx repeat: matches 4. 146 of consensus"

3205. 3215

/note="11.0 copies 1 mer T 22% conserved"

complement(3220. 3532)

/note="Alusx repeat: matches 1. 312 of consensus"

3555. 3766

/note="L2 repeat: matches 2443. 2691 of consensus"

3842. 3908

/note="L1ME repeat: matches 5672. 5727 of consensus"

3909. 4040

/note="FLAM_C repeat: matches 3. 133 of consensus"

4041. 4072

/note="L1ME repeat: matches 5727. 5761 of consensus"

complement(4073. 4399)

repeat_region /note="MT1D repeat: matches 162. .505 of consensus"
4400. .4697
/note="AluSp repeat: matches 1. .299 of consensus"
repeat_region complement(4698. .4860)
/note="MT1D repeat: matches 4. .162 of consensus"
repeat_region 4861. .4886
/note="2.2 copies 12 mer CACACATTACC 52% conserved"
repeat_region 4897. .4911
/note="2.5 copies 6 mer GGGCTG 30% conserved"
repeat_region 5073. .5113
/note="L1M1 repeat: matches 6214. .6256 of consensus"
repeat_region 5114. .5420
/note="AluX repeat: matches 1. .307 of consensus"
repeat_region 5421. .5473
/note="L1M1 repeat: matches 6256. .6302 of consensus"
repeat_region 5476. .5498
/note="23.0 copies 1 mer A 28% conserved"
repeat_region complement(5903. .5977)
/note="L2 repeat: matches 3136. .3220 of consensus"
repeat_region 6050. .6393
/note="MR83 repeat: matches 1. .355 of consensus"
repeat_region complement(6394. .6705)
/note="AluY repeat: matches 1. .311 of consensus"
repeat_region complement(6706. .7009)
/note="AluX repeat: matches 1. .305 of consensus"
repeat_region 7010. .7126
/note="MR83 repeat: matches 353. .448 of consensus"
repeat_region complement(7145. .7445)
/note="L1M4 repeat: matches 5936. .6236 of consensus"
repeat_region 7446. .7455
/note="10.0 copies 1 mer T 20% conserved"
repeat_region complement(7466. .7588)
/note="AluY repeat: matches 1. .123 of consensus"
repeat_region complement(7589. .7887)
/note="AluSp repeat: matches 1. .302 of consensus"
repeat_region complement(7898. .8117)
/note="AluSg/x repeat: matches 83. .300 of consensus"
repeat_region complement(8121. .8453)
/note="L1M4 repeat: matches 5618. .5949 of consensus"
repeat_region 8496. .8510
/note="AluSg/x repeat: matches 119. .133 of consensus"
repeat_region 8511. .8807
/note="AluX repeat: matches 1. .298 of consensus"
repeat_region 8808. .8893
/note="AluSg/x repeat: matches 133. .306 of consensus"
repeat_region 8995. .9004
/note="3.3 copies 3 mer ACC 20% conserved"
repeat_region 9031. .9082
/note="L2 repeat: matches 3106. .3160 of consensus"
repeat_region complement(9083. .9386)
/note="AluSg repeat: matches 1. .304 of consensus"
repeat_region 9387. .9522
/note="L2 repeat: matches 3160. .3282 of consensus"
repeat_region 9546. .9852
/note="AluSg1 repeat: matches 1. .306 of consensus"
repeat_region 9947. .9960
/note="2.3 copies 6 mer GGGGTG 28% conserved"
repeat_region complement(10080. .10164)
/note="MR repeat: matches 109. .206 of consensus"
repeat_region 10110. .10367
/note="match: GSS: Em:AQ416488"
misc_feature 10157. .10649
/note="CpG island"
/evidence=not_experimental
repeat_region 10299. .10316
/note="2.2 copies 8 mer CCGCCGTT 27% conserved"
repeat_region 10478. .10512
/note="7.0 copies 5 mer GAGGC 61% conserved"
repeat_region 10777. .10788
/note="2.4 copies 5 mer AAATG 24% conserved"
repeat_region 11262. .11272
/note="2.2 copies 5 mer CTTC 22% conserved"
repeat_region 11328. .11341

repeat_region /note="2.3 copies 6 mer CTCCC 28% conserved"
11490. .11499
/note="2.0 copies 5 mer CCCCT 20% conserved"
repeat_region 11583. .11595
/note="2.2 copies 6 mer ACTCCC 26% conserved"
misc_feature 12335. .13553
/note="CpG island"
/evidence=not_experimental
repeat_region 12598. .12612
/note="3.0 copies 5 mer CGGCT 21% conserved"
repeat_region 12919. .12929
/note="3.7 copies 3 mer GGC 22% conserved"

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Best Local Similarity 77.4%; Pred. No. 8e-45;
Matches 263; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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Db 64240 GGTCCGGTGGCTCATGCTATATCTAGTACATTTGGAGGCTGAGGTGGCGGAATCACC 64181

QY 131 CGAGTCAGAGTCCAAAGCCAGCTGGCCCAAGATGGTGAACCCCGTCTCTATTAAAAA 190
Db 64180 TGAGTCAGCAGTTCGAGACCCAGCTGGCCCAACACCGTGAACCCCGTCTCTACTAAAA 64121

QY 191 TACAAACATTACCTGGGCATGATGGTGGCGCTGTAAATCCAGCTACTCAGCAGGCTGA 250
Db 64120 TACAAATTTAGTGGCGTGGTGGCGGCGCTGTAAATCCAGCTACGCGGAGGCTGA 64061

QY 251 GGCAGGAGTCCCGGAGCTGGCAGATCTGCTGAGCTGGGAGCTGGGAGGTTGAGGCTACGT 310
Db 64060 GGTAGGAGATTTGTTGAACCTAGGAGAAATCGTTGAACCTGGGAGCGGAGGTTGCGT 64001

QY 311 AAGCCAAAGATCATGCCAGTATCTTACGCTGGCGCAAAAGTGAGACCGTAAACAAAAA 370
Db 64000 GAGCCAGATTTGGCCACTGTCTTACGCTGGGAGACGAGACGAGCTCATCTCAAAA 63941

QY 371 AAAAAATTTAAAAAGAAATTTAGATCAAGATCCAACT 410
Db 63940 AAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 63901

RESULT 8

AL606477/c

LOCUS AL606477

DEFINITION Human DNA sequence from clone RP11-190H11 on chromosome 1, complete

sequence.

ACCESSION AL606477.11

VERSION AL606477.11

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 139961)

AUTHORS Tracey,A.

TITLE Direct Submission

JOURNAL Submitted (13-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquerry@sanger.ac.uk

On Feb 14, 2002 this sequence version replaced gi:18250800.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at: http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> RP11-190H11 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VCUTOR: pBACE3.6
This sequence is the entire insert of clone RP11-190H11 The true left end of clone RP11-138J20 is at 32632 in this sequence. The true right end of clone RP5-930J4 is at 48503 in this sequence.

FEATURES		Location/Qualifiers	
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		/note="Sequence from uni-directional primer and dGTP big dye terminator reads only."	
misc_feature	60787..61315	/note="Single clone region. Reads generated from a transposon library derived from a single pUC clone. Restriction digest data confirm the assembly."	
	61098..61144	/note="Sequence from uni-directional dGTP big dye terminator reads only."	
misc_feature	61283..61315	/note="Sequence from uni-directional dGTP big dye terminator reads only."	
		/note="Sequence from uni-directional dGTP big dye complement(61316..61324)	
misc_feature		/note="1372 bases of IS186 transposon (X03123) removed here. This sequence represents the duplicated flanking sequence of the IS186."	
	ORIGIN		
QY	Query Match	43.0%; Score 215.6; DB 9; Length 139961;	
	Best Local Similarity	78.3%; Pred. No. 1.6e-44;	
	Matches	271; Conservative 0; Mismatches 74; Indels 1; Gaps 1;	
	44	TTGCTCTTATACATTTAAAAAATAGCGCGTGCAGTGGCTCAGCGCTGTAATCCAGCACT	103
	118004	TTTCTTTGTGAACAAACAAAGGCTGGCGCGAGTGGCTCAGCTGTAAATCCAGCACT	117945
Db	104	TTGGGAAGCCAGGCGGGGAGAACACCCGAGGTTCAGAGTCCAAAGGCCAGCTGGCCCAAG	163
	117944	TTGGGAGGCGAGGCGAGCGGATTACTTGAGTCAGGATTCAGGCGAGCTGGCCCAAC	117885
QY	164	ATGGTGAACCCCGTCTCTATTAAAAATACAAACATTACTGGGCATGATGTGGCGGCC	223
	117884	ATGGTGAACCCCGCATCTCTACTAAAAATACAAATTAGCTGGCATGTGTGGCGCATGCC	117825
QY	224	TGTAATCCCGAGTACTCAGGAGGCTGAGCAGGAGGATCCGGGAGCTGGCAGATCTGC	283
	117824	TGTAATCCCGAGTACTTGGAGGCTGAGCAGGAGGAAATTCGTTGAGGAGG-AGAAATTGC	117766
QY	284	CTGAGCTTGGGAGGTTGAGGCTACAGTAAGCCAAATCATGTCAGTATCTTTCAGGCTGC	343
	117765	TTGAGGCGAGGAGGTTGAGGTTGAGTTCAGTGAATCATGCTGCACTCCAGCTGC	117706
QY	344	GGCACAAGTGAACCGGTAAACAAAAAATAAATAAATAAATAAATAAATAAATAA	389
	117705	CGACAGAGTGAAGGCTCTGTCTCAAAAAAATAAATAAATAAATAAATAAATAA	117660

RESULT 9

AC091062/c

LOCUS

DEFINITION

AC091062

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

AC091062 81278 bp DNA linear PRI 19-FEB-2002
Homo sapiens chromosome 17, clone RP11-506D12, complete sequence.

AC091062.5 GI:18702407

HTG

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (Bases 1 to 81278)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 17, clone RP11-506D12

Unpublished

2 (Bases 1 to 81278)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,

Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,

Camrata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,

Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K.,

Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,

Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,

Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,

Maclean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,

McEwan,P., McKernan,K., McPheeters,K., Meldrum,J., Meneus,L.,

Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,

Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,

Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,

Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,

Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,

Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,

Teodorovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,

Travers,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (25-MAR-2001) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (Bases 1 to 81278)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,

Brown,A., Camrata,J., Campopiano,A., Chang,J., Chazaro,B.,

Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A.,

Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,

Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,

Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,

Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,

Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,

Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,

McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrum,J.,

Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,

Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,

Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,

Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,

Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,

Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,

Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

Travers,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (08-OCT-2001) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (Bases 1 to 81278)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,

Brown,A., Camrata,J., Campopiano,A., Chang,J., Chazaro,B.,

Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A.,

Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,

Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,


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QY 232 CAGCTACTCAGGAGCTGAGGAGGATCCGGGAGCTCGCAGATCTGCTGAGCCT 291
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Db 42961 GGGAGGTTGAGGCTACAGTAAGCAAGATCGCTTGAACCTGGGAGAT-GGAGGTTGCAT 42962

QY 352 GTGAGACCGTAAACAAAAAATTTTAAAAAGAAA 391
Db 42901 GCAAGACTCCATCTCAAAAAAATTTTAAAAAGAAA 42862

RESULT 10
AC008044/c
LOCUS AC008044 125304 bp DNA linear PRI 07-OCT-1999
DEFINITION Homo sapiens chromosome 14 BAC containing genes for ABH and nuclear
receptor coactivator NCOA-62, complete sequence.
ACCESSION AC008044
VERSION AC008044.4 GI:6015188
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 125304)
Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B.,
Bloom, S., Dors, M., Dickhoff, R., Harrison, G., James, R., Lasky, S.,
Madan, A., Ratcliffe, A., Shaffer, T. and Hood, L.
Sequencing of human chromosome 14
Unpublished
2 (bases 1 to 125304)
Rowen, L., Madan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R.,
Harrison, G., James, R., Loretz, C., Lasky, S., Madan, A., Prescott, S.,
Ratcliffe, A., Shaffer, T. and Hood, L.
Direct Submission
Submitted (14-JUL-1999) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
3 (bases 1 to 125304)
Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B.,
Bloom, S., Dors, M., Dickhoff, R., Harrison, G., James, R., Lasky, S.,
Madan, A., Ratcliffe, A., Shaffer, T. and Hood, L.
Direct Submission
Submitted (07-OCT-1999) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
COMMENT On Oct 7, 1999 this sequence version replaced gi:5708444.
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and BAC 111016, Accession AC008372"
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1. 21034
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CDS
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differences in the conceptual translation between this CDS
and the cDNA due to frameshift variations. The genomic
sequence is all high quality data"

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IMSGFRLNHAVERPVEEGELPHCLREAPLPAVLPRDSMVEFCSEMEDWQVCASYL
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Best Local Similarity 76.9%; Pred. No. 2.8e-43; Indels 0; Gaps 0;
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QY 110 AGCCAAGCGCGGAGACACCCGAGGTCAGAGTCCAGGCCAGCTGGCCCAAGATGGTG 169
Db 80991 GGTCAAGTGGGGGGATCACCTGAGTGGGAGTTCAGAGCCAGCCAGCTGGCCCAAGATGGTG 80932
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Db 80931 AAACCCCTCTCTATTAAAAATACAAACATTTAGTGGCATGTGGCGAGCGCTGTAAAT 80872
QY 230 CCCAGTACTCAGAGGTCAGGAGGATCCGCGAGGATCCGCGAGGTCGGAGATCTGCTGAGC 289
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QY 290 CTGGGAGGTTGAGGCTACAGTAAGCAAGATCATCGCAGTATATCTTCAGCTGGCGGACACA 349
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QY 350 AAGTGAGACCGTAAACAAAAAATTTTAAA 383
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RESULT 11
AF108083/c
LOCUS AF108083 65489 bp DNA linear PRI 31-AUG-2001
DEFINITION Homo sapiens chromosome 7 BAC clone F5, complete sequence.
ACCESSION AF108083
VERSION AF108083.1 GI:3941729
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 65489)
Rump, A., Rosenthal, A., Drescher, B., Weber, J., Schattevoy, R. and
Korenberg, J.
Direct Submission
TITLE

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JOURNAL Submitted (20-NOV-1998) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

FEATURES
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(30184-30224 and 42265-42300); orientation of middle
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens chromosome 17, clone RP11-463M16, complete sequence.
AC068531.9 GI:24080707
HTG.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 182555)

Homo sapiens chromosome 17, clone RP11-463M16

Unpublished

2 (bases 1 to 182555)

Barren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,

Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G.,

Capopolitano, A., Castile, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Dodge, S., Domingo, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., Laroque, K., Lamazares, R., Landers, T., Lehotzky, J.,

Levine, R., Liu, G., Locke, K., Macdonald, P., Marquis, N.,

McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,

Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,

Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,

Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,

Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,

Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (03-MAY-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 182555)

Barren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B.,

Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,

Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,

Gardyna, S., Gird, S., Graham, L., Grand-Pierre, N., Hagos, B.,

Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A.,

Karatas, A., Kellis, C., Landers, T., Levine, R., Lindblad-Toh, K.,

Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,

McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,

McConor, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,

Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,

Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,

Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,

Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (11-SEP-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 182555)

Barren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B.,

Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,

Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,

Gardyna, S., Gird, S., Graham, L., Grand-Pierre, N., Hafez, N.,

Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Kanat, A., Karatas, A., Kellis, C., Landers, T., Levine, R.,

Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J.,

Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T.,

Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,

Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,

Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R.,

TITLE

JOURNAL

COMMENT

Submitted (17-OCT-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Oct 17, 2002 this sequence version replaced gi:22779575.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WITBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L9798

Center clone name: 463_M_16

Only the first 182.6 kilobases of this clone are being submitted.

The remainder overlaps accession number AC091133 [WICGR project

L12028].

FEATURES

source

Location/Qualifiers

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10413..10580

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

QY	259	GATCCGGAGCTGCGAGACTGTCTCCTGACGCCCTGGGAGGTTGAGGCTTACAGTAGCCCAAG	318
Dd	149740	AAT-----AGCTTTGACCCCGGAGGTGGAGTGTCGCAGTTGAGCTGAG	149700
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Dd	149699	ATCAGTTCAGCGACTCCCACTTCCCTGGGTGACAGAGCAAGATGTCTCAAAAAAAAAAAAA	149640
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Dd	149639	AAAAAAAAAAAAAATATATATATATAATAATAAGAA	149601
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DEFINITION	AL353708	sequence.	
ACCESSION	AL353708		
VERSION	AL353708.10	GI:14272261	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 90125)		
JOURNAL	Martin,S.		
COMMENT	Direct Submission Submitted (30-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk requests: clonesrequest@sanger.ac.uk On May 31, 2001 this sequence version replaced gi:13992256. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; SW; SWISSPROT; Tr; TREMBL; Wp.; WORMPEP; information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl RP11-533E19 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBAC3.6 IMPORTANT: This sequence is not the entire insert of clone RP11-533E19 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-533E19 is at 90125 in this sequence. The true left end of clone RP11-521I8 is at 15352 in this sequence. The true right end of clone RP11-12M5 is at 100 in this sequence.		
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repeat_region 7493..7784
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repeat_region 8219..8308
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repeat_region 12585..12863
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repeat_region 13334..13647
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repeat_region 13819..14115
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repeat_region 14230..14324
/notes="MER58C repeat: matches 119..89 of consensus"
repeat_region 14357..14648
/notes="AluYa5 repeat: matches 1..304 of consensus"
repeat_region 14780..15076
/notes="AluSg repeat: matches 1..298 of consensus"
repeat_region 15706..15990
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repeat_region 16649..16784
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repeat_region 23525..23648
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repeat_region 24994..25299
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27036..27118
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44763..45071
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45075..45198
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45199..45548
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45551..45664
/notes="L1P3 repeat: matches 6035..6149 of consensus"
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46161..46385
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46571..46710
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 Best Local Similarity 73.0%; Pred. No. 4.1e-42;

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Db	15982	CAGAAAAAGAGCCGCGCAGGTGTCTCACACCTGTATCCAGCACTTCGGAGGCGG	16041						
Qy	115	AGCGGCGCAGAACACCCGAGGTCTCAGGATCCAGGCGCAGCTGGCCCAAGATGGTGAACC	174						
Db	16042	AAGCAGTGGATCACCTGAGATCAGGAGTTCAAGACCGCCTGGCCCAACATGGCGAAACC	16101						
Qy	175	CCGTCTCTATTAAAAATACAAACATTACCTGGGCATGATGGTGGGCGCCTGTAAATCCCAAG	234						
Db	16102	CCGTCTCTACTAAAAATACAAAAATTAGCCGCGCATGGTGGCACAAAGCCTGTAGTCCCAAG	16161						
Qy	235	CTACTCAGGAGGTGAGGAGGAGGATCCGCGAGCCTGGCAGATCTGCTGAGCCTGGG	294						
Db	16162	CTACTCGGAAACTGAGGAGGAGGATCACTTGAAACCGGGAATCACTTGAACCCCGGG	16221						
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Db	16222	AGGCAGAGGTTGCACTGAGCGGACATTCACCACTGCACCTCCAGCCTGGGTGACAGAGTG	16281						
Qy	355	AGACCGTAACAAAAAATTTTAAAAAAGAAATTTAGATCAAGATCCCACTGTAA	414						
Db	16282	AGACTCTGTCTCAAAAAAATTTTAAAAAAGAAATTTAGATCAAGATCCCACTGTAA	16341						
Qy	415	AAA	417						
Db	16342	ACA	16344						

Search completed: March 4, 2004, 15:00:23
 Job time : 2278.13 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 11:56:09 ; Search time 286.428 Seconds
(without alignments)
7430.646 Million cell updates/sec

Title: US-09-966-880A-35_COPY_5000_5500

Perfect score: 501
Sequence: 1 ataccataaaacaggtgt.....ggcttcacgatgggaatgg 501

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	100.0	11204	3 AAC55339	Aac55339 Human act
2	501	100.0	11204	6 ABS73286	Abst73286 DNA encod
3	283.4	56.6	6564	3 AAC55314	Aac55314 Human act
4	216.8	43.3	79528	6 AAL50814	Aal50814 Human can
5	197.4	39.4	164702	7 ACF62730	Acf62730 Cancer ba
6	197.4	39.4	164702	7 ADB20845	Adb20845 MRP1 base
7	197.4	39.4	164702	9 ADB87934	Adb87934 Human UGT
8	197.4	39.4	164702	9 ADB96917	Adb96917 Human MDR
9	197.4	39.4	164702	9 ADB92108	Adb92108 Human MDR
10	197.4	39.4	207433	5 ABZ72040	Abz72040 Gene 216
11	197.4	39.4	207433	7 ABX74891	Abx74891 BAC1098L2
12	196.8	39.3	1877	3 AAC93353	Aac93353 Human sec
13	196.6	39.2	8321	7 ADA98848	Ada98848 Human sec
14	196.6	39.2	8321	7 ADA44471	Ada44471 Human sec
15	196.6	39.2	8321	9 ADC20851	Adc20851 Human sec
16	196.2	39.2	1743	4 AAI62586	Aai62586 Human bre
17	196.2	39.2	1743	4 AAL03368	Aal03368 Human rep
18	196.2	39.2	1746	4 AAI62587	Aai62587 Human bre
19	196.2	39.2	1746	4 AAL03369	Aal03369 Human rep
20	196.2	39.2	249999	7 ABZ80229	Abz80229 Human tra
21	195.6	39.0	10642	5 ABA20382	Aba20382 Human ner
22	195	38.9	66566	3 AAA53450	Aaa53450 Human thi
23	195	38.9	100301	6 ABQ88176	Abq88176 Human ost

ALIGNMENTS

RESULT 1

AAC55339	24	194.4	38.8	849	4	AAH33054	Aah33054 Human col
ID AAC55339 standard; DNA; 11204 BP.	25	194.4	38.8	87350	2	AAX83003	Aax83003 Human WRN
AC AAC55339;	26	194	38.7	3172	4	AAK85276	Aak85276 Human imm
XX	27	194	38.7	3172	4	AAL05811	Aal05811 Human rep
XX	28	194	38.7	3172	4	ABL98375	Ab198375 Human tes
DT 05-FEB-2001 (first entry)	29	193.8	38.7	32176	4	AAL05628	Aal05628 Human rep
XX	30	193.8	38.7	32250	4	AAL05627	Aal05627 Human rep
DE Human activation-induced cytidine deaminase genomic DNA SEQ ID NO.35.	31	193.8	38.7	65854	4	AAK86282	Aak86282 Human imm
XX	32	193.8	38.7	189013	7	ACF62741	Acf62741 Cancer ba
KW Activation-induced cytidine deaminase; AID; cytidine deaminase; immune related disease; allergy; allergic disease; anti-allergic; antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; ashma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; Digeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IgG subclass selection disorder; ds.	33	193.8	38.7	189013	7	ADB20856	Adb20856 MRP1 base
OS Homo sapiens.	34	193.8	38.7	189013	9	ADB87945	Adb87945 Human UGT
XX	35	193.8	38.7	189013	9	ADB96928	Adb96928 Human MDR
XX	36	193.8	38.7	189013	9	ADB92119	Adb92119 Human MDR
XX	37	192.8	38.5	3121	6	ABK51416	Abk51416 cDNA encc
XX	38	192.6	38.4	111282	6	AAL44261	Aal44261 Human pho
XX	39	192.6	38.4	111282	6	ABS55190	Ab555190 Genomic D
XX	40	192.4	38.4	70000	6	AAD42934	Aad42934 Human pho
XX	41	192	38.3	499	8	ACF35649	Acf35649 Human nuc
XX	42	192	38.3	32986	4	AAK69758	Aak69758 Human imm
XX	43	192	38.3	32986	4	AAK84629	Aak84629 Human imm
XX	44	191.8	38.3	51469	4	AAK78813	Aak78813 Human imm
XX	45	191.8	38.3	51469	4	AAK70270	Aak70270 Human imm

Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies.

Claim 17; Page 163-170; 174pp; Japanese.

QY 241 AGGAGCTGAGCGCAGGAGGATCCCGAGGCTGCGAGATCTGCTGAGCTGGAGGTTG 300
Db 5240 AGGAGGCTGAGCGAGGAGGATCCCGAGGCTGCGAGATCTGCTGAGCTGGAGGTTG 5299
QY 301 AGGCTACAGTAAGCCAGATCATCCAGTATCTTCACTTCCAGCTGGCGCAAGTGAGACCG 360
Db 5300 AGGCTACAGTAAGCCAGATCATCCAGTATCTTCACTTCCAGCTGGCGCAAGTGAGACCG 5359
QY 361 TAACAAAAAAGAAAAATTTAAAAAAGAAAAATTTAGATCAAGATCCAACTGTAAAAAGTG 420
Db 5360 TAACAAAAAAGAAAAATTTAAAAAAGAAAAATTTAGATCAAGATCCAACTGTAAAAAGTG 5419
QY 421 GCCTAAACACACATTAAGAGTTGGAGTTATCTTCCAGGCGAGAGCAACATCAGG 480
Db 5420 GCCTAAACACACATTAAGAGTTGGAGTTATCTTCCAGGCGAGAGCAACATCAGG 5479
QY 481 GGGTCTTCAGCATGGGAATGG 501
Db 5480 GGGTCTTCAGCATGGGAATGG 5500
RESULT 3
AAC55314
ID AAC55314 standard; DNA; 6564 BP.
XX
AC AAC55314;
XX
DT 05-FEB-2001 (first entry)
XX
DE Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:10.
XX
KW Activation-induced cytidine deaminase; AID; cytidine deaminase;
KW immune related disease; allergy; allergic disease; antiallergic;
KW antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;
KW gene therapy; B cell associated immune system disorder; food allergy;
KW immunodeficiency disease; immunoglobulin A deficiency disease; asthma;
KW IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;
KW drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;
KW ataxia telangiectasia; common variable immunodeficiency disorder;
KW major histocompatibility class II deficiency disease;
KW auto immunodeficiency syndrome; IgG subclass selection disorder; ds.
XX
OS Homo sapiens.
XX
FN WO200058480-A1.
XX
PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-JP001918.
XX
PR 29-MAR-1999; 99JP-00087192.
PR 24-JUN-1999; 99JP-00178999.
PR 27-DEC-1999; 99JP-00371382.
XX
PA (NISH) JAPAN TOBACCO INC.
PA (HONJ) HONJO T.
PI Honjo T, Muramatsu M;
XX
DR WPI; 2000-611715/58.
XX
PT Nucleic acid encoding activation induced cytidine deaminase, useful as a
PT target for drug development for immune-related diseases including
PT allergies.
XX
PS Claim 17; Page 145-150; 174pp; Japanese.
XX
CC The present invention describes an activation-induced cytidine deaminase
CC (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has
CC cytidine activity similar to APOBEC-1. AID has antiallergic, antianemic,
CC antiasthmatic, ophthalmological, anti-HIV and dermatological activities,
CC and can be used in gene therapy. AID polynucleotides are useful in
CC methods for identifying drugs for the treatment of B cell associated

CC immune system disorders, immunodeficiency diseases and allergies, such as
CC immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-
CC globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy,
CC drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia
CC telangiectasia, common variable immunodeficiency disorder, MHC (major
CC histocompatibility class II deficiency disease, AIDS (auto
CC immunodeficiency syndrome), elevated IgE disorder, and IgG subclass
CC selection disorder. The DNA sequences encoding AID may be used for gene
CC therapy and the antibodies to the AID protein may be used for diagnosis
CC and treatment of these disorders. The present sequence represents a
CC genomic DNA sequence of human AID
XX
SQ Sequence 6564 BP; 1909 A; 1358 C; 1383 G; 1914 T; 0 U; 0 Other;
Query Match 56.6%; Score 283.4; DB 3; Length 6564;
Best Local Similarity 99.6%; Pred. No. 86-60; Mismatches 0; Gaps 0;
Matches 284; Conservative 0; Indels 1; Indels 0; Gaps 0;
QY 217 GGGCGCCTGTATCCAGCTACTCAGGAGGCTGAGGAGGAGGATCCCGAGGCTGGCA 276
Db 1 GGGGGCCTGTATCCAGCTACTCAGGAGGCTGAGGAGGAGGATCCCGAGGCTGGCA 60
QY 277 GATCTGCTGAGCCTGGGAGGTTGAGCTACAGTAAGCAAGATCCAGTATCTTTC 336
Db 61 GATCTGCTGAGCCTGGGAGGTTGAGCTACAGTAAGCAAGATCCAGTATCTTTC 120
QY 337 AGCCTGGGCGCAAAAGTGAGCCGTAAACAAAAAATTTAAAAAAGAAATTTAG 396
Db 121 AGCCTGGGCGCAAAAGTGAGCCGTAAACAAAAAATTTAAAAAAGAAATTTAG 180
QY 397 ATCAGATCCAACTGTAAAAAGTGCCCTAAACACACATTAAGAGTTTGGATTATTC 456
Db 181 ATCAGATCCAACTGTAAAAAGTGCCCTAAACACACATTAAGAGTTTGGATTATTC 240
QY 457 TCAGGCGAAGAGAACCATCAGGGGGTCTTCAGCATGGGAATGG 501
Db 241 TCAGGCGAAGAGAACCATCAGGGGGTCTTCAGCATGGGAATGG 285
RESULT 4
AAL50814/c
ID AAL50814 standard; DNA; 79528 BP.
XX
AC AAL50814;
XX
DT 30-JAN-2003 (first entry)
XX
DE Human cancer status prediction method-related DNA sequence #6.
XX
KW Human; gene therapy; cancer status prediction; cancer; ds;
KW cancer malignancy evaluation; drug design; antisense nucleic acid.
XX
OS Homo sapiens.
XX
FN WO200272828-A1.
XX
PD 19-SEP-2002.
XX
PF 07-MAR-2002; 2002WO-JP002153.
XX
PR 14-MAR-2001; 2001JP-00073063.
PR 06-APR-2001; 2001JP-00108503.
PR 02-AUG-2001; 2001JP-00234807.
XX
PA (DNAC-) DNA CHIP RES INC.
PA (HISF) HITACHI SOFTWARE ENG CO LTD.
XX
PI Kato K, Iwao K, Noguchi S, Matoba R;
XX
DR WPI; 2002-713517/77.
XX
PT Computer-aided statistical method for predicting cancer, applicable in
PT gene therapy for evaluating cancer malignancy with data for use in drug

XX Heinrich G, Kerb R;
XX WPI; 2003-268144/26.
DR
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX
XX Disclosure; SEQ ID NO 658; 86pp; English.
PS
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5), polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 164702 BP; 52399 A; 32545 C; 31423 G; 48335 T; 0 U; 0 Other;
SQ
Query Match 39.4%; Score 197.4; DB 7; Length 164702;
Best Local Similarity 74.9%; Pred. No. 2.5e-38;
Matches 269; Conservative 0; Mismatches 71; Indels 19; Gaps 1;
QY 51 TATACATTAATAAATAGCCGGTGCAGTGGCTCAGCCTGTAAATCCAGCACTTTGGGAA 110
DB 138901 TAAAAAGTAATAAGAGCGCGGTGGTAGCCCAACCTGTAAATCCTAGCACTTTGGGAG 138942
QY 111 GCCAAGCGCGGAGCAACACCCGAGGTCCAGGAGTCCAGGCCAGCCTGGCCCAAGATGGTGA 170
DB 138841 GCAGAGCGGGGAGATCACTCAGCTCAGGAGTTCAAGACCAAGCTGGCCCAATGGTGA 138782
QY 171 AACCCCGTCTCTATTAAAAATACAAATACCTACCTGGGATGATGGCGGCTGTATTC 230
DB 138781 AACCCCGTCTCTACTAAAAATACAAATATAGTGGCGGTGGTGGCAAGCACTGTATTC 138722
QY 231 CCAGCTACTCAGGAGGCTGAGGAGGATCCGGGAGCCTGGCGAGATCTGCCTGAGCC 290
DB 138721 CCAGCTACTTGGAGGCTGAGGAGGAGAT-----TGCTTGAACC 138681
QY 291 TGGGAGGTTGAGGCTACAGTAAGCCAGATCATGCGAGTATATCTCAGCCTGGGCGACAA 350
DB 138680 TGGGAGGTTGAGGTTGCAAGTGGCGGAGATCCGCCACTGCACCTGGCGGCGAG 138621
QY 351 AGTGAGACCGTAACAAAAAATAAATTTAAAAAAGAAATTTAGATCAAGATCAAC 409
DB 138620 AGTGAGACTCTGACTCMAAAAAAATAAAGTAATAAAGAAAGAAAGAAATTAAC 138562
RESULT 6
ADB20845/c
ID ADB20845 standard; DNA; 164702 BP.
XX
XX ADB20845;
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX MRP1 based cancer related nucleic acid SEQ ID NO:658.
DE
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW variant allele; multidrug resistance protein 1; MRP1; cytosolic; gene;
KW ds.
XX

PT design.
XX
PS Disclosure; Page 84-131; 182pp; Japanese.
XX
CC The invention comprises a method for predicting cancer status. The method
CC involves: measuring expression doses of genes obtained from specimens;
CC selecting at least one gene as the gene for an assay; using the
CC measurement results on expression doses of the selected genes for
CC multivariate analysis; and classifying the specimens in analogous groups
CC with results of the multivariate analysis on expression patterns of the
CC genes. The method of the invention is useful for predicting cancer, which
CC is applicable in gene therapy for evaluating cancer malignancy with data
CC for use in drug design (e.g. antisense nucleic acids for use in gene
CC therapy to treat cancer). The present DNA sequence represents a human
CC nucleic acid of the invention
XX
XX Sequence 79528 BP; 19015 A; 20270 C; 20468 G; 19775 T; 0 U; 0 Other;
SQ
Query Match 43.3%; Score 216.8; DB 6; Length 79528;
Best Local Similarity 77.4%; Pred. No. 3.3e-43;
Matches 263; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 71 GGTGAGTGGCTCAGCCTGTAAATCCAGCACTTTGGGAAGCCAGGCGGAGCAACACC 130
DB 64240 GGTGCGGTGGCTCATGCTTAATCTAGCACTTTGGGAGGCTGAGGTGGGCGAATCACC 64181
QY 131 CGAGTCCAGGATCCAGGCCAGCCTGCCAGATGGTGAACCCCGCTCTATTAAAA 190
DB 64180 TGACGTCCAGGATTCGAGACAGCCTGGCCAAACAGGTGAACCCCGCTCTATTAAAA 64121
QY 191 TACAAACATTAATCTGGGATGATGTGGCGGCTGTAAATCCAGCTACTCAGGAGGCTGA 250
DB 64120 TACAAATATTAGTGGCGGTGGTGGCGGCGCTGTAAATCCAGTACGCGGAGGCTGA 64061
QY 251 GCAGAGGATCCGCGGAGCTGGCAGATCTGCTGAGCCTGGAGGTTGAGGCTACAGT 310
DB 64060 GGTAGGAGAAATGCTTGAACCTAGGAGATCGCTTGAACCTGGGAGCGGAGGTTGCACT 64001
QY 311 AAGCCAAAGATATGCCAGTATATCTCAGCCTGGGCGCAAAAGTGAGACCGTAACAAAAA 370
DB 64000 GAGCCAAAGATTTGCCACTGTACTTACGCTGGGAGACAGACAGACTCCATCTCAAA 63941
QY 371 AAAAAATTTAAAAAGAAATTTAGATCAAGATCCAACT 410
DB 63940 AAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 63901
RESULT 5
ACF62730/c
ID ACF62730 standard; DNA; 164702 BP.
XX
XX ACF62730;
XX
XX 08-OCT-2003 (first entry)
DT
XX
XX Cancer based on CYP3A5 related polynucleotide SEQ ID NO:658.
DE
XX
XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KW cytostatic; gene; ds.
XX
XX Unidentified.
OS
XX
XX WO2003013534-A2.
FN
XX
XX 20-FEB-2003.
PD
XX
XX 23-JUL-2002; 2002WO-EP008219.
PF
XX
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
PA

Db 138620 AGTCAGACTCTGACTCAAAAAAAAAAAAAAAAAAGTAAAGAAAGAAAGAAAGAAATTAAC 138562

RESULT 8

ADB96917/c

ID ADB96917 standard; DNA; 164702 BP.

XX

AC ADB96917;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human MDR1 related DNA sequence SEQ ID NO:658.

XX

DE irinotecan; colorectal cancer; cervical cancer; gastric cancer;

XX

KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;

XX

KW multidrug resistance 1; MDR1; cytosstatic; human; CYP3A5; MRP1; MDR1;

XX

XX TOP1; ds.

XX

OS Homo sapiens.

XX

OS WO2003013537-A2.

PN

XX

XX 20-FEB-2003.

PD

XX

XX 23-JUL-2002; 2002WO-EP008218.

PF

XX

XX 23-JUL-2001; 2001EP-00117608.

PR

XX

XX 24-MAY-2002; 2002EP-00011710.

PR

XX

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

PA

XX

XX Heinrich G, Kerb R;

PI

XX

XX WPI; 2003-268145/26.

DR

XX

XX New use of irinotecan for preparation of pharmaceutical compositions for

PT

PT treating cancer in subject having genome with variant allele comprising

PT

PT multidrug resistance 1 polynucleotide.

XX

XX Disclosure; SEQ ID NO 658; 130pp; English.

XX

XX The invention relates to the novel use of irinotecan or its derivative

CC

CC for the preparation of pharmaceutical compositions for treating

CC

CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or

CC

CC malignant glioma in a subject having a genome with a variant allele which

CC

CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition

CC

CC of the invention has cytostatic activity. The invention is useful for the

CC

CC preparation of pharmaceutical compositions for treating colorectal,

CC

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC

CC glioma in a subject (preferably human, more preferably African or Asian)

CC

CC or a mouse. The present sequence is used in the exemplification of the

CC

CC invention.

XX

XX Sequence 164702 BP; 52399 A; 32545 C; 31423 G; 48335 T; 0 U; 0 Other;

SQ

Query Match 39.4%; Score 197.4; DB 9; Length 164702;

Best Local Similarity 74.9%; Pred. No. 2.5e-38;

Matches 269; Conservative 0; Mismatches 71; Indels 19; Gaps 1;

QY 51 TATACATTAAAAATAGCCGGTGCAGTGGCTCAGCTGTAAATCCAGACATTGGGAA 110

Db 138901 TAAAAAGTAAAGAGCGGGGTGTGTAGCCACACCTGTAACTTAGCATTGGGAG 138842

QY 111 GCCAAGCGGGCAGAACCCGAGGTCAAGAGTCCAGCCAGCCCTGGCCCAAGATGTGA 170

Db 138841 GCAGAGCGGGCAGATCACCTGAGGTCAAGAGTTCAAGACCAGCCCTGGCCCAATGTGA 138782

QY 171 AACCCCGTCTCTATTAAAAATACAAACATTACCTGGGCGATCATGTGGGGCCCTGTATC 230

Db 138781 AACCCCGTCTCTATTAAAAATACAAACATTAGCTGGGCGTGGTGGCAGACCTGTATC 138722

QY 231 CCAGTACTCAGGCGGTGAGCGAGGAGATCCCGGAGCCCTGGCAGATCTGCCTGAGCC 290

Db 138721 CCAGCTACTTGGGAGGCTGAGGCAGGAGAT-----TGCTTGAACC 138681

QY 291 TGGGAGGTTGAGGCTACAGTAAGCCAGATCATCGCAGTATACTTCCAGCTGGCGCAAA 350

Db 138680 TGGGAGGTTGAGGTTGAGTGCAGTGCAGCCAGATCGCCCTGGCGCGCAG 138621

QY 351 AGTGAGACCGTAAACAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCCAAC 409

Db 138620 AGTGAGACTCTGACTCAAAAAAAGTAAAGAAAGAAAGAAATTAAC 138562

RESULT 9

ADB92108/c

ID ADB92108 standard; DNA; 164702 BP.

XX

AC ADB92108;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human MDR1 related DNA sequence SEQ ID NO:658.

XX

DE irinotecan; colorectal cancer; cervical cancer; gastric cancer;

XX

KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;

XX

KW multidrug resistance 1; MDR1; cytosstatic; human; UGT1A1; MRP1; TOP1; ds.

XX

XX Homo sapiens.

XX

XX WO2003013535-A2.

PN

XX

XX 20-FEB-2003.

PD

XX

XX 23-JUL-2002; 2002WO-EP008220.

PF

XX

XX 23-JUL-2001; 2001EP-00117608.

PR

XX

XX 24-MAY-2002; 2002EP-00011710.

PR

XX

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

PA

XX

XX Heinrich G, Kerb R;

PI

XX

XX WPI; 2003-342400/32.

DR

XX

XX New use of irinotecan for preparation of pharmaceutical compositions for

PT

PT treating cancer in subject having genome with variant allele comprising

PT

PT multidrug resistance 1 polynucleotide.

XX

XX Disclosure; SEQ ID NO 658; 104pp; English.

XX

XX The invention relates to a novel use of irinotecan or its derivative for

CC

CC the preparation of a pharmaceutical composition for treating colorectal,

CC

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC

CC glioma in a subject having a genome with a variant allele which comprises

CC

CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the

CC

CC invention has cytostatic activity. The present sequence is used in the

CC

CC exemplification of the invention.

XX

XX Sequence 164702 BP; 52399 A; 32545 C; 31423 G; 48335 T; 0 U; 0 Other;

SQ

Query Match 39.4%; Score 197.4; DB 9; Length 164702;

Best Local Similarity 74.9%; Pred. No. 2.5e-38;

Matches 269; Conservative 0; Mismatches 71; Indels 19; Gaps 1;

QY 51 TATACATTAAAAATAGCCGGTGCAGTGGCTCAGCTGTAAATCCAGACATTGGGAA 110

Db 138901 TAAAAAGTAAAGAGCGGGGTGTGTAGCCACACCTGTAACTTAGCATTGGGAG 138842

QY 111 GCCAAGCGGGCAGAACCCGAGGTCAAGAGTCCAGCCAGCCCTGGCCCAAGATGTGA 170

Db 138841 GCAGAGCGGGCAGATCACCTGAGGTCAAGAGTTCAAGACCAGCCCTGGCCCAATGTGA 138782

QY 171 AACCCCGTCTCTATTAAAAATACAAACATTACCTGGGCGATCATGTGGGGCCCTGTATC 230

Db 138781 AACCCCGTCTCTATTAAAAATACAAACATTAGCTGGGCGTGGTGGCAGACCTGTATC 138722

2007 7C:CE:CA C TAB7 TTT

231	CCAGCTACTCAGGAGGCTGAGGCAGGAGGATCCGCGAGCCTGGCAGATCTGCCTGAGCC	290
138721	CCAGCTACTTCGGAGGCTGAGGCAGGAGAT-----TGCATTGAACC	138681
291	TGGGAGGTTGAGGCTACAGTAAGCCAGATCATGCCAGTATCTTCAGCCTGGGCGCAA	350
138680	TGGGAGGTGGAGGTTTCAGTGAGCCGAGATCGCGCACTGCATCTCAGCCTGGGCGGCG	138621
351	AGTGAGCCGTAACAAAAAATAAATTTAAAAAAGAAATTTAGATCAAGATCCAAC	409
138620	AGTGAGACTCTGACTCAAAAAAATAAAGTTAAAGAAAGAAAGAAAGAAATTAAC	138562

RESULT 10
ABZ72040/C
ID ABZ72040 standard; DNA; 207433 BP.

AC ABZ72040;
XX
DT 03-APR-2003 (first entry)

Gene 216 H194BAC1098L22 nucleotide sequence SEQ ID NO 5.

Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic; antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma; obesity; inflammatory bowel disease; promoter; gene; ss.

OS Homo sapiens.

PN WO200178894-A2.
yy

PD 25-OCT-2001.

PF 13-APR-2001; 2001WO-US012245.

13-APR-2000; 2000US-00548797.

AA
PA
(GENO-) GENOME THERAPEUTICS CORP.

Keith T;

DR WPI; 2001-639428/73.

XX
XX

PT of asthma, obesity and inflammatory bowel disease.

Example 4; Fig 7; 520pp; English.

The invention relates to isolated genes (Gene 216) from human chromosome 20p13-p12 and the proteins they encode. The nucleic acids and proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate Gene 216 expression. For example, the nucleic acids (or vectors) and proteins may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of gene 216 by expressing inactive proteins or to supplement the patients own production of Gene 216 proteins. Additionally, the nucleic acids may be used to produce the secreted Gene 216 protein, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples and therefore which patients may be in need of restorative therapy. The Gene 216 protein may also be used as antigens in the production of antibodies against Gene 216 and in assays to identify modulators of Gene 216 expression and activity. The anti-Gene 216 antibodies and antigens may also be used to down regulate expression and activity. The anti-Gene 216 antibodies may also be used as diagnostic agents for detecting the presence of Gene 216 proteins in samples (e.g. by enzyme linked immunosorbent assay or ELISA). Disorders that may be prevented, diagnosed and/or treated by the above methods include, for

XX New isolated gene 216 nucleic acids, useful for diagnosing, preventing or
PT treating a disorder, such as asthma, bronchial hyper-responsiveness,
PT chronic obstructive pulmonary disease, obesity or inflammatory bowel
PT syndrome.
XX
PS Example 6; Fig 7; 650pp; English.
XX
XX This invention relates to a novel isolated nucleic acid, gene 216,
CC identified from human chromosome 20p13-p12. The invention also discloses
CC regions of the 216 gene that contain single nucleotide polymorphisms
CC (SNP's) which may be used as markers for disease susceptibility or
CC severity. The nucleotides of the invention may have antiasthmatic,
CC antiinflammatory or anorectic activities and may be used in gene therapy.
CC The nucleic acids, antibodies or its fragments are useful for diagnosing,
CC preventing or treating a disorder, such as respiratory diseases (e.g.
CC asthma, bronchial hyper-responsiveness, chronic obstructive pulmonary
CC disease or adult respiratory distress syndrome), obesity, or inflammatory
CC bowel syndrome. The nucleic acids are also useful for identifying
CC increased susceptibility of a subject to the disorders mentioned. The
CC nucleic acids can also be used as primers and templates for the
CC recombinant production of disorder-associated peptides or polypeptides,
CC for chromosome and gene mapping, or for tissue distribution studies. The
CC present sequence represents a gene 216 cDNA sequence used in the scope of
CC the invention
XX
SQ Sequence 207433 BP; 52775 A; 51289 C; 51698 G; 51671 T; 0 U; 0 Other;
Query Match 39.4%; Score 197.4; DB 7; Length 207433;
Best Local Similarity 71.2%; Pred. No. 2.7e-38;
Matches 284; Conservative 0; Mismatches 96; Indels 19; Gaps 1;
QY 10 AAACAGGTTGAGCCAGTCCAGCCAGCAGTATTGCTTATATCAATTAATAAATAGGC 69
Db 199036 AAACAGGTTAATCAACCCGCGCTAGGTTAACTTAATCAGCAGATGAGCC 198977
QY 70 CGGTGAGTGGTCCAGCTGTAATCCAGACCTTTGGGAAGCCAGCGGCGAGACAC 129
Db 198976 GGGCACGTTGGTCCAGCTGTAATCCAGACCTTTGGGAAGCCAGCGGCGTAAATCAC 198917
QY 130 CGAGTCCAGGAGTCCAGCCAGCCTGGCCAGATGTTGAACCCCGTCTTATAAAA 189
Db 198916 CTGAGTTCAGGATTCAGACCCAGCTGTTCAATGCGGAACCCCGTCTTATAAAA 198857
QY 190 ATACAAACATTAACCTGGGATGATCGTGGGCGCTGTTAATCCAGTACTCAGAGGCTG 249
Db 198856 ATACAAATTAAGCGGCGTGGTGGTATGCTGTAAACCCAGCTACTCAGAGGCTG 198797
QY 250 AGCAGGAGATCCCGGAGCCTGGCAGATCTGCTGAGCTGGGAGGTTGAGGCTACAG 309
Db 198796 AGCAGGAGATC-----GCTTGAAACCCGAGGAGTGGAGTTGAG 198756
QY 310 TAAGCCAGATCATGCCAGTATATCTCAGCTGGGCGCAAAAGTGAGACCGTAACAAAA 369
Db 198755 GGAACCAAGATCATGCCAGGCACTCCAGCTGGGCAACAGAGTGAGATCCATTTCAAA 198696
QY 370 AAAAAAATTTAAAAAAGAAATTTAGATCAAGTCCAA 408
Db 198695 AACAAAGGAAAAAGAAAGAAATCAGCAGATGAGTGAA 198657
RESULT 12
AAC93353
ID AAC93353 standard; cDNA; 1877 BP.
XX
AC AAC93353;
XX
DT 16-FEB-2001 (first entry)
XX
DE Human secreted protein cDNA sequence #44.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;

KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; ss.
XX
OS Homo sapiens.
XX
PN WO200058495-A1.
XX
PD 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-US0007661.
XX
PR 26-MAR-1999; 99US-0126504P.
PR 07-JAN-2000; 2000US-0174847P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX WPI: 2000-611720/58.
XX P-PSDB; AAB51422.
XX
PT New nucleic acid molecules encoding 45 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Claim 1; Page 352; 410pp; English.
XX
CC The invention relate to the isolation of genes AAC93310-C93354 encoding
CC 45 human secreted proteins AAB5130-B51423. The genes can be used to
CC generate fusion proteins by linking to the gene for the human
CC immunoglobulin G Fc portion (AAC93301) for increasing the stability of
CC the fusion protein as compared to the human protein only. The genes and
CC proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b)
CC immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections
XX
SQ Sequence 1877 BP; 543 A; 358 C; 372 G; 596 T; 0 U; 8 Other;
Query Match 39.3%; Score 196.8; DB 3; Length 1877;
Best Local Similarity 73.3%; Pred. No. 9.9e-39;
Matches 252; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 42 TATTGCTCTTATACATTAATAAATAGCGGTGAGTGGCTCAGCGCTGTATATCCAGCA 101
Db 1529 TATAGATAATTAAGAAATAAATTTGGTAGGCACTGTGCTCATCGCTGTATATCCATCA 1588
QY 102 CTTTGGGAAGCCAGCGGCGAGACACCCGAGGTTCAGAGTCCAGGCGAGCTGGCCCA 161
Db 1589 CTTTGGGAGCTGAAGTGGGTGGATTGGCTGAGGTTCAGATTTCAGACACAGCTTGACCA 1648
QY 162 AGATGGTGAACCCCGTCTCTATTAAAAATACAAACATTTACCTGGGCGATGATGGTGGCG 221
Db 1649 ATATGGGGAACCCCATCTCTACTAATAATAAAGTTAGCTGGCATGGTGGCATGG 1708
QY 222 CTTGTATCCAGCTACTCAGGAGGCTGAGGAGGAGGATCCGCGGAGCTGGCAGATCT 281
Db 1709 CTTGTAGTCCAGCTATTTCAGGAGGCTGAGACAGGAGAAATTCCTTGAACCCCGTGAAT 1768
QY 282 GCCTGAGCTGGGAGGTTTCAGGCTACAGTAAGCCAGATCATGCCAGTATATTCAGCCT 341
Db 1769 GCTTGAAACCGGAGCGGAGGTTGCAGTGAGCCGAGATCATGCCATTGCATCCAGTCT 1828

QY 342 GGGCGCAAAAGTGAGACCGTAACAAAAAATTTAAAAA 385
Dd 1829 AGGCAACAGGCGCAAACTCCATCTCCAAAAAATTTAAAAA 1872

RESULT 13
ID ADA98848 standard; DNA; 8321 BP.
AC ADA98848;
XX
XX 20-NOV-2003 (first entry)
XX Human secreted protein-related DNA sequence #441.
XX human; secreted protein; cardiovascular disorder; arrhythmia;
KW atherosclerosis; stroke; endocarditis; congestive heart failure;
KW rheumatic heart disease; cardiomyopathy; hemorroids; varicose veins;
KW migraine; thrombosis; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; renal disorder; proliferative disorder; cancer; ds.
XX
XX Homo sapiens.
XX
XX WO2003004623-A2.
XX 16-JAN-2003.
XX
XX 26-MAR-2002; 2002WO-US009922.
XX 27-MAR-2001; 2001US-0278650P.
XX 12-SEP-2001; 2001US-00950082.
XX 12-SEP-2001; 2001US-00950083.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2003-247946/24.
XX
XX New human secreted polypeptide and nucleic acid molecules, useful for
PT diagnosing, preventing, prognosticating or treating cardiovascular
PT disorders (e.g. arrhythmia, atherosclerosis, cardiomyopathy, or
PT thrombosis).
XX
XX Disclosure; SEQ ID NO 957; 1572pp; English.
XX
XX The invention comprises the amino acid and coding sequence of human
CC secreted proteins. The DNA and protein sequences of the invention are
CC useful in the treatment of cardiovascular disorders, such as: arrhythmia,
CC atherosclerosis, stroke, endocarditis, congestive heart failure,
CC rheumatic heart disease, cardiomyopathy, hemorroids, varicose veins,
CC migraine, or thrombosis. The DNA and protein sequences may also be used
CC for treating or preventing: neural disorders, immune system disorders,
CC muscular disorders, reproductive disorders, gastrointestinal disorders,
CC pulmonary disorders, renal disorders, proliferative disorders and/or
CC cancerous diseases. The present DNA sequence is used in the
CC exemplification of the invention. NOTE: The present sequence is shown on
XX the WPI website.
XX
SQ Sequence 8321 BP; 1704 A; 2261 C; 2254 G; 2102 T; 0 U; 0 Other;
Query Match 39.2%; Score 196.6; DB 7; Length 8321;
Best Local Similarity 75.2%; Pred. No. 1.7e-38;
Matches 261; Conservative 0; Mismatches 79; Indels 7; Gaps 1;

QY 43 ATTGCTCTTATACATTAATAATAGGCGGTGAGTGGCTCACGCCCTGTATCCAGCAC 102
Dd 2907 ATGCTTTTAAAAAATAAAGGTTGGGCGCGGTGCTCATGCTGTATCTAGCAC 2966
QY 103 TTTGGGAAGCCAGCGCGGCGAGACACCCAGGTGAGGATCCAGGATCCAGGCTGGGCAA 162

Dd 2967 TTTGGGAGGCTGAGGTGGGTGGATCACTTGAGGTTCAGAGTTCAGACCCAGCTGGGCAA 3026
QY 163 GATGTTGAACCCCGTCTCTTATTAATAATCAACATCTCTGGCATGATGTTGGGCGC 222
Dd 3027 CATGGCGAARCCCGTCTCTACTATAAATACAAAAATAGCCAGGCTGGTGGCGCAAGC 3086
QY 223 CTGTAATCCAGCTACTCAGGAGGCTGAGGAGGATCCGCGAGGCTGGCAGATCTG 282
Dd 3087 CTGTAATCCAGCTCTCAGGAGGCTGAGGCAAGAGCTGAGGC-----AAGAGAATGG 3139
QY 283 CCTGAGCCTGGAGGTTGAGGCTACAGTACGCCAAGATCATGCCAGTATATCTTACGCTG 342
Dd 3140 CTTGAACCTGGGAGGTGGAGATTGCGAGTGGCCAGGATCGTCCACTGAACTCCAGCTG 3199
QY 343 GGGCAAAAGTGAGACCGTAACAAAAAATTTAAAAAAGA 389
Dd 3200 GGGCAAGTGAGACTTTGACTCAGAAAAAATAAAGAAAGAAA 3246

RESULT 14
ID ADA44471 standard; DNA; 8321 BP.
XX ADA44471;
XX
XX 20-NOV-2003 (first entry)
XX Human secreted protein DNA SEQ ID 664.
XX Gene therapy; human; Antidiabetic; Anorectic; Ophthalmological;
KW Neuroprotective; Cerebroprotective; Antianemic; ds.
XX
XX Homo sapiens.
XX WO2003000865-A2.
XX 03-JAN-2003.
XX
XX 26-MAR-2002; 2002WO-US009105.
XX 27-MAR-2001; 2001US-0278650P.
XX 12-SEP-2001; 2001US-00950082.
XX 12-SEP-2001; 2001US-00950083.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2003-184045/18.
XX
XX A human secreted protein and nucleic acids useful for preparing a
PT diagnostic or pharmaceutical composition for diagnosing or treating
PT diabetes or conditions related to diabetes, e.g. hyperglycemia, obesity,
PT retinopathy, neuropathy.
XX
XX Disclosure; SEQ ID NO 664; 701pp; English.
XX
XX The invention relates to novel genes and their fragments which are useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids and proteins
CC are useful in the diagnosis, treatment and prevention of conditions
CC related to diabetes, e.g. hyperglycaemia, obesity, retinopathy,
CC polynuropathy, atherosclerosis, anaemia, stroke, gangrene, impotence,
CC infection, cataract, renal disorders, or endocrine disorders. The present
CC sequence was used to illustrate the invention.
XX
SQ Sequence 8321 BP; 1704 A; 2261 C; 2254 G; 2102 T; 0 U; 0 Other;
Query Match 39.2%; Score 196.6; DB 7; Length 8321;
Best Local Similarity 75.2%; Pred. No. 1.7e-38;
Matches 261; Conservative 0; Mismatches 79; Indels 7; Gaps 1;

QY 43 ATTGCTTTATACATTAATAAATAGGCGGTGACGCTCAGCCCTGTATCCAGCAC 102
 Db 2907 ATGCTTTTAAATAAATAAAGGTGGGCGCGTGGCTCATGCTGTATCTAGCAC 2966
 QY 103 TTTGGGAAGCCAGCGGCGAGAACACCCGAGGTTCAGAGTCCAAAGGCCAGCTGGCCAA 162
 Db 2967 TTTGGGAGGCTGAGGTGGGTGGATCCTTTGAGGTTCAGAGTTCAGAGCCAGCTGGCCAA 3026
 QY 163 CATGCTGAACCCCGCTCTCTATTAAATAAATAAATACAAACATTACCTGGCATGATGGTGGCGC 222
 Db 3027 CATGGGAACCCCGCTCTCTATTAAATAAATAAATACAAACATTACCTGGCATGATGGTGGCGC 3086
 QY 223 CTGTAAATCCAGCTACTCAGAGGCTGAGGAGGAGGATCCGCGAGGAGCTGGGAGATCTG 282
 Db 3087 CTGTAAATCCAGCTACTCAGAGGCTGAGGAGGAGGATCCGCGAGGAGCTGGGAGATCTG 3139
 QY 283 CCTGAGCTGGGAGGTTGAGGCTACAGTAAGCCAAAGATCATGCGCAGTATATCTTCAGGCTG 342
 Db 3140 CTGTAACCTGGGAGGTGAGATTGAGTGAGCCAAAGATCTGCGCACTGAATCCAGGCTG 3199
 QY 343 GCGCAAAAGTGAGACCGTATCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 389
 Db 3200 GCGCACAGAGTGAGACTTTGACTCAGAAAAAATAAATAAATAAATAAATAAATAAATAA 3246

RESULT 15

ADC20851

ID ADC20851 standard; DNA; 8321 BP.

AC ADC20851;

XX 18-DEC-2003 (first entry)

DT 18-DEC-2003 (first entry)

DE Human secreted protein-related DNA sequence #269.

XX gene therapy; human; secreted protein; haemopoietic disorder;
 KW haematological disorder; anaemia; haemophilia; inflammatory disorder;
 KW inflammatory bowel disease; Crohn's disease; neoplastic disease; cancer;
 KW leukaemia; wound healing; epithelial cell proliferation disorder;
 KW immune disorder; autoimmune disorder; asthmatic disorder;
 KW cardiovascular disorder; atherosclerosis; myocarditis;
 KW infectious disease; HIV; AIDS; endocrine disorder; diabetes;
 KW gastrointestinal disorder; duodenal ulcer; gastroenteritis; gene; ds.

OS Homo sapiens.

XX WO200292787-A2.

PN 21-NOV-2002.

XX 26-MAR-2002; 2002WO-US009257.

XX 27-MAR-2001; 2001US-0278650P.

PR 12-SEP-2001; 2001US-00950082.

PR 12-SEP-2001; 2001US-00950083.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Ruben SM;

XX WPI; 2003-129287/12.

DR New human secreted proteins and nucleic acid molecules, useful for

PT preparing a diagnostic or pharmaceutical composition for diagnosing,

PT preventing or treating hematopoietic or hematologic disorders, e.g.

PT anemia or hemophilia.

XX Disclosure; SEQ ID NO 805; 1512pp; English.

PS The invention comprises the amino acid and coding sequences of human

XX secreted proteins. The DNA and protein sequences of the invention are

CC useful for detecting, preventing, diagnosing, prognosticating, treating

CC or ameliorating: haematopoietic or haematological disorders (e.g. anaemia

CC

CC and haemophilia); inflammatory disorders (e.g. inflammatory bowel disease
 CC and Crohn's disease); neoplastic disease (e.g. cancer and leukaemia);
 CC wound healing and disorders of epithelial cell proliferation; immune
 CC disorders (e.g. autoimmune disorders and asthmatic disorders);
 CC cardiovascular disorders (e.g. atherosclerosis and myocarditis);
 CC infectious disease (e.g. HIV/AIDS); endocrine disorders (e.g. diabetes);
 CC and gastrointestinal disorders (e.g. duodenal ulcers and
 CC gastroenteritis). The present DNA sequence was used in the
 CC exemplification of the invention.

XX Sequence 8321 BP; 1704 A; 2261 C; 2254 G; 2102 T; 0 U; 0 Other;

SQ Query Match 39.2%; Score 196.6; DB 9; Length 8321;

Best Local Similarity 75.2%; Pred. No. 1.7e-38;

Matches 261; Conservative 0; Mismatches 79; Indels 7; Gaps 1;

QY 43 ATTGCTTTATACATTAATAAATAGGCGGTGACGCTCAGCCCTGTATCCAGCAC 102

Db 2907 ATGCTTTTAAATAAATAAAGGTGGGCGCGTGGCTCATGCTGTATCTAGCAC 2966

QY 103 TTTGGGAAGCCAGCGGCGAGAACACCCGAGGTCAGAGTCCAAAGGCCAGCTGGCCAA 162

Db 2967 TTTGGGAGGCTGAGGTGGGTGGATCCTTTGAGGTTCAGAGTTCAGAGCCAGCTGGCCAA 3026

QY 163 GATGGTGAACCCCGCTCTCTATTAAATAAATAAATACAAACATTACCTGGCATGATGGTGGCGC 222

Db 3027 CATGGGAACCCCGCTCTCTATTAAATAAATAAATACAAACATTACCTGGCATGATGGTGGCGC 3086

QY 223 CTGTAAATCCAGCTACTCAGGAGGCTGAGGAGGAGGATCCGCGAGGAGCTGGGAGATCTG 282

Db 3087 CTGTAAATCCAGCTACTCAGGAGGCTGAGGAGGAGGATCCGCGAGGAGCTGGGAGATCTG 3139

QY 283 CCTGAGCTGGGAGGTTGAGGCTACAGTAAGCCAAAGATCATGCGCAGTATATCTTCAGGCTG 342

Db 3140 CTGTAACCTGGGAGGTGAGATTGAGTGAGCCAAAGATCTGCGCACTGAATCCAGGCTG 3199

QY 343 GCGCAAAAGTGAGACCGTATCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 389

Db 3200 GCGCACAGAGTGAGACTTTGACTCAGAAAAAATAAATAAATAAATAAATAAATAAATAA 3246

Search completed: March 4, 2004, 13:06:20

Job time : 292.428 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 13:06:29 ; Search time 55.5558 Seconds
(without alignments)
5004.527 Million cell updates/sec

Title: US-09-966-880A-35_COPY_5000_5500

Perfect score: 501

Sequence: 1 ataccataaaacaggtgt.....ggcttcacgacgggaatgg 501

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	195.6	39.0	98844	US-09-791-211-10	Sequence 10, Appl
C 2	194.4	38.8	87350	US-08-781-891-79	Sequence 79, Appl
C 3	194.4	38.8	87350	US-09-618-166-79	Sequence 79, Appl
C 4	194.4	38.8	87543	US-09-791-211-3	Sequence 3, Appl
C 5	192.6	38.4	111282	US-09-754-250-3	Sequence 3, Appl
C 6	192.4	38.4	70000	US-09-851-896-3	Sequence 3, Appl
C 7	189.6	37.8	55298	US-09-491-356C-1	Sequence 1, Appl
C 8	189	37.7	2841	US-09-526-133A-24	Sequence 24, Appl
C 9	189	37.7	63000	US-09-780-172-18	Sequence 18, Appl
C 10	188.8	37.7	11288	US-08-646-301A-1	Sequence 1, Appl
C 11	188.8	37.7	11288	US-08-481-968A-4	Sequence 4, Appl
C 12	188.8	37.7	11288	US-08-154-712B-4	Sequence 4, Appl
C 13	188.8	37.7	15056	US-09-474-699-10	Sequence 10, Appl
C 14	188	37.5	7676	US-08-451-777A-7	Sequence 7, Appl
C 15	188	37.5	7676	US-08-451-778A-7	Sequence 7, Appl
C 16	188	37.5	7676	US-08-598-208-7	Sequence 7, Appl
C 17	188	37.5	7676	PCT-US95-06743-7	Sequence 7, Appl
C 18	187.2	37.4	319608	US-09-539-333D-1	Sequence 1, Appl
C 19	186.6	37.2	1301	US-09-539-333D-36	Sequence 36, Appl
C 20	186.6	37.2	1386	US-09-539-333D-40	Sequence 40, Appl
C 21	186.2	37.2	112132	US-09-741-150-3	Sequence 3, Appl
C 22	186.2	37.2	112132	US-10-160-187-3	Sequence 3, Appl
C 23	186	37.1	13608	US-09-679-409-1	Sequence 1, Appl
C 24	185.4	37.0	128779	US-09-497-855A-38	Sequence 38, Appl
C 25	185.2	37.0	29629	US-09-729-995-3	Sequence 3, Appl
C 26	185.2	37.0	29629	US-10-135-689-3	Sequence 3, Appl
C 27	184.8	36.9	4823	US-08-457-254-5	Sequence 5, Appl

C 28	184.8	36.9	4823	2	US-08-484-257-20	Sequence 20, Appl
C 29	184.8	36.9	4823	3	US-08-999-927-5	Sequence 5, Appl
C 30	184.8	36.9	4823	4	US-08-461-819-5	Sequence 5, Appl
C 31	184.8	36.9	4823	5	PCT-US94-08806-28	Sequence 28, Appl
C 32	184.8	36.9	4823	5	PCT-US95-01829-5	Sequence 5, Appl
C 33	184.8	36.9	4823	5	PCT-US95-16626-5	Sequence 5, Appl
C 34	184.6	36.8	36651	4	US-09-738-894A-3	Sequence 3, Appl
C 35	184.6	36.8	36651	4	US-09-964-469-3	Sequence 3, Appl
C 36	184.6	36.8	42571	4	US-09-810-347-3	Sequence 3, Appl
C 37	184	36.7	21234	4	US-09-810-671-3	Sequence 3, Appl
C 38	184	36.7	21234	4	US-10-109-854-3	Sequence 3, Appl
C 39	183.6	36.6	1001	4	US-09-671-317-457	Sequence 457, App
C 40	183.6	36.6	1019	4	US-09-177-650-128	Sequence 128, App
C 41	183.4	36.6	55827	4	US-09-813-133A-3	Sequence 3, Appl
C 42	183.2	36.6	21968	4	US-09-851-985-3	Sequence 3, Appl
C 43	183	36.5	3694	3	US-09-232-200-46	Sequence 46, Appl
C 44	183	36.5	3694	4	US-09-232-197-46	Sequence 46, Appl
C 45	183	36.5	3694	4	US-09-232-201-45	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-09-791-211-10/c
; Sequence 10, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTIGENSE MODULATION OF WRN EXPRESSION
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791,211
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 98844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 24962
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 64383
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65468
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65469
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65470
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65471
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 87130
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 89049
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
US-09-791-211-10

Query Match 39.0%; Score 195.6; DB 4; Length 98844;
Best Local Similarity 71.3%; Pred. No. 1.3e-42;
Matches 281; Conservative 0; Mismatches 94; Indels 19; Gaps 1;
QY 66 AGSCCGGTGACGTGCTACGCTGTAAATCCAGCACTTGGGAAGCCAGCGGCGAGA 125
||||| |

OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 63290
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 66614
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68660
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68697
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68718
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68739
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 69785
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79134
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79198
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 86336
OTHER INFORMATION: unknown
OTHER INFORMATION:
US-09-791-211-3

Query Match 38.8%; Score 194.4; DB 4; Length 87543;
Best Local Similarity 75.4%; Pred. No. 2,7e-42;
Matches 263; Conservative 0; Mismatches 67; Indels 19; Gaps 1;
QY 57 TTTAAAAATAGCCGGTGCAGTGGCTCAGCGCTGTAATCCAGACACTTTGGGAAGCCAAAG 116
Db 42168 TTTTAAAAAGCTGGCATGGTGGCTCAGCGCTGTAATCCAGACACTTTGGGAGCCGAG 42227
QY 117 GCGGGCAGAACCCCGAGTCAAGAGTCAAGGCGAGCGCTGGCCAGATGTGAAACCCC 176
Db 42228 GCAGGCAGATCACTTGAGTCAAGAGTTCAGACCCAGCGCTGGCCAAACATGATGAAACTCC 42287
QY 177 GTCTCTATTAAAAATACAAACATTACCTGGGCGATGATGTGGGCGCTGTAATCCAGCT 236
Db 42288 GTTCTTACTTAAAGTACAAAATTTAGCTGGGCGTGTGTGGTGCCCTGTAATCCAGCT 42347
QY 237 ACTCAGGAGCTGAGGCAGAGGATCCGCGGAGCGCTGGCAGATCTGCTGAGCGCTGGGAG 296
Db 42348 ATTCAGGAGCTGAGGCAGGAGT-----TGCTTGAACCCAGGAG 42388
QY 297 GTTGGAGTACAGTAAAGCAAGATCATGCCAGTACTTACGCTGGGCGGCAAGAGTGGAG 356
Db 42389 GTGGAGTGGAGTGAAGTCAAGATTTGCCACTGCGACTTCAGCTTGGGAGACAGGCGAG 42448
QY 357 ACCGTACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 405
Db 42449 ACTCTGTCTCNAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 42497

RESULT 5
US-09-754-250-3/c
Sequence 3, Application US/09754250
Patent No. 6376225
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001063
CURRENT APPLICATION NUMBER: US/09/754,250
CURRENT FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 111282
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(111282)
OTHER INFORMATION: n = A, T, C or G
US-09-754-250-3

Query Match 38.4%; Score 192.6; DB 4; Length 111282;
Best Local Similarity 76.7%; Pred. No. 8.9e-42;
Matches 257; Conservative 0; Mismatches 59; Indels 19; Gaps 1;
QY 67 GCGCGTGCAGTGGCTCAGCGCTGTAATCCAGACACTTTGGGAAGCCAAAGCGGCAGAA 126
Db 18615 GCCAGGTGCAGTGGCTCAGCGCTGTAATCCAGACACTTTGGGAGGTCAAGCGCGCAGAT 18556
QY 127 CACCCGAGTCAAGAGTCCAGGCCAGCGCTGCCCAAGATGTGAAACCCCGTCTCTATTA 186
Db 18555 CACCTGAGGCGCAGGAGTTCGAGACAGCGCTGCCCAATATGTGAAACCCCGTCTCTACCA 18496
QY 187 AAATACAAACATTACCTGGGCGATGATGGTGGGCGCTGTAATCCAGCTACTCAGGAGG 246
Db 18495 AAAGTACAAAATTTAGCGGCGCATGCTGGCAGTCCCTGTGATCCAGCTACTTGGGAGG 18436
QY 247 CTGAGGCAGGAGATCCGCGGAGCGCTGGCAGATCTGCCCTGAGCGCTGGGAGGTGAGGCTA 306
Db 18435 CTGAGGCAGGACATC-----ACTTGAACCCAGGAGGTGGAGGTG 18395
QY 307 CAGTAGCCAGATCATGCCAGTACTTACGCTGGGCGCAAAAGTGAACCGTAAACAA 366
Db 18394 CAGTGAGCAAGATCCACCTGCACTCCAGCTGGGCGACAGAGCAAGCTGTCTCAA 18335
QY 367 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 401
Db 18334 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 18300

RESULT 6
US-09-851-896-3/c
Sequence 3, Application US/09851896
Patent No. 6410325
GENERAL INFORMATION:
APPLICANT: Susan M. Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPE)
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0220
CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
LENGTH: 70000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-851-896-3

Query Match 38.4%; Score 192.4; DB 4; Length 70000;
Best Local Similarity 77.3%; Pred. No. 8.4e-42;
Matches 255; Conservative 0; Mismatches 56; Indels 19; Gaps 1;
QY 67 GCGCGTGCAGTGGCTCAGCGCTGTAATCCAGACACTTTGGGAAGCCAAAGCGGCAGAA 126

Db 1407 TTAAGAGCTGAACAGGCGCTGGCGTAGTGGCTCAGCGCTGTAAATCCAGCAGCTTTGGGA 1348
Qy 110 AGCCAAGCGGGGAGAACACACCGAGGTTCAGAGTCCAGGCGCAGCTTGGCCAGATGGTG 169
Db 1347 GSCCGAGGCGGTGTGATCACCTGAGTTCAGGAATTCAGAGCAGCTAGCCACACGCG 1288
Qy 170 AAACCCCTCTCTATTAATAATACAAATTAACCTGGGCATGATGGTGGCGCTGTAAAT 229
Db 1287 AAACCCCTCTCTATTAATAATACAAATTAACCTGGGCATGATGGTGGCGCTGTAAAT 1228
Qy 230 CCCAGTACTCAGGAGGTGAGGCGAGGAGTCCGCGAGCTGGCAGATCTGCTGAGC 289
Db 1227 CCCAGTACTCAGGAGGTGAGGCGAGGAGTCCGCGAGCTGGCAGATCTGCTGAGC 1187
Qy 290 CTGGAGGTGAGGCTCAGTAAAGCAAGTATCCAGTATCTTCAAGCTGGCGGACCA 349
Db 1186 CTGGAGGTGAGGCTCAGTAAAGCAAGTATCCAGTATCTTCAAGCTGGCGGACCA 1127
Qy 350 AAGTACAGCGGTAAACAAAAAATTTAAAAAAGAAATTTAGATCAAGATCC 406
Db 1126 GAGCAGACTCCGCTCAGAAAAAATTTAAAAAAGAAATTTAGATCAAGATCC 1070

RESULT 9
US-09-780-172-18/c
; Sequence 18, Application US/09780172
; Patent No. 6607916
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0159
; CURRENT APPLICATION NUMBER: US/09/780,172
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 63000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-172-18

Query Match 37.7%; Score 189; DB 4; Length 63000;
Best Local Similarity 74.1%; Pred. No. 6.7e-41;
Matches 275; Conservative 0; Mismatches 75; Indels 21; Gaps 2;
Qy 52 ATACATTAATAATAGGCGGTGCTCAGTGGCTCAGCGCTGTAAATCCAGCAGCTTTGGGAAG 111
Db 19563 AAATTTTAAATTCGGCTGGCGCAGTGGCTCAGCGCTGTAAATCCAGCAGCTTTGGGAAG 19504
Qy 112 CCAAGCGGCGAGAACACCGAGGTTCAGAGTCCAGGCGAGCTGGCCAGATGGTGAA 171
Db 19503 CTGAGCGGCGGATCA--CGAGGTCAAGATCGAGCCACCTGGCTTAACATGGTGAA 19446
Qy 172 ACCCGCTCTCTATTAAAAATACAAATTAACCTGGGCATGATGGTGGCGCTGTAAATCC 231
Db 19445 ACCCGCTCTCTATTAAAAATACAAATTAACCTGGGCATGATGGTGGCGCTGTAAATCC 19386
Qy 232 CAGCTACTCAGGAGGTGAGGCGAGGAGTCCCGGAGCTGGCAGATCTGCTGAGCT 291
Db 19385 CAGCTACTCAGGAGGTGAGGCGAGGAGTCCCGGAGCTGGCAGATCTGCTGAGCT 19345
Qy 292 GCGAGGTGAGGTTCAGTAAAGCAAGATCATGCCAGTATCTTCAAGCTGGCGGACAA 351
Db 19344 GCGAGGTGAGGTTCAGTAAAGCAAGATCATGCCAGTATCTTCAAGCTGGCGGACAA 19285
Qy 352 GTGAGCCGCTAACAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAACTG 411
Db 19284 GCGAGCTCCATCTCAAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAACTG 19225
Qy 412 TAAAAAGTGGC 422

Db 19224 TGCACAGTGGC 19214
RESULT 10
US-08-646-301A-1
; Sequence 1, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
; TITLE OF INVENTION: Antigen for Expression Targeting
; FILE REFERENCE: PB1508USW
; CURRENT APPLICATION NUMBER: US/08/646,301A
; CURRENT FILING DATE: 1996-05-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-646-301A-1

Query Match 37.7%; Score 188.8; DB 3; Length 11288;
Best Local Similarity 73.0%; Pred. No. 3.9e-41;
Matches 279; Conservative 0; Mismatches 82; Indels 21; Gaps 2;
Qy 60 AAAATAGGCGGTGCTCAGTGGCTCAGCGCTGTAAATCCAGCAGCTTTGGGAAGCCAGGCG 119
Db 529 AAAATCAGCGCGCGGTGGCTCAGCGCTGTAAATCCAGCAGCTTTAGAAAGCTGAGGTG 588
Qy 120 GCGAGAACCCGAGGTTCAGGAGTTCAGGCGAGCTGGCCAGATGGTGAACCCGCTC 179
Db 589 GCGAGATTAATCTGAGGTTCAGGAGTTCAGGCGAGCTGGCCAGATGGTGAACCCGCTC 648
Qy 180 TCTATTAAAAATACAAATTAACCTGGGCATGATGGTGGCGCTGTAAATCCAGCTACT 239
Db 649 TCTATTAAAAATACAAATTAACCTGGGCATGATGGTGGCGCTGTAAATCCAGCTACT 708
Qy 240 CAGGAGCTCAGGCGAGGATCCGCGAGCTGGCGAGATCTGCTGAGCTGGGAGTT 299
Db 709 CCGGAGGCTCAGGCTGGCAAT-----TGCCTGGACCCAGGAAGCA 749
Qy 300 GAGGCTACACTAAGCCAGATCATGCGAGTATCTTCAAGCTGGCGCACAAGTGA-- 357
Db 750 GAGGCTCAGTGGCGAGGATTTGTGCACTGCACTGCGCTGGGCAACAGAGCCAGCT 809
Qy 358 CCCTAACAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAACTGTGTAATAA 417
Db 810 CTGTAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAACTGTGTAATAA 869
Qy 418 GTGGCTTAACACACCATTTAA 439
Db 870 ATCTCTTTGGGTAAACAAAAA 891

RESULT 11
US-08-481-968A-4
; Sequence 4, Application US/08481968A
; Patent No. 6300490
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (C
; FILE REFERENCE: PB1087US4
; CURRENT APPLICATION NUMBER: US/08/481,968A
; CURRENT FILING DATE: 1998-06-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 11288

Search completed: March 4, 2004, 16:42:01
Job time : 59.5558 secs

PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 284984
LENGTH: 669
TYPE: DNA
ORGANISM: Human
US-10-027-632-284984

Query Match 39.7%; Score 198.8; DB 15; Length 669;
Best Local Similarity 76.0%; Pred. No. 9.5e-43;
Matches 260; Conservative 0; Mismatches 77; Indels 5; Gaps 1;

QY 79 GCTCAGCGCTGTAATCCAGCACTTTGGGAAGCCAGCGGGGCGAAGACCCCGAGGTCA 138
Db 464 GCTCAGCGCTGTAATCCAGCACTTTGGGAAGCCAGCGGGGCGAAGACCCCGAGGTCA 405
QY 139 GGAGTCCAAAGGCGAGCTGGCCAGATGGTGAACCCCGTCTCTATTAAAAATCAAAACA 198
Db 404 GGAGTTTGAGACCGCTGGCCAGATGGTGAACCCCGTCTCTATTAAAAATCAAAACA 345
QY 199 TTACCTGGGCATGATGGTGGGCGCTGTAAATCCAGCTACTCAGGAGCTCAGGAGGAG 258
Db 344 TGAGCCAGCATGGTGGGCGCGCTGTAAATCCAGCTACTCAGGAGCTCAGGAGGAG 285
QY 259 GATCCGCGAGCTGCGAGA-----TCTGCTTGGAGCTGGAGGTTGAGGCTACAGTAAG 313
Db 284 ATCTCTTCTCTGCTGGTGAAGCCCGAGCCCTGAACCCAGGAGCGGAGTTGAGTAAG 225
QY 314 CCAAGATCATGCGATATCTTACGCTGGGCGCAAAAGTGAGACCGGTAAACAAAAAAA 373
Db 224 CCAAGATCTGCGCACTGCACTCCAGCTGGGAGCAAAAGTGAGACTCAGTCTCAAAAAA 165
QY 374 AAAATTTAAAAAGAAATTTAGATCAAGATCCCACTGTAA 415
Db 164 AAAAAAAGAAAAAGAAAGAAATTTATTTATGTGTAA 123

RESULT 5
US-10-277-216-5/c
Sequence 5, Application US/10277216
Publication No. US20040002470A1
GENERAL INFORMATION:
APPLICANT: KEITH, TIM
TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES,
FILE REFERENCE: 2976-4051
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/10/277,216
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 10/126,022
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 09/834,597
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/548,797
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 420
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 207433
TYPE: DNA
ORGANISM: Homo sapiens
US-10-277-216-5

Query Match 39.4%; Score 197.4; DB 15; Length 207433;
Best Local Similarity 71.2%; Pred. No. 2.7e-41;
Matches 284; Conservative 0; Mismatches 96; Indels 19; Gaps 1;

QY 10 AAAACAGGTGTGAGCCACTGCGCCAGCCAGGATTTGCTCTTATATCAATTAATAATAGGC 69
Db 199036 AAAACAGGTGTGAGCCACTGCGCCAGCCAGGATTTGCTCTTATATCAATTAATAATAGGC 129
QY 70 CGGTGCAAGTGGCTGAGCGCTGTAATCCAGCACTTTGGGAAGCCAGCGGGGCGAGAACAC 129
Db 198976 GGGCAGGTGGCTGAGCGCTGTAATCCAGCACTTTGGGAAGCCAGCGGGGCGAGAACAC 198917
QY 130 CCGAGGTGAGGAGTCCAGGCGCAGCTGCGCCAGGATGGTGAACCCCGTCTCTATTAAAA 189
Db 198916 CTGAGGTGAGGAGTCCAGGCGCAGCTGCGCCAGGATGGTGAACCCCGTCTCTATTAAAA 198857
QY 190 ATACAAACATTTACCTGGGCGATGATGGTGGGCGCTGTAATCCAGCTACTCAGGAGGCTG 249
Db 198856 ATACAAACATTTACCTGGGCGATGATGGTGGGCGCTGTAATCCAGCTACTCAGGAGGCTG 198797
QY 250 AGGCGAGGATCCGCGGAGCCTGGCGAGATCTGCTGAGCCTGGGAGGTTGAGGCTACAG 309
Db 198796 AGGCGAGGATCCGCGGAGCCTGGCGAGATCTGCTGAGCCTGGGAGGTTGAGGCTACAG 198756
QY 310 TAAGCAAGATCATGCGCACTATCTTACGCTGGGCGCAAAAGTGAGACCGGTAAACAAAA 369
Db 198755 GGAACCAAGATCATGCGCACTATCTTACGCTGGGCGCAAAAGTGAGACCGGTAAACAAAA 198696
QY 370 AAAAAAATTTAAAAAGAAATTTAGATCAAGATCCAA 408
Db 198695 AAAAAAAGAAAGAAAGAAATTTAGATCAAGATCCAA 198657

RESULT 6
US-10-126-022-5/c
Sequence 5, Application US/10126022
Publication No. US20040023215A1
GENERAL INFORMATION:
APPLICANT: KEITH, TIM
TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES,
FILE REFERENCE: 2976-4039US2
CURRENT FILING DATE: US/10/126,022
PRIOR APPLICATION NUMBER: 09/834,597
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/548,797
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 420
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 207433
TYPE: DNA
ORGANISM: Homo sapiens
US-10-126-022-5

Query Match 39.4%; Score 197.4; DB 16; Length 207433;
Best Local Similarity 71.2%; Pred. No. 2.7e-41;
Matches 284; Conservative 0; Mismatches 96; Indels 19; Gaps 1;

QY 10 AAAACAGGTGTGAGCCACTGCGCCAGCCAGGATTTGCTCTTATATCAATTAATAATAGGC 69
Db 199036 AAAACAGGTGTGAGCCACTGCGCCAGCCAGGATTTGCTCTTATATCAATTAATAATAGGC 129
QY 70 CGGTGCAAGTGGCTGAGCGCTGTAATCCAGCACTTTGGGAAGCCAGCGGGGCGAGAACAC 129
Db 198976 GGGCAGGTGGCTGAGCGCTGTAATCCAGCACTTTGGGAAGCCAGCGGGGCGAGAACAC 198917
QY 130 CCGAGGTGAGGAGTCCAGGCGCAGCTGCGCCAGGATGGTGAACCCCGTCTCTATTAAAA 189
Db 198916 CTGAGGTGAGGAGTCCAGGCGCAGCTGCGCCAGGATGGTGAACCCCGTCTCTATTAAAA 198857


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RESULT 7
US-10-027-632-119235
/ Sequence 119235, Application US/10027632
/ Publication NO. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ POLYMORPHISMS IN THE HUMAN GENOME
/ FILE REFERENCE: 108827,129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: PastSeq for Windows Version 4.0
/ SEQ ID NO 119235
/ LENGTH: 1138
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-119235

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QY 354 GAGACCGTACACAAAAAATTTTAAAAAAGAAATTT 394
DB 510 GAGACTCCATCTCAAAAAAATTTTAAAAAAGAAATTT 550

RESULT 8
US-10-027-632-119236
; Sequence 119236, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,216
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 119236
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-119236

Query Match 39.3%; Score 197; DB 15; Length
Best Local Similarity 76.8%; Pred. No. 3.6e-42;
Matches 262; Conservative 0; Mismatches 60; Index

QY 54 ACATTAAAAAATAGGCGGTGCAGTGGCTCACGCCCTGTATCCCA
DB 229 ACTCAAGATTTTGGCGGCACAGTGGCTCACACCTGTATCCCTC

QY 114 AAGCGGGGAGAACACCCGAGGTGAGAGTCCAAAGCCAGCCTGGG
DB 289 GAGGCGAGGTGGATTACCGGAGTTCACACCCAGCCTGGG

QY 174 CCGCTCTCTATTTAAAAATACAAACATTACCTGGGCATGATGGTGGG
DB 349 CCCTCTCTACTTAAATAACAAAATAGCTGGCATGGTGGCAGG

QY 234 GCTACTCAGAGGCTGAGGCGAGGAGATCCGCGAGCGCTGGCAGAG
DB 409 GCTACTCAGAGGCTGAGGCGAGGAGAT-----

QY 294 GAGGTTCAGGCTACAGTAAGCCAAAGATCATGCCAGTATACTTCAGAG
DB 450 GAGTTGAGGTTTGCAGTGAGCCGAGATCATGCCATTCGCACTCCAGG

QY 354 GAGACCGTACACAAAAAATTTTAAAAAAGAAATTT 394
DB 510 GAGACTCCATCTCAAAAAAATTTTAAAAAAGAAATTT 550

RESULT 9
US-10-027-632-119237
; Sequence 119237, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119237
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-119237

Query Match      39.3%; Score 197; DB 15; Length 1138;
Best Local Similarity 76.8%; Pred. No. 3.6e-42;
Matches 262; Conservative 0; Mismatches 60; Indels 19; Gaps 1;

QY 54 ACATTAAATAAGCGCGTGCAGTGGCTCAGCGCTGTAATCCAGCAGCTTTGGAGGCC 113
DB 229 ACTCAAGAAATTTGGCGGCACAGTGGCTCAGCGCTGTAATCCCTGCACTTTGGAGGCC 288
QY 114 AAGCGGGGAGAACACCCGAGGTCAGGAGTCAAGCGGCGAGCGCTGGCCAAAGTGGTGAAC 173
DB 289 GAGCGAGGTGGATTACCGAGGTGAGGATTCACACAGCTGCGCCACATGATGAAT 348
QY 174 CCGCTCTCTATTAAAAATAACAAATACCTGGGCGATGATGGTGGCGCCCTGTAATCCCA 233
DB 349 CCGCTCTCTATTAAAAATAACAAATATAGTGGCGATGATGGTGGCGACACACCTGTAATCCCA 408
QY 234 GCTACTCAGAGGCTGAGCGAGGATCGCGGAGCGCTGGCGAGATCTGCTGAGCGCTGG 293
DB 409 GCTACTCAGAGGCTGAGCGAGGAT-----TGCTTGAACCCGG 449
QY 294 GAGGTTGAGGCTACAGTAAGCCAGATCATGCCAGTATATTCAGCCTGGGCGCAAAAGT 353
DB 450 GAGTTGAGGTTGCACTGAGCGGAGATCATGCCATTGCACTCCAGCCTGGGCGCAGAGG 509
QY 354 GAGACCGTAACAAAAAATAAAAAAATTTAAAAAAGAAATTT 394
DB 510 GAGACTCCATCTCAAAAAAATAAAAAAATTTAAAAAAGAAATTT 550

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RESULT 10
US-10-027-632-187984
; Sequence 187984, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483

```

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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187984
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-187984

Query Match      39.2%; Score 196.2; DB 15; Length 676;
Best Local Similarity 73.7%; Pred. No. 4.7e-42;
Matches 272; Conservative 0; Mismatches 78; Indels 19; Gaps 1;

QY 35 AGCCAGGATTGCTCTTATACATTAAAAAATAGGCGGTGCAGTGGCTCACGCTGTAAT 94
DB 168 AGCCAGACTTCCTTAAATTTAAAAACGAGTAGGCGAGGTGCGGTGGCTCATGCTGTAAT 227
QY 95 CCCAGCATTGGGAAGCCAGCGGCGAGACACCCGAGGTCAGGAGTCCAGGCCAGC 154
DB 228 CTGAGCATTGGGAGKAGCAGAGCGGCTGATCACCCTGAGGTGAGGAGTTCAAGACCAGC 287
QY 155 CTGCGCAAGATGGTGAACCCCGCTCTCTATTAAAAATAACAAATATACCTGGGCGATG 214
DB 288 CTGCGCAACATGCGGAAACCCCTGCTCTACTAAAAATAACAAATATAGCTGGGTGGTG 347
QY 215 GTGGGCGCTGTAATCCAGCTACTCAGGAGGTGAGGAGTCCGCGAGGAGTCCGCGAGCCTGG 274
DB 348 GTGGGCGCTGTAATCCAGCTACTCAGGAGGTGAGGAGTCCGCGAGGCTGAGG-----TGG 388
QY 275 CAGATCTGCTGAGCTGGGAGGTTGAGGCTCAGTAAAGCCAGATCATGCCAGTATATCT 334
DB 389 GAGAAATGCTTGACCCAGGAGTAGAGGTTGCACTAAAGTCCGAGCTGTGCCACTGCCT 448
QY 335 TCAGCTGGGCGCAAGAGTGAAGCCGTAAACAAAAAATAAAAAAATTTAAAAAAGAAATTT 394
DB 449 TCAGCTGGGCGCAAGAGTGAAGCTCTGTCAAAAAAATAAAAAAATTTAAAAAAGCTATGCTT 508
QY 395 AGATCAAGA 403
DB 509 TGTAAGA 517

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RESULT 11
US-09-764-891-6056/c
; Sequence 6056, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6056
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-6056

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Query Match      39.2%; Score 196.2; DB 10; Length 1743;
Best Local Similarity 75.4%; Pred. No. 7.1e-42;
Matches 266; Conservative 0; Mismatches 68; Indels 19; Gaps 1;

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QY	35	ACCCAGGATTGCTCTTATACATTTAAAAAATAGCGCGGTGAGTGGCTCAGCGCTGTAAT	94
Db	464	AGCCAGACTTCTTTAAAAATTAAAAACGAGTAGGCGAGGTGCGGTGCTCATGCTGTAAAT	405
QY	95	CCACGACATTTTGGGAAGCCCAAGCGGGGCGAGAACACCCGAGGTACAGGAGTCCAAGGCCAGC	154
Db	404	CTCAGCATTTTGGGAGCGAGAGCGGGTGGATCACCTGAGTCAAGGAGTTCAGACCCAGC	345
QY	155	CTGGCCAAAGATGGTGAACCCCGTCTCTATTAAAAAATACAAACATTACCTGGGCGATGATG	214
Db	344	CTGGCCAAACATGGCGAAACCCCTGTCTCTACTAAAAATACAAAGAATTAGCTGGGTGTGGTG	285
QY	215	GTGGGGCGCTGTAAATCCACAGCTACTCAGGAGGCTTGAGGCGAGGAGGATCCGCGGAGCTGG	274
Db	284	GTGGGCACTGTAAATCCACAGCTACTCAGGAGGCTGAGG-----TGG	244
QY	275	CAGATCTGCTGAGCCTGGGAGTTGAGGCTACAGTAAAGCCAGATCATGCCAGTACT	334
Db	243	GAGAATTGCTTGAACCCAGGAGGTAGAGGTTGCAGTAACTGCAGACTGTGCCACTGCAC	184
QY	335	TCAGCTGGGCGACAAAGTAGACCGTAAACAAAAAATAAAAAAATTTAAAAAGAAATTT	394
Db	183	TCAGCTGGGCAACAGAGTGAGACTCTCTCAAAAAAATAAAAAAATTTAAAAACCTATGCTT	124
QY	395	AGATCAAGA 403	
Db	123	TGTAAGA 115	

RESULT 14

US-10-210-723-13

; Sequence 13, Application US/10210723

; Publication No. US20040023382A1

; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean

; APPLICANT: C. Frank Bennett

; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION

; FILE REFERENCE: PTS-0028

; CURRENT APPLICATION NUMBER: US/10/210,723

; CURRENT FILING DATE: 2002-07-31

; NUMBER OF SEQ ID NOS: 141

; SEQ ID NO 13

; LENGTH: 70000

; TYPE: DNA

; ORGANISM: H. sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 63612-63711

; OTHER INFORMATION: n = A,T,C or G

US-10-210-723-13

	Query Match	39.0%;	Score 195.2;	DB 16;	Length 70000;
	Best Local Similarity	73.6%;	Pred. No. 6.6e-41;		
	Matches 271;	Conservative 0;	Mismatches 78;	Indels 19;	Gaps 1;
QY	67	GGCGGTGTCAGTGGCTCAGCGCTGTAAATCCACAGCACTTTGGGAAGCCAAAGCGGGCAGAA	126		
Db	19129	GCCAGTGCAGTGGCTCATGCTGTATATCCAGAACTTTGGGAAGCCAAAGCGGGCAGAT	19188		
QY	127	CACCCGAGTTCAGGAGTCCAAAGCCAGCGCTGGCCAAAGATGGTGAACCCCGCTCTCTATTA	186		
Db	19189	CACCTGAGTTCAGGAGTTCGACCAAGCCGCTGGCCCAACATGGTGAACCCCGCTCTCTACTA	19248		
QY	187	AAAAATCAAAATTAACCTGGGATGATGCTGGGCGCCTGTAAATCCAGCTACTCAGAGG	246		
Db	19249	AAAAATCAAAATTAAGCTGGGCAATGATGGCGATGCTCTGTATATCCAGCTACTCGGAGG	19308		
QY	247	CTGAGCAGAGGATCCGCGAGCCTGGCAGATCTGCCTGAGCTGGGAGTTGAGGCTA	306		
Db	19309	CTGAGCAGAGGAATCC-----CTTGAACCGGAGCGGAAGTTG	19349		

Qy 405 CCAACTGTAAAA 417
Db 502 ATATATATATATA 514

Search completed: March 4, 2004, 19:00:17
Job time : 248.513 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:54:45 ; Search time 1959.09 Seconds
(without alignments)
7636.686 Million cell updates/sec

Title: US-09-966-880A-35_COPY_5000_5500
Perfect score: 501
Sequence: 1 atacattataaacaggtgt.....ggtcttcagcagtggaatgg 501

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pin:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_pug:*
- 27: em_gss_vri:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	203.6	40.6	666	28	B88182
C 2	201.6	40.2	678	28	AQ387027
C 3	200.2	40.0	3.4	9	AA828637
C 4	198.2	39.6	736	13	BUS54403

C 5	196.6	39.2	445	12	BQ023922
C 6	196.6	39.2	607	28	AQ554450
C 7	195.6	39.0	495	28	AQ336857
C 8	195.6	39.0	530	13	BUT52902
C 9	195.4	39.0	370	13	EX485214
10	194.8	38.9	374	28	AQ021361
11	194.6	38.8	607	28	BZ603708
12	192.4	38.4	393	10	BF805088
C 13	192.4	38.3	617	28	AQ383054
C 14	192	38.3	895	12	BM452899
C 15	190.8	38.1	501	9	AA722505
C 16	190.8	38.1	603	28	AQ381919
C 17	190.8	38.1	945	13	BUT17036
C 18	190.4	38.0	879	13	BQ708582
C 19	190.2	38.0	493	13	EX486751
C 20	190.2	38.0	602	13	EX480725
C 21	190.2	38.0	664	28	AQ581318
C 22	190	37.9	452	14	T74524
C 23	190	37.9	462	28	AQ504564
24	189.8	37.9	966	28	BZ773416
C 25	189.6	37.8	342	13	EX484854
26	189.6	37.8	589	13	EX464260
27	189.6	37.8	642	28	B59854
28	189.6	37.8	648	28	BZ611349
29	189.4	37.8	711	28	AQ415030
30	189.4	37.8	1389	11	BC019872
C 31	189.2	37.8	619	12	B1870387
C 32	189.2	37.8	687	29	AG085195
C 33	189.2	37.8	688	29	AG118999
C 34	188.8	37.7	689	13	BU661880
35	188.8	37.7	814	28	AQ780979
36	188.8	37.7	1538	10	BG036370
37	188.6	37.6	703	28	AQ035234
38	188.6	37.6	711	13	EX454025
39	188.4	37.6	411	9	A1590458
C 40	188.4	37.6	673	29	AG046383
41	188.4	37.6	4125	11	BC028413
C 42	188.2	37.6	739	28	AQ035003
C 43	188	37.5	601	13	EX506204
C 44	188	37.5	623	28	AQ055264
C 45	187.8	37.5	432	12	B1496637

ALIGNMENTS

RESULT 1
B88182/c
LOCUS B88182 666 bp DNA linear GSS 09-APR-1999
DEFINITION B88182 666 bp DNA linear GSS 09-APR-1999
ACCESSION B88182 666 bp DNA linear GSS 09-APR-1999
VERSION B88182 666 bp DNA linear GSS 09-APR-1999
KEYWORDS B88182 666 bp DNA linear GSS 09-APR-1999
SOURCE B88182 666 bp DNA linear GSS 09-APR-1999
ORGANISM B88182 666 bp DNA linear GSS 09-APR-1999
REFERENCE B88182 666 bp DNA linear GSS 09-APR-1999
AUTHORS B88182 666 bp DNA linear GSS 09-APR-1999
TITLE B88182 666 bp DNA linear GSS 09-APR-1999
JOURNAL B88182 666 bp DNA linear GSS 09-APR-1999
COMMENT B88182 666 bp DNA linear GSS 09-APR-1999

7912 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdaadams@igrr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong

(pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES

Location/Qualifiers
1..666

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7508725"
/db_xref="taxon:9606"
/clone="RPC1-11-23L14"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPC1-11"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
RPC111 Human Male BAC Library"

ORIGIN

Query Match 40.6%; Score 203.6; DB 28; Length 666;
Best Local Similarity 72.7%; Pred. No. 1.8e-24;
Matches 263; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
Qy 65 TAGCCCGGTGCAGTGGCTCAGCTGTATCCAGCAGCTTTGGGAAGCCAAAGCGGGCAG 124
Db 362 TGGCCAGGCACAGTGTCTCACACTGTATACAGCAGCTTTGAGAGGCCAAGSCAGGCG 303
Qy 125 AACACCCGAGTCCAGGAGTCAAGCCAGCTGCCAGAGTGTGAAGCCCGTCTCTAT 184
Db 302 ATCACCTGAGTCCAGGAGTTCGAGACAGCCTGACCAACATGGCGAAACCTGCTCTAC 243
Qy 185 TAAATAACAAACATTAACCTGGCGCATGATGGTGGGCGCTGTATATCCAGCTACTCAGGA 244
Db 242 TAAATAACAAACATTAAGCCAGCATGTTGGTGGTGGTGTATCTCAGCTACTCAGGA 183
Qy 245 GGCTGAGGAGGAGTCCGGAGCTGCGCATGCTGCAGATCTGCTGAGCTGGAGGTTGAGC 304
Db 182 GGCTGAGGAGGAGTCCGGAGTTCATTTGGAGCAGGAGATCATTTGAACCCAGGAGCAGAGT 123
Qy 305 TACAGTAAGCCAAAGATCATGCCAGTATATCTCAGCTGGGCGCAACAAAGTGAGACCCGTAAC 364
Db 122 TGCACTGAGCAGAGATTTGCCCGCACTGTATTTAGCTGGGCAACAGTGAGACTCTGCTC 63
Qy 365 AAAAAAATAAATTTAAAAAAGAAATTTAGATCAAGATCCAACTGTGTAAGAGTGGCT 424
Db 62 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3
Qy 425 AA 426
Db 2 CA 1

RESULT 2

AQ387027
LOCUS RPC111-153C12.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-153C12,
DEFINITION genomic survey sequence.
ACCESSION AQ387027
VERSION AQ387027.1 GI:4358050
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Zhao, S., Adams, W.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
TITLE Use of BAC End Sequences from Library RPC1-11 for Sequence-Ready Map Building
JOURNAL Map Building (1997)
COMMENT Other GSSs: RPC111-153C12.TV
Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org

Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:758427"
/db_xref="taxon:9606"
/clone="RPC1-11-153C12"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPC1-11"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
RPC111 Human Male BAC Library"

ORIGIN

Query Match 40.2%; Score 201.6; DB 28; Length 678;
Best Local Similarity 73.2%; Pred. No. 3.8e-24;
Matches 281; Conservative 0; Mismatches 84; Indels 19; Gaps 1;
Qy 22 AGCCACTGGCCCGCCAGCAGGTATTGCTCTTATACATTAAAAAATAGCCCGTGCAGTGGC 81
Db 38 AGCCTGGGTGACACAGCAGACCATCTCTAAAAATAAAATAAGGCGCGGTGGC 97
Qy 82 TCAGCCTGTATCCAGCAGCTTTGGGAAGCCAGGCGGCAGACACCCAGGTCAAGGA 141
Db 98 TCAGCCTGTATCCAGCAGCTTTGGGAGGCTTAAGCGGCGCAGATCACTGAGTCAAGGA 157
Qy 142 GTCCAAAGCCAGCCTGGCCAGATGGTGAACCCCGTCTCTATTAAAAATACAAACATTA 201
Db 158 GTTCGAGACACAGCCTGGCCACATGGTGAACCCCATCTCTCTAAAAATAAAAAATTA 217
Qy 202 CTGGGCAATGATGTGGCGGCTGTATCCAGCTACTCAGGAGGCTGAGCAGGAGAT 261
Db 218 GCCGGGCAATGGTGTGGTGGTGGTGTATATCCAGCTACATGGGAGGCTGAGCAGGAGAT 277
Qy 262 CCGCGGAGCCTGGCAGATCTGCCTGAGCCTGGGAGGTTGAGGCTACAGTAAAGCCAGATC 321
Db 278 -----TCTTGAACCTGGGAGGCGGAGGTTGCACTGAGCGGAGATC 318
Qy 322 ATGCCAGTATCTCAGCCTGGGCGCAAGTAGAGCCGTAAACAAAAAATAAAAAATTA 381
Db 319 GTGCCATTGCACTCCAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 378
Qy 382 AAAAAAGAAATTTAGATCAAGATC 405
Db 379 ATAAAAACATCTCTCTCCATCATC 402

RESULT 3

AQ828637
LOCUS AA828637/c 314 bp mRNA linear EST 07-APR-1998
DEFINITION cd79d11.s1 NCI CGAP Ov2 Homo sapiens cDNA clone IMAGE:1374165 similar to contains Alu repetitive element;; mRNA sequence.
ACCESSION AA828637
VERSION AA828637.1 GI:2901736
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 314)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicqap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Krizman, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Cloning by: Washington University Genome Sequencing Center
 Cloning by: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 405 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES

Location/Qualifiers
 1..314
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1374165"
 /sex="female"
 /tissue_type="ovary"
 /lab_host="DH10B"
 /clone_lib="NCI-CCAP Ovs2"
 /note="Vector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 40.0%; Score 200.2; DB 9; Length 314;
 Best Local Similarity 79.1%; Pred. No. 8.7e-24;
 Matches 238; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
 QY 77 GTGGCTCAGCGCTGTAATCCAGACATTTGGAGCCAGGCGGGCAGACACCCGAGGT 136
 Db 301 GTACTATACCTGTAATCTTAGACATTTGGAGCCAGGCGGAGATCACTGAGGT 242
 QY 137 CAGAGTCCAAAGGCGGCTGGCCAAAGATGGTGAACCCCGTCTCTATTAAATACAA 196
 Db 241 TCGGAGTTCAGGACCGCTGGCCAAATGGTGAACCCCATCTCTACTAAATACAA 182
 QY 197 CATTAAGTGGCGATGATGGGCGCTGTAATCCAGCTACTCAGGAGGCTGAGCAGG 256
 Db 181 AATCAGCTGGGTATGGTGGTGGCGCTCTAATCTTAGCTACTTGGGAGGCTTAGGCGG 122
 QY 257 AGGATCCGCGAGCGCTGGCAGATCTGCTGAGCCTGGGAGGTTGAGGCTACAGTAAAGCCA 316
 Db 121 AGAATCACTTCAACGCGAGGAGATCACTTGAACCCAGGAGGCTTGCAGTGAGCCG 62
 QY 317 AGATCATGCCAGTATATCTTACGCTGGGCGCAAGTGAACCCGCTAACCAAAAAA 376
 Db 61 AGATCATGCCAGTCTCAGCTCCAGCTGGGCAACAGAGACGCGCATCTCAAAAAA 2
 QY 377 A 377
 Db 1 A 1

RESULT 4

BUS54403/c
 LOCUS BUS54403 736 bp mRNA linear EST 16-OCT-2002
 DEFINITION AGENCOURT_10410045 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6621672
 5', mRNA sequence.
 ACCESSION BUS54403
 VERSION BUS54403.1 GI:24039369
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 736)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Cloning by: Agencourt Bioscience Corporation
 Cloning by: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LCM2873 row: 1 column: 24
 High quality sequence stop: 517.

FEATURES

Location/Qualifiers
 1..736
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6621672"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_82"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCCC-3' and 3' adaptor sequence: 5'-ATTTAGAGCCGAGCGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 39.6%; Score 198.2; DB 13; Length 736;
 Best Local Similarity 76.4%; Pred. No. 1.3e-23;
 Matches 256; Conservative 0; Mismatches 78; Indels 1; Gaps 1;
 QY 67 GCGCGGTGAGTGGCTCAGCGCTGTAATCCAGACATTTGGAGCCAGGCGGGCAGAA 126
 Db 548 GCGCGGTGAGTGGCTCAGCGCTGTAATCCAGACATTTGGAGCCAGGCGGGCAGAA 489
 QY 127 CACCCGAGTCAAGGAGTCCAAAGGCCAGCCTGGCCAAAGATGGTGAACCCCGTCTCTATTA 186
 Db 488 AACCTGAGGTCAAGAGTCTGAGACAGCCTGGCCAAATGTTGTTGAACCCCGTACTACTA 429
 QY 187 AAAATACAAACATTACCTGGGCGATGATGGTGGGCGCTGTAAATCCAGCTACTCAGGAGG 246
 Db 428 AAAATGCAAAATTTAGCTGGGCGATGGTGGGCGACCTGTAAATCCAGCTACTCAGGAGG 369
 QY 247 CTGAGCGAGGAGTCCGC-GGAGCCTGGCAGATCTGCTGAGCCTGGGAGGTTGAGGCT 305
 Db 368 CTGAGGTAGGAGATTTGCTCAAGCAATTTCTTGGCTTGAACCCAGAGGGGAGGCT 309
 QY 306 ACAGTAAGCCAAAGATCATGCCAGTATATCTCAGGCTGGGCGCAAAAGTGAGACCGTAACA 365
 Db 308 GCAGTGAGCCAAAGATTGCACCACTGCACTCCAGTATGGGTGACAGAGCGAGACTCCGTCT 249
 QY 366 AAAAAAAAAATTTAAAAAAGAAATTTAGATCA 400
 Db 248 CAAAAAATAAATAACAAATATGCAATTTTAAACA 214

RESULT 5

BQ023922/c
 LOCUS BQ023922 445 bp mRNA linear EST 27-MAR-2002
 DEFINITION UI-1-BBip-aun-b-07-0-UI.sl NCI-CCAP_P16 Homo sapiens cDNA clone
 UI-1-BBip-aun-b-07-0-UI 3', mRNA sequence.
 ACCESSION BQ023922
 VERSION BQ023922.1 GI:19759201


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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 445)
JOURNAL NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Steven Brown
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 11-307, xLUJ (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..445
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-1-BB1p-aun-b-07-0-UI"
/tissue_type="Placenta"
/dev_stage="Full Term"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Pl6"
/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with
a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Pl6 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are GA, AGGAA. For
additional information, contact: Bento Soares,
bento-soares@uiowa.edu
TAG TISSUE=placenta human full term
TAG LIB=UI-1-BB1p
TAG_SEQ=AGGAA"

ORIGIN
Query Match 39.2%; Score 196.6; DB 12; Length 445;
Best Local Similarity 77.2%; Pred. No. 3e-23;
Matches 257; Conservative 0; Mismatches 64; Indels 12; Gaps 1;

QY 52 ATACATTAAATAAGCGGTGAGTGGCTCAGCGCTGTATCCAGCACTTTGGGAGG 111
DB 321 ATATCTATATTTGGTGGGTGAGTGGCTGTATCCAGCACTTCGGAGG 262

QY 112 CCAAGCGGGCAGAACACCCGAGGTCAGAGTCCAGGCCAGCTGGCCAGAGTGGTAA 171
DB 261 CCGAGGCGAGGAGATCACTGAGGTCAGAGTTTAAAGACCAGCGCTGGCCACATGGTAA 202

QY 172 ACCCGCTCTCTATTAATAAATAAATAAATAAGCCGGCATGTGGGCGCTCTATCC 231
DB 201 ATCCCGTCTCTATTAATAAATAAATAAATAAGCCGGCATGTGGGCGCTCTATCC 142

QY 232 CAGCTACTCAGGAGGCTGAGGCGAGGATCCGCGAGCCCTGGCAGATCTGCCTGAGCCT 291
DB 141 CAGCTACTTGGAGGCTGAGGCGAGGATCACTTGAAC-----CCAGAACCT 94

QY 292 GGGAGGTTGAGCTACAGTAAAGCAAGATCATGCCAGTACTTTCAGCTGGCGACAA 351

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DB 93 GGGAGGCAGAGGTTGAGTGGAGCCGAGATTGTGCCACTGTACTCCTCGGTGACAGA 34
QY 352 GTGAGACCGCTAACCAAAAAAATTTAAAA 384
DB 33 GGGAGACTTCGTGCGCAAAAAAATTTAAAA 1

RESULT 6
AQ554450/c 607 bp DNA linear GSS 28-MAY-1999
LOCUS RPCI-11-422120.TU RPCI-11 Homo sapiens genomic clone
DEFINITION RPCI-11-422120, genomic survey sequence.
ACCESSION AQ554450
VERSION AQ554450.1 GI:4913627
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 607)
AUTHORS Zhao,S.; Adams,M.D.; Niernan,W., Malek,J., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: RPCI-11-422120.TV
Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbs@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pister@dejong.med.buffalo.edu). Clones may be purchased from
BACAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..607
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7661875"
/db_xref="taxon:9606"
/clone="RPCI-11-422120"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
RPCI11 Human Male BAC Library"

ORIGIN
Query Match 39.2%; Score 196.6; DB 28; Length 607;
Best Local Similarity 74.6%; Pred. No. 2.7e-23;
Matches 247; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 65 TAGCCCGGTGAGTGGCTCAGCGCTGTATCCAGCACTTTGGGAGCCAGCGCGGAG 124
DB 337 TGCCAGGCACAGTGTCTCACACCTGTATCACAGCACTTTGAGAGGCGGCGG 278

QY 125 AACACCCGAGGTCAGAGTCCAGGCCAGCTGGCCAGAGTGGTGAACCCCGCTCTAT 184
DB 277 ATCACTGAGTTCAGAGTTCGAGACCAGCTGACCAACATGGCGAACCTCGTCTAC 218

QY 185 TAAATAACAACATTAACCTGGGCGATGATGGTGGCGGCTGTATCCAGCTACTCAGA 244
DB 217 TAAATAACAACAAATAGCCAGGCATGGTGGTGGCTGTATCTCAGCTACTCAGA 158

QY 245 GGCCTGAGGCGAGGAGTCCGCGAGCTGCGAGATCTGCCTGAGCTGGGAGTTGAGC 304

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DB 157 GGCTGACGAGGAGATCATTTGGACGAGGAGATCATTTGAACCCAGGAGGAGAGGT 98
 QY 305 TACAGTAAGCCAGATCATGCGAGTATCTTTCAGCTGGCGGACAAAGTGAGACCGTAAC 364
 DB 97 TGCAGTGAGCCAGATGTCCTCCACTGTATTTTCAGCTGGCGGACAAAGTGAGACTCTGTCTC 38
 QY 365 AAAAAAATTTTAAAAAAGAAATTTA 395
 DB 37 AAGAGAAACAAACCAACCAACCAACCAATTA 7

RESULT 7
 A0236857/c
 LOCUS A0236857 495 bp DNA linear GSS 21-APR-1999
 DEFINITION RPII11-71K16.TJ RPII-11 Homo sapiens genomic clone RPII-11-71K16,
 genomic survey sequence.
 ACCESSION A0236857
 VERSION A0236857
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
 Berry,K., Granger,D., Suh,B., Wible,C., de Jong,P. and Venter,J.C.
 TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
 JOURNAL Unpublished (1998)
 COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org

Clones are derived from the human BAC library RPII-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@jong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 Location/Qualifiers
 1..495
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:7527135"
 /db_xref="taxon:9606"
 /clone="RPII-11-71K16"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPII-11"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPII11 Human Male BAC Library"

ORIGIN
 Query Match 39.0%; Score 195.6; DB 28; Length 495;
 Best Local Similarity 71.3%; Pred. No. 4.2e-23;
 Matches 258; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 65 TAGGCGGTCAGTGGCTCACCGCTGTAATCCAGCACTTTGGGAAGCGCAAGCGGGCAG 124
 DB 403 TGGCAGGACACAGTGTCTCACACCTGAATCACAGCACTTTGAGAGCCAGGACAGCG 344
 QY 125 AACACCCGAGGTTCAGAGTTCAGGCGCAGCTGGCGGACAGATGGTGAACCCCGTCTTAT 184
 DB 343 ATCACCTGAGGTTCAGAGTTCAGAGCCAGCTGGACCAATGGCGGAAACCTAGTCTATAC 284
 QY 185 TAAATATCAACATTTACCTGGGCGCTGATGGGCGCTGTAAATCCAGCTACTTCAGGA 244
 DB 283 TAAATATCAACATTTAGCAGCATGGTGGTGGCTGTAAATCTCAGTACTCAGGA 224

QY 245 GGCTGAGGAGGAGGATCGCGAGCTGGCGAGATCTGCTGAGCTGGGAGGTTGAGGC 304
 DB 223 GGCTGAGGAGGAGATCATTTTGGACGCGAGGAGATCATTTTGAACCCAGGAGGAGGT 164
 QY 305 TACAGTAAGCCAGATCATGCGAGTATCTTTCAGCTGGCGGACAAAGTGAGACCGTAAC 364
 DB 163 TGCAGTGAGCCAGATGTCCTCCACTGTATTTTCAGCTGGCGGACAAAGTGAGACTCTGTCTC 104
 QY 365 AAAAAAATTTTAAAAAAGAAATTTAGATCAAGATCCCACTGTAAAGTGGCGCT 424
 DB 103 AAGAAAAAATTTTAAAAAAGAAATTTTCTCTGCAATATGAAGCGCAAGTGGACT 44
 QY 425 AA 426
 DB 43 CA 42

RESULT 8
 BU752902/c
 LOCUS BU752902 530 bp mRNA linear EST 10-OCT-2002
 DEFINITION UI-1-BB1-aic-b-04-0-UI.s1 NCI CGAP P15 Homo sapiens cDNA clone
 UI-1-BB1-aic-b-04-0-UI 3', mRNA sequence.

ACCESSION BU752902
 VERSION BU752902.1 GI:23710587
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-z@mail.nih.gov
 Tissue Procurement: Dr. Steven Brown
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Cloning Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 10-306, >ALU (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 Location/Qualifiers
 1..530
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-1-BB1-aic-b-04-0-UI"
 /tissue_type="Placenta"
 /dev_stage="Full Term"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP P15"
 /note="Organ: Placenta; Vector: pTTT3-Pac (Pharmacia) with
 a modified polylinker; Site_1: EcoRI; Site_2: Not I;
 NCI-CGAP P15 is a subtracted cDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pTTT3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for this library are GA, AGGAA. For
 additional information, contact: Bento Soares,
 bento-soares@uiowa.edu
 TAG TISSUE=placenta human full term
 TAG_LIB=UI-1-BB1
 TAG_SEQ=AGGAA"

```
ORIGIN
Query Match      39.0%; Score 195.6; DB 13; Length 530;
Best Local Similarity 77.1%; Pred. No. 4.1e-23;
Matches 256; Conservative 0; Mismatches 64; Indels 12; Gaps 1;

QY 52 ATACATTAAAAATAGCGCGTGCAGTGGCTCAGCCCTGTAATCCCGACACTTTGGGAAG 111
Db 320 ATATACTATATTTGGCTGGGTGCAGTGGCTCATGCCCTGTAATCCCGACACTTCGGGAG 261
QY 112 CCAGGGCGGCGAGACACCCCGAGTCCAGAGTCCAGCGCAGCTGGCCAGATGGTGA 171
Db 260 CCGAGGCGAGGAGATCCTCAGGTCAGAGTTTAAGACCGCTGGCCACATCGGTGA 201
QY 172 ACCCGCTCTTATTAATAATCAAAATACCTCGGCATGATGGTGGCGCTGTAAATCC 231
Db 200 ATCCCGTCTCTACTAAAAATACAAAATAAGCGGCGATGGTGGTGAACGCTGTAAATCC 141
QY 232 CAGCTACTCAGAGGCTCAGCGAGGAGATCCGGGAGCTGGCGATCTGCCTGAGCT 291
Db 140 CAGCTACTTGGAGGCTCAGCGAGGAGATCATTGAAC-----CCGAACT 93
QY 292 GGGAGGTTGAGGCTACAGTAAGCAAGATCATGCCAGTATATCTTTCAGCTGGGCGACAAA 351
Db 92 GGGAGGCGAGGTTGCACTGAGCGAGATTTGCGCACTGTACTCCTCTGGGTGACAGA 33
QY 352 GTGAGACCGTACAAAAAATAAAAAATTTAA 383
Db 32 GGGAGACTTCGTCGCAAAAAAATAAAAAA 1

RESULT 9
BX485214      370 bp  mRNA  linear  EST 04-SEP-2003
LOCUS DKEZp686E14246 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKEZp686E14246 5', mRNA sequence.
ACCESSION BX485214
VERSION BX485214.1 GI:31947745
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 370)
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
EST (Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by BMPZ (Biomedical Research Center at the Heinrich-
Heine-University, Dueseldorf/Germany) within the cDNA sequencing
consortium of the German Genome Project. No sl sequence available.
This clone (DKEZp686E14246) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
Location/Qualifiers
1..370
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKEZp686E14246"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pRipEx2; Site_1: SfIIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN
Query Match      39.0%; Score 195.4; DB 13; Length 370;
Best Local Similarity 75.6%; Pred. No. 5.1e-23;
Matches 264; Conservative 0; Mismatches 66; Indels 19; Gaps 1;

QY 69 CCGGTGCAGTGGCTCAGCCCTGTAATCCCGACACTTTGGGAAGCCAGCGGCGAACA 128
Db 2 CCGGTGCAGTGGCTCAGCCCTGTAATCCCGACACTTTGGGAAGCCAGCGGCGAACA 61
QY 129 CCGGAGGTCAGAGTCCCAAGCCAGCTGGCGCAGATGGTGAACCCCGCTCTTATTTAA 188
Db 62 CCAGAGGTCAGAGTTCGAGACCCCTAGCAACATGCAAAACCCCGCTCTTACTAA 121
QY 189 AATACAAATCATCTCGGCATGATGGTGGGCGCTGTAAATCCAGCTACTCAGGAGCT 248
Db 122 AATACAAATCATCTCGGCATGATGGTGGGCGCTGTAAATCCAGCTACTCAGGAGCT 181
QY 249 GAGGCGAGGAGGATCCCGGAGCTGGCAGATCTGCTCAGCTGGGAGGTTGAGGCTACA 308
Db 182 GAGGCGAGGAT-----AGCTTGCAGCCCGGAGTGGAGTTCGCA 222
QY 309 GTAAGCAGATCATGCCAGTATATCTCAGCTGGGCGACAAAGTGAGACCGTAACAAA 368
Db 223 GTGAGCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 282
QY 369 AAAAAAATTTAAAAAAGAAATTTAGATCAAGATCAAGTCAAGTCAAGTCAAGTCAAG 417
Db 283 AAAAAAATTTAAAAAAGAAATTTAGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 331

RESULT 10
AQ021361      374 bp  DNA  linear  GSS 09-JUN-1998
LOCUS CIT-HSP-2307K5 TF CIT-HSP Homo sapiens genomic clone 2307K5,
DEFINITION genomic survey sequence.
ACCESSION AQ021361
VERSION AQ021361.1 GI:3200097
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 374)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other-GSSs: CIT-HSP-2307K5.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamas@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
Location/Qualifiers
1..374
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2307K5"
/sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
HindIII"

ORIGIN
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Query Match	38.9%; Score 194.8; DB 28; Length 374;
Best Local Similarity	76.3%; Pred. No. 5.4e-23;
Matches	261; Conservative 0; Mismatches 62; Indels 19; Gaps 1;
QY	67 GCGCGGTGAGTGGTCAAGCTGTAATCCAGACATTTGGGAAGCAAGCGGGCAGAA 126
DB	4 GCGAGGTGCGGTGCTCATGCTGCTGTAATCCAGACATATGGGAGGCCAGGAGGAT 63
QY	127 CACCGAGGTGAGGAGTCCAGAGCCAGCGCTGGCCAAAGATGGTGAACCCGCTCTTATTA 186
DB	64 CTCAGAGGTGAGGAGTTCGAGACAGCGCTGGCCAAATGGTGAACCCGCTCTTATTA 123
QY	187 AAAATACAAACATTAACCTGGGCGATGATGGTGGGGCGCTGTAATCCAGACATCTCAGGAGG 246
DB	124 AAAATACAAACATTAAGCTGGGCGATGATGGGAGGACCTGTAATCCAGACATCTCAGGAGG 183
QY	247 CTGAGGCGAGGAGATCCGCGAGCGCTGGCAGATCTGCTGAGCTGGGAGTTGAGGCTA 306
DB	184 CTGAGGCGAGGAGAT-----TGCTTGAATGGGAGGCGAGGTTG 224
QY	307 CAGTGAAGCAAGATCATCCAGTATCTTACGCTGGCGGCGACAAAGTGAGACCGTAAACAA 366
DB	225 CAGTGAAGCAAGATCACCTCACTCTTACGCTGGCGGCGACAGAGTGATCTCCATCTC 284
QY	367 AAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAA 408
DB	285 AAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAA 326
RESULT 11	
BZ603705	
LOCUS	607 bp DNA linear GSS 08-JUN-2003
DEFINITION	WHAP212TR Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_1-22D18, genomic survey sequence.
ACCESSION	BZ603705
VERSION	BZ603705.1 GI:31512167
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q., Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P., Gray, J.W., and Collins, C.
TITLE	End-sequence profiling: Sequence-based analysis of aberrant genomes
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
MEDLINE	12709111
PUBMED	12788976
COMMENT	Contact: Volik SV Colin Collins' lab UCSF Comprehensive Cancer Center UCSF Box 0808, San Francisco, CA 94143-0808, USA Tel: 415 502 7066 Fax: 415 502 5665 Email: svolik@cc.ucsf.edu This clone is available from Amplicon Express http://www.genomex.com Class: BAC ends.
FEATURES	location/Qualifiers 1..607 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="MCF7_1-22D18" /sex="female" /clone_lib="Human MCF7 breast cancer cell line library (MCF7_1)" /note="Vector: pSCBAC1; Site:1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

source 1. 393
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="C10150"
 /note="Organ: colon,ins; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (O.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 38.4%; Score 192.4; DB 10; Length 393;
 Best Local Similarity 75.0%; Pred. No. 1.6e-22;
 Matches 261; Conservative 0; Mismatches 68; Indels 19; Gaps 1;

QY 44 TTGCTCTTATACATATAAATAGCCGGTCCAGTGGCTCAGCTGTGTAATCCAGCACT 103
 DB 54 TGGGTGTTAAACATTAAGGATAGCCGGCGCGTGGCTCAGCTGTATCCAGCACT 123
 QY 104 TTGGGAACCAAGGGGCGAGAACACCGAGGTGAGAGTCCAGGCCAGCTGGCCAG 163
 DB 124 TTGGGAGCCGAGGCGAGACGATCACCTGAGATTAGGATTTCCAGACCGCTGGCTAAC 183
 QY 164 ATGGTGAACCCCGCTCTTATATAAATACAAACATTACCTGGGCATGATGGTGGGCGCC 223
 DB 184 ATGGTGAACCCCGCTCTTACCAAAATACAAATTAAGCCGGCATGGTGGCAGGCCCC 243
 QY 224 TGTATCCAGCTACTCAGAGGCTGAGCGAGGAGTCCCGGAGCGCTGCGAGATCTGC 283
 DB 244 TGTATCCAGCTACTCAGAGGCTGAGCGAGGAGTCCCGGAGCGCTGCGAGATCTGC 284
 QY 284 CTGACCTGGAGGTTGAGGCTTACAGTAAGCCAGATCATGCCAGTATATCTTACGCTGG 343
 DB 285 TTGAACCCGGAGGTGGAGGTTGAGTGGCGAGATCAGCCACTGCATCCAGCGCTGG 344
 QY 344 GCGACAAAGTGAGACCGCTAACAAAAAATTTTAAAAAAGAAA 391
 DB 345 GTGACAGGTGAGACTCCATCTCTCANAAGAAAAAACAACAAACANA 392

RESULT 13
 AQ383054/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 617)
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
 Venter, J. C
 Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other GSSs: RPCI11-139K16.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeet@ig.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/>) or from
 Research Genetics (<http://info@resgen.com>). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1. 617
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:753247"
 /db_xref="taxon:9606"
 /clone="RPCI-11-139K16"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
 RPCI11 Human Male BAC Library"

OR-IGIN

Query Match 38.3%; Score 192; DB 28; Length 617;
 Best Local Similarity 74.1%; Pred. No. 1.5e-22;
 Matches 243; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 90 GTAATCCAGCACTTTGGAGAGCCAGCGGCGAGACACCCGAGTCCAGAGTCCCAAGG 149
 DB 617 GTAATCCTAGCACTTTGGGGGCCAAAGACGCGCGGATCACCTAAGTCAGGAGTTAAGG 558
 QY 150 CCAGCTGCGCAAGATGGTGAACCCCGTCTCTTATAAATAACAAACATTACCTGGGCA 209
 DB 557 CCAGCTGCGCAACACCGGTGAACCCCTCTCTACTATAAATAACAAATTTAGTCAGCGC 498
 QY 210 TGATGTGGGCGCCCTGTAATCCAGCTACTCAGAGGCTGAGGAGGAGGATCCGCGGAG 269
 DB 497 TGGTGGCGGCGACCTGTATTCACAGTACTGGGGAGGCTGAGGCGAGAGATCGCTTGA 438
 QY 270 CCTGGCAGATCTGCTGAGCGCTGGGAGGTTCAGGCTACAGTAAGCAAGATCATGCCAGT 329
 DB 437 CGCAGGAGATCGCTTGACCCAGGCGCGGAGGTTTCAGTAAGCTGAGATCACACCACT 378
 QY 330 ATACTTCAGCTGGGCGCAAAAGTGAGACCGCTAACAAAAAATTTTAAAAAAGA 389
 DB 377 GCATCCAGCTGGGTGACAGGTGAGACTCCATCTCAAAAAAATTTTAAAAAAGA 318
 QY 390 AATTTAGATCAAGATCCAACTGTAATAA 417
 DB 317 AAAGAAAAAGAAAGAAAGTGAAGAGA 290

RESULT 14

BAC452899
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 895)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Cloned through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM12203 row: n column: 03

High quality sequence stop: 657.

Location/Qualifiers

FEATURES

source

1. .895

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5527874"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 72"

/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life

Technologies."

ORIGIN

```

Query Match      38.3%; Score 192; DB 12; Length 895;
Best Local Similarity 75.1%; Pred. No. 1.3e-22;
Matches 257; Conservative 0; Mismatches 75; Indels 10; Gaps 1;

QY 48 TCCTATACATATAAATAGCCGGTGCAGTGCCTCAGCGCTGTATCCAGCAGCTTGG 107
Db 421 TCTAAGAAAATAAAGGCTGCCAGGTGAGTAGGTACGCGCTGTATCCAGCAGCTTAG 480
QY 108 GAAGCCAAAGCGGCGCAGAACACCCGAGGTCCAGAGTCCAAAGCCAGCCTGGCCAGATGG 167
Db 481 GAGGCCAAGGTGGTGTGATCACTCAGGTTCAGAGTTCAGACCCAGCTGGCCACATGG 540
QY 168 TGAACCCCTCTCTATTAAATAATACAAATACCTGGGCATGATGGTGGCGCTGTGA 227
Db 541 TGAACCCCTCTCTATTAAATAATACAAATATAGTGGGCATGATGGCGGTGCTGTGA 600
QY 228 ATCCCACTACTCAGGAGGTGAGGAGGAGGATCCGCGAGGCTGGCAGATCTGCTCA 287
Db 601 ATCTACTACTCAGGAGGTGAGGCGGAGATCGTTGAACCCGGGA-----A 650
QY 288 GCCTGGAGGTTAGGCTACAGTAAGCAAGATCATGCCAGTATATTAGCTTGGCGCA 347
Db 651 GCCCAGGAGGAGGTTGAGTGAGTGAGTGGCCATTGCACTCCGGCTGGGCAA 710
QY 348 CAAGTCAGACCGGTAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 389
Db 711 CTGAGCAAACTCCATCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 752

```

RESULT 15

AA722505/c

LOCUS

DEFINITION

z31908.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone

IMAGE:413726 3' similar to contains Alu repetitive element;; mRNA

sequence.

AA722505

AA722505.1 GI:2740212

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 501)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,

Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,

Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

Contact: Willson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40ml3 fwd. Et from Amersham

High quality sequence stop: 478.

Location/Qualifiers

FEATURES

source

1. .501

/organism="Homo sapiens"

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/notes="Organ: pineal gland; Vector: pT7T3D (Pharmacia)

with a modified polylinker; Site 1: Not I; Site 2: Eco RI;

1st strand cDNA was primed with a Not I - oligo(dT) primer

[5' TGTTACCAATCTGAAGTGGAGCGCGGCTTTTTTTTTTTTTTTTTTTT

3'), double-stranded cDNA was size selected, ligated to

Eco RI adapters (Pharmacia), digested with Not I and

cloned into the Not I and Eco RI sites of a modified pT7T3

vector (Pharmacia). Library constructed by Bento Soares

and M.Fatima Bonaldo."

ORIGIN

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Query Match      38.1%; Score 190.8; DB 9; Length 501;
Best Local Similarity 71.9%; Pred. No. 2.6e-22;
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Search completed: March 4, 2004, 16:38:38

Job time : 1964.09 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:50:45 ; Search time 2291.28 Seconds
(without alignments)
9552.848 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_hg.*
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41: em_hgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	505	100.0	11204	6	BD016860	BD016860 Novel cyt
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4	505	100.0	71132	9	AC092184	AC092184 Homo sapi
5	429.4	85.0	2818	6	BD016833	BD016833 Novel cyt
6	428	84.8	2172	6	BD016840	BD016840 Novel cyt
7	428	84.8	2791	9	AB040431	AB040431 Homo sapi
8	79	15.6	166447	2	BX323824	BX323824 Danio rer
9	73.2	14.5	3000	6	AX822415	AX822415 Sequence
10	73.2	14.5	3000	6	AX825612	AX825612 Sequence
11	73.2	14.5	3000	6	AX826055	AX826055 Sequence
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13	71.8	14.2	144493	9	AP001547	AP001547 Homo sapi
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16	71.6	14.2	3000	6	AX825927	AX825927 Sequence
17	71.6	14.2	6375	6	AX346926	AX346926 Sequence
18	71.6	14.2	29993	6	AX825188	AX825188 Sequence
19	71.6	14.2	38342	6	AX351503	AX351503 Sequence
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ALIGNMENTS

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LOCUS BD016835
DEFINITION Novel cytidine deaminase.
ACCESSION BD016835
VERSION BD016835.1 GI:22558011
KEYWORDS JP 2001245669-A/8.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Honjo, T. and Muramatsu, M.
TITLE Novel cytidine deaminase
JOURNAL Patent: JP 2001245669-A 8 11-SEP-2001;

Pred. No. is the number of results predicted by chance to have a

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COMMENT      JAPAN TOBACCO INC, TASUKU HONJO
OS           Homo sapiens (human)
PN           JP 2001245669-A/8
PD           11-SEP-2001
PF           28-MAR-2000 JP 2000092981
PI           TASUKU HONJO, MASAMICHI MURAMATSU
PC           C12N15/09, A61K39/395, A61P1/00, A61P11/06, A61P13/12,
PC           A61P17/00,
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DEFINITION Novel cytidine deaminase.
ACCESSION  BD016860
VERSION    BD016860.1 GI:22558036
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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 11204)

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AUTHORS      Honjo, T. and Muramatsu, M.
TITLE        Novel cytidine deaminase
JOURNAL      Patent: JP 2001245669-A 33 11-SEP-2001;
              JAPAN TOBACCO INC, TASUKU HONJO
COMMENT      OS Homo sapiens (human)
              PN JP 2001245669-A/33
              PD 11-SEP-2001
              PF 28-MAR-2000 JP 2000092981
              PI TASUKU HONJO, MASAMICHI MURAMATSU
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Best Local Similarity 100.0%; Pred. No. 1.4e-64;
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RESULT 3
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LOCUS       AB040430
DEFINITION Homo sapiens AID gene for activation-induced cytidine deaminase,
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ACCESSION  AB040430
VERSION    AB040430.1 GI:9989407
KEYWORDS   AID; activation-induced cytidine deaminase.
            Homo sapiens (human)
SOURCE     Homo sapiens (human)

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AC092184.7 GI:21206067
HTG.
Homo sapiens (human)
ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
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Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
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Weinstock, G. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 71132)

TITLE
JOURNAL
REFERENCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Muro, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.
Isolation, tissue distribution, and chromosomal localization of the
human activation-induced cytidine deaminase (AID) gene
Genomics 68 (1), 85-88 (2000)
20408890
PUBMED
10950930
REFERENCE
AUTHORS
Muro, T., Muto, T., Levy, Y., Geissmann, F., Plebani, A., Sanal, O.,
Catalan, N., Forveille, M., Dufourcq-Lageouise, R., Gennery, A.,
Tescan, I., Ersoy, F., Kayserili, H., Ugazio, A.G., Brousse, N.,
Muramatsu, M., Notarangelo, L.D., Kinoshita, K., Honjo, T., Fischer, A.
and Durandy, A.
Activation-induced cytidine deaminase (AID) deficiency causes the
autosomal recessive form of the Hyper-IgM syndrome (HIGM2)
Cell 102 (5), 565-575 (2000)
20460541
PUBMED
11007475
REFERENCE
AUTHORS
Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.
Direct Submission
Submitted (18-MAR-2000) Tasuku Honjo, Kyoto University, Department
of Medical Chemistry, Faculty of Medicine, Yoshida, Sakyo-ku,
Kyoto, Kyoto 606-8501, Japan (E-mail: honjo@four.med.kyoto-u.ac.jp,
Tel:81-75-753-4371 (ex.4371), Fax:81-75-753-4388)
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Best Local Similarity 100.0%; Pred. No. 1.4e-64;
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 121 TTTATTAACATGATTTCTTTTCGATATATGAAATGGAGTCTCAAGGCTTCATAAAT 180
Db 10820 TTTATTAACATGATTTCTTTTCGATATATGAAATGGAGTCTCAAGGCTTCATAAAT 10879
Qy 181 TATAACTTAGAATGATTCATAAACAACGTATGATTAATGTACATTCAGTAATGGTG 240
Db 10880 TATAACTTAGAATGATTCATAAACAACGTATGATTAATGTACATTCAGTAATGGTG 10939
Qy 241 CTACGAAGCCATTTCTCTTGATTTTGTAGTAACCTTTATGACACAAATTTGCTTCGGC 300
Db 10940 CTACGAAGCCATTTCTCTTGATTTTGTAGTAACCTTTATGACACAAATTTGCTTCGGC 10999
Qy 301 TCACCTTCAATCAGTTAAATTAATGATTAATAATTTTGGAGCTGTGAAGATAAAATACC 360

AUTHORS	Worley, K.C.	STS	/standard_name="57233"
TITLE	Direct Submission	repeat_region	439..560
JOURNAL	Submitted (25-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	repeat_region	774..881
REFERENCE	3 (bases 1 to 71132)	repeat_region	903..1190
AUTHORS	Worley, K.C.	repeat_region	/rpt_family="AluSq"
TITLE	Direct Submission	repeat_region	1191..1213
JOURNAL	Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	STS	/rpt_family="AT_rich"
REFERENCE	4 (bases 1 to 71132)	STS	/standard_name="6612"
AUTHORS	Worley, K.C.	repeat_region	1744..1819
TITLE	Direct Submission	repeat_region	/standard_name="8198"
JOURNAL	Submitted (25-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	repeat_region	1966..2264
REFERENCE	5 (bases 1 to 71132)	repeat_region	/rpt_family="AluSq"
AUTHORS	Worley, K.C.	repeat_region	3296..3328
TITLE	Direct Submission	repeat_region	/rpt_family="(TTTC)n"
JOURNAL	Submitted (12-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	repeat_region	4097..4249
COMMENT	On May 25, 2002 this sequence version replaced gi:20901754. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu	repeat_region	/rpt_family="AluSq"
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		repeat_region	complement(5140..5262)
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		repeat_region	6020..6336
		repeat_region	/rpt_family="AluSx"
		repeat_region	6337..6629
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		repeat_region	/rpt_family="AluY"
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Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TTAATAATTTGATCTTCATGATTAATCAATTTATATTTATTTTTCGCTCAATGATTT 120
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Db 45363 TTTTATTAACATGATTTCTTTCTGATATATTTGAAATGGAGTCTCAAAGCTTCATAAAT 45422
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Db 45543 TCACCTTCAATCAGTAAATGATTAATTTTGGAAAGCTGTGGAAGTAAATATACC 45602
QY 361 AATAAATAATATATAAAGTATTTATATGAAGTTTAAATATAAATAACAGTATGATGAA 420
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Db 45663 TAAACTTGAGAGTCCAGAGTTATCCCATACATCTGTAATCAACTAATTTCTCAAGGG 45722
QY 481 TGTAGGAGCCATTCATGAGGAAA 505
Db 45723 TGTAGGAGCCATTCATGAGGAAA 45747

RESULT 5
BD016833
LOCUS BD016833 2818 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel cytidine deaminase.
ACCESSION BD016833
VERSION BD016833.1 GI:22558009
KEYWORDS JP 2001245669-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Honjo, T. and Muramatsu, M.
TITLE Novel cytidine deaminase
JOURNAL Patent: JP 2001245669-A 6 11-SEP-2001;
JAPAN TOBACCO INC. TASUKU HONJO
COMMENT
OS Homo sapiens (human)
PN JP 2001245669-A/6
PD 11-SEP-2001
PF 28-MAR-2000 JP 2000092981
PI TASUKU HONJO, MASAMICHI MURAMATSU
PC C12N15/09, A61K39/395, A61P1/00, A61P11/06, A61P13/12,
PC A61P17/00.
PC A61P27/02, A61P27/16, A61P37/02, A61P37/08, C07K16/18, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12N9/78, C12P21/02, C12P21/08, C12N1/21, C12R1/19, PC
(C12N5/10, C12R1/91), C12N15/00, C12N5/00, C12N5/00, C12R1/91) CC
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FT CDS (80) . (676)
FT 3'UTR (677) . (2818).
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Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 1.8e-53;
Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAACCTGGAATGACCAACTGCTCTTATTTTAAATCTTATTTGACATAAGTTTGTAAAGAG 60
Db 2367 GAAACCTGGAATGACCAACTGCTCTTATTTTAAATCTTATTTGACATAAGTTTGTAAAGAG 2426
QY 61 TTAATAATTTGATCTTCATGATTAATCAATTTATATTTTATTTTTCGCTCAATGATTT 120
Db 2427 TTAATAATTTGATCTTCATGATTAATCAATTTATATTTTATTTTTCGCTCAATGATTT 2486
QY 121 TTTTATTAACATGATTTCTTTCTGATATATTTGAAATGGAGTCTCAAAGCTTCATAAAT 180
Db 2487 TTTTATTAACATGATTTCTTTCTGATATATTTGAAATGGAGTCTCAAAGCTTCATAAAT 2546
QY 181 TATAACTTTAGAAATGATTTCTAATAACACGATATGTAATGTAACATGTCAGTAATGGTG 240
Db 2547 TATAACTTTAGAAATGATTTCTAATAACACGATATGTAATGTAACATGTCAGTAATGGTG 2606
QY 241 CTACGAAGCCATTTCTCTGATTTTCTGATTAATTTAGTAACTTTTATGACAGCAAAATTTGCTTCGGC 300
Db 2607 CTACGAAGCCATTTCTCTGATTTTCTGATTAATTTAGTAACTTTTATGACAGCAAAATTTGCTTCGGC 2666
QY 301 TCACCTTCAATCAGTAAATGATTAATTTTGGAAAGCTGTGGAAGTAAATATACC 360
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QY 361 AATAAATAATATATAAAGTATTTATATGAAGTTTAAATATAAATAACAGTATGATGAA 420
Db 2727 AATAAATAATATATAAAGTATTTATATGAAGTTTAAATATAAATAACAGTATGATGAA 2786
QY 421 TAAACTTGAGA 431
Db 2787 TAAACTTGAGA 2797

RESULT 6
BD016840
LOCUS BD016840 2172 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel cytidine deaminase.
ACCESSION BD016840
VERSION BD016840.1 GI:22558016
KEYWORDS JP 2001245669-A/13.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Honjo, T. and Muramatsu, M.
TITLE Novel cytidine deaminase
JOURNAL Patent: JP 2001245669-A 13 11-SEP-2001;
JAPAN TOBACCO INC. TASUKU HONJO
COMMENT
OS Homo sapiens (human)
PN JP 2001245669-A/13
PD 11-SEP-2001
PF 28-MAR-2000 JP 2000092981
PI TASUKU HONJO, MASAMICHI MURAMATSU
PC C12N15/09, A61K39/395, A61P1/00, A61P11/06, A61P13/12,
PC A61P17/00.
PC A61P27/02, A61P27/16, A61P37/02, A61P37/08, C07K16/18, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12N9/78, C12P21/02, C12P21/08, C12N1/21, C12R1/19, PC
(C12N5/10, C12R1/91), C12N15/00, C12N5/00, C12N5/00, C12R1/91) CC
FH Key Location/Qualifiers
FT 5'UTR (1) . (79)
FT CDS (80) . (676)
FT 3'UTR (677) . (2818).
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Best Local Similarity 100.0%; Pred. No. 3.1e-53;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TTAATAATGTTTACTTCATGATTCATTTATATTTTATTTATTTTGGTCTCAATGATTT 120
DB 1805 TTAATAATGTTTACTTCATGATTCATTTATATTTTATTTTGGTCTCAATGATTT 1864
QY 121 TTTATTAACATGATTTCCCTTTCTGATATTTGAATGAGTCTCAAGCTTCATAAAT 180
DB 1865 TTTATTAACATGATTTCCCTTTCTGATATTTGAATGAGTCTCAAGCTTCATAAAT 1924
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DB 2045 TCACATTTCAATCAGTAAATGATTAATGATTAATTTTGAAGCTGTGAAGATAAATACC 2104
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QY 421 TAAACTTG 428
DB 2165 TAAACTTG 2172

RESULT 7
AB040431
LOCUS
DEFINITION Homo sapiens AID mRNA for activation-induced cytidine deaminase, complete CDS.
ACCESSION AB040431.1 GI:9988409
VERSION
KEYWORDS AID; activation-induced cytidine deaminase; Human AID.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.,
Isolation, tissue distribution, and chromosomal localization of the human activation-induced cytidine deaminase (AID) gene
Genomics 68 (1), 85-88 (2000)
JOURNAL MEDLINE
PUBMED 20408890
PUBMED 10950930
REFERENCE 2 (sites)
Rev, P., Muto, T., Levy, Y., Geissmann, F., Plebani, A., Sanal, O., Catalan, I., Forveille, M., Dufourcq-Lageleuse, R., Gennery, A., Tezcan, I., Ersoy, F., Kayserili, H., Ugazio, A.G., Brucse, N., Muramatsu, M., Notarangelo, L.D., Kinoshita, K., Honjo, T., Fischer, A. and Durandy, A.
Activation-induced cytidine deaminase (AID) deficiency causes the autosomal recessive form of the Hyper-IgM syndrome (HIGM2)
Cell 102 (5), 565-575 (2000)
JOURNAL MEDLINE
PUBMED 20460541
PUBMED 11007475
REFERENCE 3 (bases 1 to 2791)
Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.

Direct Submission
Submitted (18-MAR-2000) Tasaku Honjo, Kyoto University, Department of Medical Chemistry, Faculty of Medicine, Yoshida, Sakyo-ku, Kyoto, Kyoto 606-8501, Japan (E-mail:honjo@four.med.kyoto-u.ac.jp, Tel:81-75-753-4371(ex.4371), Fax:81-75-753-4388)
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ORIGIN

Query Match 84.8%; Score 428; DB 9; Length 2791;
Best Local Similarity 100.0%; Pred. No. 2.9e-53;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAACTTGAATGCACTGCTTATTTAATCTTATGATACATAAGTTGTAAGAG 60
DB 2364 GAAACTTGAATGCACTGCTTATTTAATCTTATGATACATAAGTTGTAAGAG 2423
QY 61 TTAATAATGTTTACTTCATGATTCATTTATATTTTATTTTGGTCTCAATGATTT 120
DB 2424 TTAATAATGTTTACTTCATGATTCATTTATATTTTATTTTGGTCTCAATGATTT 2483
QY 121 TTTATTAACATGATTTCCCTTTCTGATATTTGAATGAGTCTCAAGCTTCATAAAT 180
DB 2484 TTTATTAACATGATTTCCCTTTCTGATATTTGAATGAGTCTCAAGCTTCATAAAT 2543
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DB 2544 TATACTTTAGAAATGATTTCTAATAACACGATGATTAATTTGAAGCTGTGAAGATAAATACC 2603
QY 241 CTACGAAGCAATTTCTTTGATTTTATGAACTTTTAAATTAATAAATAAAGTATGATGAA 300
DB 2604 CTACGAAGCAATTTCTTTGATTTTATGAACTTTTAAATTAATAAATAAAGTATGATGAA 2663
QY 301 TCACATTTCAATCAGTAAATGATTAATGATTAATTTTGAAGCTGTGAAGATAAATACC 360
DB 2664 TCACATTTCAATCAGTAAATGATTAATGATTAATTTTGAAGCTGTGAAGATAAATACC 2723
QY 361 AAATAAATAATATAAAGTATTTATGAACTTTTAAATTAATAAATAAAGTATGATGAA 420
DB 2724 AAATAAATAATATAAAGTATTTATGAACTTTTAAATTAATAAATAAAGTATGATGAA 2783
QY 421 TAAACTTG 428
DB 2784 TAAACTTG 2791

RESULT 8
BX323824/c
LOCUS
DEFINITION Danio rerio clone DKEY-37F18, *** SEQUENCING IN PROGRESS ***, 19 unordered pieces.
ACCESSION BX323824
VERSION BX323824.4 GI:37805603
KEYWORDS HTG; HTGS PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Cypriniformes: Cyprinidae; Danio.
1 (bases 1 to 166447)
Sims, S.
Direct Submission
Submitted (20-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 21, 2003 this sequence version replaced gi:30026999.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zk37f18
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 15874 bases at least Q40
Consensus quality: 15843 bases at least Q30
Consensus quality: 160876 bases at least Q20
Insert size: 164647; sum-of-contigs
Insert size: 181199; 3.2% error; agarose-fp
Quality coverage: 6.51x in Q20 bases; sum-of-contigs Quality
coverage: 6.15x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 22674: contig of 22674 bp in length
22675 22774: gap of 100 bp
22775 31865: contig of 9091 bp in length
31866 31965: gap of 100 bp
31966 38565: contig of 6500 bp in length
38566 42826: gap of 100 bp
42827 42926: contig of 4261 bp in length
42927 48541: contig of 5615 bp in length
48542 48641: gap of 100 bp
48642 56767: contig of 8126 bp in length
56768 56867: gap of 100 bp
56868 76763: contig of 19796 bp in length
76764 88853: contig of 12090 bp in length
88854 95380: gap of 100 bp
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125338 125337: gap of 100 bp
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149511 152311: contig of 2702 bp in length
152312 152311: gap of 100 bp
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Best Local Similarity 48.1%; Pred. NO. 0.004;
Matches 202; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

Qy 41 TACATAAGTTTGTAAGAAGATTAAATAATTTGTTACTTCATGATTCATTATATATATAT 100
Db 152852 TAAATAGTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 152793
Qy 101 TATTTTGGCTCAATGATTTTATTAATTAACATGATTTCCCTTTCTGATATATGAATGA 160
Db 152792 AATTTATTTATATATATATATATATATATATATATATATTTTNTTNTTNTT 152733

QY 161 GTCTCAAGCTTCATPAATTTTAACTTTAGAAATGATTTCTAATAACAACGCTATGTAAT 220
Db 152732 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 152673
QY 221 GTAACATTCGAGTATGCTACGAGCCATTTCTCTGATTTTCTAGTAACTTTTATG 280
Db 152672 AATAATATGTTTAAATTAATTAATTAATTAATTTTNTTTTATTTTAAATAATTTATTT 152613
QY 281 ACAGCAAAATTTGCTTCTGCTCACCTTCAATCAGTTAAATAAATGATAAATAATTTTGG 340
Db 152612 ATTAATTTTAAATTTTATTTTAAATTAATTAATTAATTAATTTTAAATAATTTTATTTT 152553
QY 341 ACCTGTGAGATTAATACCAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 400
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QY 401 AAAAAATCAGTATGATGAATAAATTCGAGAGTCGAGAGTTCAGAGTATCCCATACATCTGAAT 460
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RESULT 9
AX822415
LOCUS AX822415 3000 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 307 from Patent EP1340818
ACCESSION AX822415
VERSION AX822415.1 GI:39749043
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL proliferative disorder
Patent: EP 1340818-A 307 03-SEP-2003;
EpiGenomics AG (DE)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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Query Match 14.5%; Score 73.2; DB 6; Length 3000;
Best Local Similarity 48.6%; Pred. No. 0.078;
Matches 201; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 2 AAAACTTGAATGCACACGCTGCTTATTTTAACTTTATTTGTCATAGTTTGTAAAGAGT 61
Db 164 AAAATTTGAGTTTTAGTTTTTATATGTGAAATGGAGAAATAAATTTCTAAATTA 223
QY 62 TAAAAATTTGTTACTTCATGTTTCAATTTATATTTTATATTTTTCGCTCTAATGATTTT 121
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QY 242 TAGGAAGCCATTTCTCTGATTTTATGTAACCTTTTATGACAGCAAAATTTGCTTCGGCT 301
Db 404 AATAAATTTTGTAGGAAGAATATTTTAGTAAGTATGAGAGTAGTAATGATTTGTTTTATT 463
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Db 464 ATTTTAAATTTAATAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 523
QY 362 AATAAATTAATAAAGTATTTATGAACTTTTATGAACTTTAAATAAATAAATCAGTATGA 415
Db 524 TTTATTAATAAATAAATTTGTAATTTAATTTAGTATTTAGGGTTGATATTTGTTTTGA 577

QY 362 AATAAATAATAAAGTATTTATGAACTTTAAATAAATAAATAAATCAGTATGA 415
Db 524 TTTATTAATAAATAAATTTGTAATTTAATTTAGTATTTAGGGTTGATATTTGTTTTGA 577

RESULT 10
AX825612
LOCUS AX825612 3000 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 20 from Patent WO03072820.
ACCESSION AX825612
VERSION AX825612.1 GI:39751139
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Lesche,R., Cottrell,S. and
Mooney,S.
TITLE Method and nucleic acids for the analysis of colon cell
JOURNAL proliferative disorders
Patent: WO 03072820-A 20 04-SEP-2003;
EpiGenomics AG (DE)
FEATURES
source Location/Qualifiers
1..3000
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN
Query Match 14.5%; Score 73.2; DB 6; Length 3000;
Best Local Similarity 48.6%; Pred. No. 0.078;
Matches 201; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 2 AAAACTTGAATGCACACGCTGCTTATTTTAACTTTATTTGTCATAGTTTGTAAAGAGT 61
Db 164 AAAATTTGAGTTTTAGTTTTTATATGTGAAATGGAGAAATAAATTTGTAATTA 223
QY 62 TAAAAATTTGTTACTTCATGTTTCAATTTATATTTTATATTTTTCGCTCTAATGATTTT 121
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QY 122 TTATTAACATGATTTCCCTTTCTGATATATTTGAATGGAGTCTCAAGCTTCATAAATTT 181
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QY 182 ATAACTTTAGAATGATTTCTAATAACAACGATATGTAATTTGAACATTCAGTAATGGTGC 241
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Db 464 ATTTTAAATTTAATAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 523
QY 362 AATAAATTAATAAAGTATTTATGAACTTTTATGAACTTTAAATAAATAAATCAGTATGA 415
Db 524 TTTATTAATAAATAAATTTGTAATTTAATTTAGTATTTAGGGTTGATATTTGTTTTGA 577

RESULT 11
AX826055
LOCUS AX826055 3000 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 307 from Patent WO03072821.
ACCESSION AX826055
VERSION AX826055.1 GI:39751569
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Lesche,R., Cottrell,S. and
Mooney,S.
TITLE Method and nucleic acids for the analysis of colon cell
JOURNAL proliferative disorders
Patent: WO 03072820-A 20 04-SEP-2003;
EpiGenomics AG (DE)
FEATURES
source Location/Qualifiers
1..3000
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN
Query Match 14.5%; Score 73.2; DB 6; Length 3000;
Best Local Similarity 48.6%; Pred. No. 0.078;
Matches 201; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 2 AAAACTTGAATGCACACGCTGCTTATTTTAACTTTATTTGTCATAGTTTGTAAAGAGT 61
Db 164 AAAATTTGAGTTTTAGTTTTTATATGTGAAATGGAGAAATAAATTTCTAAATTA 223
QY 62 TAAAAATTTGTTACTTCATGTTTCAATTTATATTTTATATTTTTCGCTCTAATGATTTT 121
Db 224 TTAATTTGTTTATTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 283
QY 122 TTATTAACATGATTTCCCTTTCTGATATATTTGAATGGAGTCTCAAGCTTCATAAATTT 181
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QY 182 ATAACTTTAGAATGATTTCTAATAACAACGATATGTAATTTGAACATTCAGTAATGGTGC 241
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QY 242 TAGGAAGCCATTTCTCTGATTTTATGTAACCTTTTATGACAGCAAAATTTGCTTCGGCT 301
Db 404 AATAAATTTTGTAGGAAGAATATTTTAGTAAGTATGAGAGTAGTAATGATTTGTTTTATT 463
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Db 464 ATTTTAAATTTAATAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 523


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Matches 231; Conservative 0; Mismatches 227; Indels 3; Gaps 2;
QY 8 TGAATGACAACTGCTCTATTTTAACTTATGTACATAAGTTTGTAAAGAGTTAAAAA 67
Db 27301 TAAATATGTAATGTTTATGTAATTTATATAAATAATGTAATGTTTATGTAATATATA 27242
QY 68 TTGTACTTCATGTAATCAATTAATATATTTTATATTTTTCGCTCTAATGATTTTATTA 127
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Db 27121 ATATAATATATGTTT-TATGTAATTTATATAAATAATATATATGTTTATGTAATATATA 27063
QY 248 GCCATTTCTCTGATTTTATGTAATTTTATGTAATTTTATGTAATTTTATGTAATTTTAT 307
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Db 26882 ACTATATATATATATATATATATTTTATATATATATATA 26842

RESULT 14
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LOCUS AX822287 3000 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 179 from Patent EP1340818.
ACCESSION AX822287
VERSION AX822287.1 GI:39748915
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,
Rujan, T. and Schmitt, A.
TITLE Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL Patent: EP 1340818-A 179 03-SEP-2003;
EpiGenomics AG (DE)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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Query Match 14.2%; Score 71.6; DB 6; Length 3000;
Best Local Similarity 48.3%; Pred. No. 0.13;
Matches 200; Conservative 0; Mismatches 214; Indels 0; Gaps 0;
QY 2 AAACCTTGAATGCACAACTGCTCTATTTTAACTTATGTAATGTAATGTAATGTAATGTAATGTAAT 61
Db 164 AAATTTTGGATTTTATGTTTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 223
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RESULT 15
AX825602
LOCUS AX825602 3000 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 10 from Patent WO03072820.
ACCESSION AX825602
VERSION AX825602.1 GI:39751129
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Lesche, R., Cottrell, S. and
Mooney, S.
TITLE Method and nucleic acids for the analysis of colon cell
proliferative disorders
JOURNAL Patent: WO 03072820-A 10 04-SEP-2003;
EpiGenomics AG (DE)
FEATURES
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/mol_type="unassigned DNA"
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/note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN
Query Match 14.2%; Score 71.6; DB 6; Length 3000;
Best Local Similarity 48.3%; Pred. No. 0.13;
Matches 200; Conservative 0; Mismatches 214; Indels 0; Gaps 0;
QY 2 AAACCTTGAATGCACAACTGCTCTATTTTAACTTATGTAATGTAATGTAATGTAATGTAATGTAAT 61
Db 164 AAATTTTGGATTTTATGTTTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 223
QY 62 TAAATGTTTACTTCATGTAATTTATATTTTATATTTTATATTTTATGCTCTAATGATTTT 121
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Qy 362 AATTAATAATATAAAGTGATTTATATGAAGTTAAAAATAAAAAATCAGTATGA 415
Db 524 TTTATTAATAATAAATTTGTAATTATTAAGTATTTAGGGTTGATATGTTTTTGA 577

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GenCore version 5.1.6
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	505	100.0	6564	3 AAC55314	AAC55314 Human act
2	505	100.0	11204	3 AAC55339	AAC55339 Human act
3	505	100.0	11204	6 ABL33286	ABL33286 DNA encod
4	429.4	85.0	2818	3 AAC55312	AAC55312 Human act
5	428	84.8	2172	3 AAC55319	AAC55319 Human act
6	428	84.8	2791	6 ABL33287	ABL33287 DNA encod
7	428	84.8	2791	6 ABL33288	ABL33288 DNA encod
8	418	82.8	574	6 AAK81089	AAK81089 Human imm
9	73.2	14.5	3000	9 ADB54251	ADB54251 Pretreate
10	73.2	14.5	3000	9 ADB37774	ADB37774 Human che
11	73.2	14.5	29993	9 ADB37662	ADB37662 Human che
12	71.6	14.2	3000	9 ADB54123	ADB54123 Pretreate
13	71.6	14.2	3000	9 ADB37764	ADB37764 Human che
14	71.6	14.2	6375	6 ABL34024	ABL34024 Human imm
15	71.6	14.2	29993	9 ADB37660	ADB37660 Human che
16	71.6	14.2	38342	4 AAS46745	AAS46745 Tumour su
17	71.6	14.2	38342	6 ABL31506	ABL31506 Signal tr
C 18	67.8	13.4	8056	7 ABL10100	ABL10100 Haematopo
C 19	66.4	13.1	24000	7 ACD13446	ACD13446 Human DNA
C 20	64.6	12.8	8056	7 ABL10246	ABL10246 Haematopo
C 21	64.2	12.7	6370	6 ABL31349	ABL31349 Signal tr
C 22	64.2	12.7	6370	6 ABL70568	ABL70568 Chemical
C 23	64	12.7	1925	6 ABL77997	ABL77997 Human bre

ALIGNMENTS

RESULT 1

AAC55314
ID AAC55314 standard; DNA; 6564 BP.

XX AAC55314;

XX 05-FEB-2001 (first entry)

XX Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:10.

XX Activation-induced cytidine deaminase; AID; cytidine deaminase;
XX immune related disease; allergy; allergic disease; antiallergic;
XX antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;
XX gene therapy; B cell associated immune system disorder; food allergy;
XX immunodeficiency disease; immunoglobulin A deficiency disease; asthma;
XX IGA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;
XX drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;
XX ataxia telangiectasia; common variable immunodeficiency disorder;
XX major histocompatibility class II deficiency disease;
XX auto immunodeficiency syndrome; Igg subclass selection disorder; ds.

XX Homo sapiens.

XX WO200058480-A1.

XX PD 05-OCT-2000.

XX 28-MAR-2000; 2000WO-JF001918.

XX 29-MAR-1999; 99JP-00087192.

XX 24-JUN-1999; 99JP-00178999.

XX 27-DEC-1999; 99JP-00371382.

XX (NISR) JAPAN TOBACCO INC.

XX (HONJ/) HONJO T.

XX Honjo T, Muramatsu M;

XX WPI; 2000-611715/58.

XX Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies.

XX Claim 17; Page 145-150; 174pp; Japanese.

CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This represents the DNA sequence of a chromosome aberration
XX
SQ Sequence 11204 BP; 3305 A; 2273 C; 2373 G; 3253 T; 0 U; 0 Other;

Query Match 100.0%; Score 505; DB 6; Length 11204;
Best Local Similarity 100.0%; Pred. No. 7.7e-72;
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAACTTGAATGCACAACTGCTCTATTATCTTATTGATACATAGTTGTGTAAGAG 60
Db 10700 GAAACTTGAATGCACAACTGCTCTATTATTTTATTGATACATAGTTGTGTAAGAG 10759

QY 61 TTAAAAATGTTACTTCACTGATTTCAATTTATATTTTATATTTTTCCTCTCAATGATT 120
Db 10760 TTAAAAATGTTACTTCACTGATTTCAATTTATATTTTATATTTTTCCTCTCAATGATT 10819

QY 121 TTTATTAAACATGATTTCTTCTGATATATTAATGATGAGTCTCAAGCTTCATAAAT 180
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QY 181 TATAACTTTAGAAATGATTTCTATAACAACGATGTAATTTGTAACATTCAGTAATGGTG 240
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QY 301 TCACCTTCAATCAGTTAAATGATTAATTAATTTTGAAGCTGTGAAGATAAAATACC 360
Db 11000 TCACCTTCAATCAGTTAAATGATTAATTAATTTTGAAGCTGTGAAGATAAAATACC 11059

QY 361 AAATAAAATATATAAAAGTATTATGTAAGTTAAATATAAAATATGATGATGAGAA 420
Db 11060 AAATAAAATATATAAAAGTATTATGTAAGTTAAATATAAAATATGATGATGAGAA 11119

QY 421 TAAACTTGAGTCCAGAGTATCCCATACATCTCTTAATCACTAATTTCTCACAAGGG 480
Db 11120 TAAACTTGAGTCCAGAGTATCCCATACATCTCTTAATCACTAATTTCTCACAAGGG 11179

QY 481 TGTAAGGACCATTCATGAGAGAAA 505
Db 11180 TGTAAGGACCATTCATGAGAGAAA 11204

RESULT 4
AAC55312
ID AAC55312 standard; cDNA; 2818 BP.
XX
AC AAC55312;
XX
DT 05-FEB-2001 (first entry)
XX
DE Human activation-induced cytidine deaminase encoding cDNA SEQ ID NO:7.
XX
KW Activation-induced cytidine deaminase; AID; cytidine deaminase;
KW immune related disease; allergy; allergic disease; anti-allergic;
KW antianemic; antiaesthetic; ophthalmological; anti-HIV; dermatological;
KW gene therapy; B cell associated immune system disorder; food allergy;
KW immunodeficiency disease; immunoglobulin A deficiency disease; asthma;
KW IGA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;
KW drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;
KW ataxia telangiectasia; common variable immunodeficiency disorder;

QY 241 CTACGAAGCCATTTCTTCTGATTTTATGTAAGTTAAATTTTATGACAGCAAAATTTGCTTCGGC 300
Db 10940 CTACGAAGCCATTTCTTCTGATTTTATGTAAGTTAAATTTTATGACAGCAAAATTTGCTTCGGC 10999

QY 301 TCACCTTCAATCAGTTAAATGATTAATTAATTTTGAAGCTGTGAAGATAAAATACC 360
Db 11000 TCACCTTCAATCAGTTAAATGATTAATTAATTTTGAAGCTGTGAAGATAAAATACC 11059

QY 361 AAATAAAATATATAAAAGTATTATGTAAGTTAAATATAAAATATGATGATGAGAA 420
Db 11060 AAATAAAATATATAAAAGTATTATGTAAGTTAAATATAAAATATGATGATGAGAA 11119

QY 421 TAAACTTGAGTCCAGAGTATCCCATACATCTCTTAATCACTAATTTCTCACAAGGG 480
Db 11120 TAAACTTGAGTCCAGAGTATCCCATACATCTCTTAATCACTAATTTCTCACAAGGG 11179

QY 481 TGTAAGGACCATTCATGAGAGAAA 505
Db 11180 TGTAAGGACCATTCATGAGAGAAA 11204

RESULT 3
ABS73286
ID ABS73286 standard; DNA; 11204 BP.
XX
AC ABS73286;
XX
DT 04-DEC-2002 (first entry)
XX
DE DNA encoding human translocation del(12p) protein #1.
XX
KW Chromosome aberration; oncogenic fusion protein; cancer;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
OS
XX Homo sapiens.
XX
PN WO200269900-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US006518.
XX
PR 01-MAR-2001; 2001US-0272751P.
XX
PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI Fritz LC, Burrows FU;
XX
DR WPI; 2002-698710/75.
DR P-PSDB; ABG95082.
XX
PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90.
XX
PS Disclosure; Page 242-245; 389pp; English.
XX
CC The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogenous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock protein
CC (HSP)-90, or selectively treating cells expressing (II) involving
CC administering HSP90-inhibitor. The method is useful for treating
CC genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion

KW major histocompatibility class II deficiency disease;
KW auto immunodeficiency syndrome; IgG subclass selection disorder; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 80..676
FT /*tag= a
FT /product= "activation-induced cytidine deaminase"
XX
FN WO200058480-A1.
XX
XX 05-OCT-2000.
XX
XX 28-MAR-2000; 2000WO-JP001918.
XX
XX 29-MAR-1999; 99JP-00087192.
PR 24-JUN-1999; 99JP-00178999.
PR 27-DEC-1999; 99JP-00371382.
XX
XX (NIBS) JAPAN TOBACCO INC.
PA (HONJ/) HONJO T.
XX
XX Honjo T, Muramatsu M;
XX
XX WPI; 2000-611715/58.
DR P-PSDB; AAB24198.
XX
XX Nucleic acid encoding activation induced cytidine deaminase, useful as a
PT target for drug development for immune-related diseases including
PT allergies.
XX
XX Claim 3; Page 135-139; 174pp; Japanese.
XX
XX The present sequence encodes human activation-induced cytidine deaminase
CC (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has
CC cytidine activity similar to APOBEC-1. AID has anti-allergic, anti-naeemic,
CC antiasthmatic, ophthalmological, anti-HIV and dermatological activities,
CC and can be used in gene therapy. AID polynucleotides are useful in
CC methods for identifying drugs for the treatment of B cell associated
CC immune system disorders, immunodeficiency diseases and allergies, such as
CC immunoglobulin A (IGA) deficiency disease, IGA nephritis, gamma-
CC globulinemia, atopic dermatitis, allergic colitis, asthma, food allergy,
CC telangiectasia, atopic rhinitis, Rosen disease, DiGeorge disease, ataxia
CC (major histocompatibility class II deficiency disease, AIDS (auto
CC immunodeficiency syndrome), elevated IgE disorder, and IGG subclass
CC selection disorder. The DNA sequences encoding AID may be used for gene
CC therapy and the antibodies to the AID protein may be used for diagnosis
CC and treatment of these disorders
XX
SQ Sequence 2818 BP; 868 A; 548 C; 626 G; 776 T; 0 U; 0 Other;

Query Match 85.08; Score 429.4; DB 3; Length 2818;
Best Local Similarity 99.8%; Pred. No. 8.7e-60;
Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAAAACTTGAATGCACAACTGCTCTATTATTTAACTTATTGTACATAAGTTTGTAAAGAG 60
DB 2367 GAAAACTTGAATGCACAACTGCTCTATTATTTAACTTATTGTACATAAGTTTGTAAAGAG 2426
QY 61 TTAATAATTTGTTACTTCATGTTATTTATTTATTTATTTATTTTTCGCTCTAATGATTT 120
DB 2427 TTAATAATTTGTTACTTCATGTTATTTATTTATTTATTTATTTTTCGCTCTAATGATTT 2486
QY 121 TTTATTAACATGATTTCTTTTCTGATATATTGAATGGAGTCTCAAGCTTCATAAAT 190
DB 2487 TTTATTAACATGATTTCTTTTCTGATATATTGAATGGAGTCTCAAGCTTCATAAAT 2546
QY 181 TATTAACCTTAGAATGATTTCTTAATAACAAGTATGTAATTTGAACATTTGAGTAAGGTG 240
DB 2547 TATAACTTTGAAATGATTTCTTAATAACAAGTATGTAATTTGAACATTTGAGTAAGGTG 2606

QY 241 CTACGAAGCCATTCTCTTTGATTTTATGTAAGTCTTTTATGACAGCAAAATTTCTCTTGGC 300
DB 2607 CTACGAAGCCATTCTCTTTGATTTTATGTAAGTCTTTTATGACAGCAAAATTTCTCTTGGC 2666
QY 301 TCACCTTCAATCAGTTTAAATGATTAATTTTGAAGTCTGTAAGATATAAATACC 360
DB 2667 TCACCTTCAATCAGTTTAAATGATTAATTTTGAAGTCTGTAAGATATAAATACC 2726
QY 361 AAATAAATAAATAAATAAAGTGAATTTATATCAAGTTTAAAAATAAATAATCAATGATGAA 420
DB 2727 AAATAAATAAATAAATAAAGTGAATTTATATGAACTTAAAAATAAATAATCAATGATGAA 2786
QY 421 TAAACTTGACA 431
DB 2787 TAAACTTGAAA 2797
RESULT 5
AAC55319
ID AAC55319 standard; DNA; 2172 BP.
XX
XX AAC55319;
XX
XX 05-FEB-2001 (first entry)
XX
XX Human activation-induced cytidine deaminase exon 5 SEQ ID NO:15.
XX
XX Activation-induced cytidine deaminase; AID; cytidine deaminase;
KW immune related disease; allergy; allergic disease; anti-allergic;
KW antinaeemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;
KW gene therapy; B cell associated immune system disorder; food allergy;
KW immunodeficiency disease; immunoglobulin A deficiency disease; asthma;
KW IGA nephritis; gamma-globulinemia; atopic dermatitis; allergic colitis;
KW drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;
KW ataxia telangiectasia; common variable immunodeficiency disorder;
KW major histocompatibility class II deficiency disease;
KW auto immunodeficiency syndrome; IGG subclass selection disorder; ds.
XX
XX Homo sapiens.
PN WO200058480-A1.
XX
XX 05-OCT-2000.
XX
XX 28-MAR-2000; 2000WO-JP001918.
XX
XX 29-MAR-1999; 99JP-00087192.
PR 24-JUN-1999; 99JP-00178999.
PR 27-DEC-1999; 99JP-00371382.
XX
XX (NIBS) JAPAN TOBACCO INC.
PA (HONJ/) HONJO T.
XX
XX Honjo T, Muramatsu M;
XX
XX WPI; 2000-611715/58.
XX
XX Nucleic acid encoding activation induced cytidine deaminase, useful as a
PT target for drug development for immune-related diseases including
PT allergies.
XX
XX Claim 18; Page 152-153; 174pp; Japanese.
XX
XX The present invention describes an activation-induced cytidine deaminase
CC (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has
CC cytidine activity similar to APOBEC-1. AID has anti-allergic, antinaeemic,
CC antiasthmatic, ophthalmological, anti-HIV and dermatological activities,
CC and can be used in gene therapy. AID polynucleotides are useful in
CC methods for identifying drugs for the treatment of B cell associated
CC immune system disorders, immunodeficiency diseases and allergies, such as
CC immunoglobulin A (IGA) deficiency disease, IGA nephritis, gamma-
CC globulinemia, atopic dermatitis, allergic colitis, asthma, food allergy,
CC drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia

CC telangiectasia, common variable immunodeficiency disorder, MHC (major
 CC histocompatibility class II deficiency disease, AIDS (auto
 CC immunodeficiency syndrome), elevated IGE disorder, and IgG subclass
 CC selection disorder. The DNA sequences encoding AIB may be used for gene
 CC therapy and the antibodies to the AIB protein may be used for diagnosis
 CC and treatment of these disorders. The present sequence represents the
 CC exon 5 genomic DNA sequence of human AIB
 XX
 SQ Sequence 2172 BP; 702 A; 379 C; 465 G; 626 T; 0 U; 0 Other;
 Query Match 84.8%; Score 428; DB 3; Length 2172;
 Best Local Similarity 100.0%; Pred. No. 1.5e-59;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAACTTGAATGCAACATGCTTATTTATCTTATGATACATAAGTTGTAAAGAG 60
 DB 1745 GAAACTTGAATGCAACATGCTTATTTATCTTATGATACATAAGTTGTAAAGAG 1804
 QY 61 TTAATAAATGTTACTTCATGATTCATTTATATTTATTTATTTTGGTCTAATGATT 120
 DB 1805 TTAATAAATGTTACTTCATGATTCATTTATATTTATTTATTTTGGTCTAATGATT 1864
 QY 121 TTATTAAACATGATTTCCCTTTCTGATATATTGAATGGAGTCTCAAGCTTCATAAATT 180
 DB 1865 TTATTAAACATGATTTCCCTTTCTGATATATTGAATGGAGTCTCAAGCTTCATAAATT 1924
 QY 181 TATAACTTTAGAAATGATTTCTAATAACAACGATGATTAATGTAATGCGATGATGTTG 240
 DB 1925 TATAACTTTAGAAATGATTTCTAATAACAACGATGATTAATGTAATGCGATGATGTTG 1984
 QY 241 CTACGAAGCCATTTCTCTGATTTTATGATTAATGATGATGATGATGATGATGATG 300
 DB 1985 CTACGAAGCCATTTCTCTGATTTTATGATTAATGATGATGATGATGATGATGATG 2044
 QY 301 TCACCTTCATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 360
 DB 2045 TCACCTTCATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 2104
 QY 361 AAATAAATAATATAAAGTATTTATGATTAATGATTAATGATTAATGATTAATGATTAATG 420
 DB 2105 AAATAAATAATATAAAGTATTTATGATTAATGATTAATGATTAATGATTAATGATTAATG 2164
 QY 421 TAAACTTG 428
 DB 2165 TAAACTTG 2172
 RESULT 6
 ABS73287
 ID ABS73287 standard; DNA; 2791 BP.
 XX
 AC ABS73287;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE DNA encoding human translocation del (12p) protein #2.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200269900-A2.
 PN
 XX
 PD 12-SEP-2002.
 XX
 PF 01-MAR-2002; 2002WO-US006518.

XX 01-MAR-2001; 2001US-0272751P.
 PR (CONF-) CONFORMA THERAPEUTICS CORP.
 PA Fritz LC, Burrows RJ;
 PI WPI; 2002-698710/75.
 XX P-PSDB; ABG95083.
 DR
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90.
 XX
 PS Disclosure; Page 246-247; 389pp; English.
 XX
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock protein
 CC (HSP)-90, or selectively treating cells expressing (II) involving
 CC administering HSP90-inhibitor. The method is useful for treating
 CC genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This represents the DNA sequence of a chromosome aberration
 XX
 SQ Sequence 2791 BP; 842 A; 548 C; 625 G; 776 T; 0 U; 0 Other;
 Query Match 84.8%; Score 428; DB 6; Length 2791;
 Best Local Similarity 100.0%; Pred. No. 1.4e-59;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAACTTGAATGCAACATGCTTATTTATCTTATTTATTTATTTTGGTCTCAATGATT 60
 DB 2364 GAAACTTGAATGCAACATGCTTATTTATCTTATTTATTTATTTTGGTCTCAATGATT 2423
 QY 61 TTAATAAATGTTACTTCATGATTTATTTATTTATTTATTTTGGTCTCAATGATT 120
 DB 2424 TTAATAAATGTTACTTCATGATTTATTTATTTATTTATTTTGGTCTCAATGATT 2483
 QY 121 TTATTAAACATGATTTCCCTTTCTGATATATTGAAATGGAGTCTCAAGCTTCATAAATT 180
 DB 2484 TTATTAAACATGATTTCCCTTTCTGATATATTGAAATGGAGTCTCAAGCTTCATAAATT 2543
 QY 181 TATAACTTTAGAAATGATTTCTAATAACAACGATGATTAATGTAATGCGATGATGTTG 240
 DB 2544 TATAACTTTAGAAATGATTTCTAATAACAACGATGATTAATGTAATGCGATGATGTTG 2603
 QY 241 CTACGAAGCCATTTCTCTGATTTTATGATTAATGATGATGATGATGATGATGATG 300
 DB 2604 CTACGAAGCCATTTCTCTGATTTTATGATTAATGATGATGATGATGATGATGATG 2663
 QY 301 TCACCTTCATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 360
 DB 2664 TCACCTTCATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 2723
 QY 361 AAATAAATAATATAAAGTATTTATGATTAATGATTAATGATTAATGATTAATGATTAATG 420
 DB 2724 AAATAAATAATATAAAGTATTTATGATTAATGATTAATGATTAATGATTAATGATTAATG 2783
 QY 421 TAAACTTG 428
 |||||

D	B		2784 TAAACTTG 2791	
RESULT 7				
ABS73288				
ID	ABS73288 standard; DNA; 2791 BP.			
XX				
AC	ABS73288;			
DT	04-DEC-2002 (first entry)			
DE	DNA encoding human translocation del(12p) protein #3.			
KW	Chromosome aberration; oncogenic fusion protein; cancer;			
KW	HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;			
KW	T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;			
KW	acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;			
KW	acute lymphoblastic leukaemia; ALL; APL; solid tumour;			
KW	papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;			
KW	rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.			
OS	Homo sapiens.			
PN	WO200269900-A2.			
XX				
PD	12-SEP-2002.			
XX				
PF	01-MAR-2002; 2002WO-US006518.			
XX				
PR	01-MAR-2001; 2001US-0272751P.			
XX				
PA	(CONF-) CONFORMA THERAPEUTICS CORP.			
PI	Fritz LC, Burrows FJ;			
DR	WPI; 2002-698710/75.			
DR	P-PSTDB; ABG95084.			
XX				
PT	Treating genetically-defined disease associated with chromosomal			
PT	aberrations yielding oncogenic fusion proteins, e.g. cell proliferative			
PT	diseases, involves administering an inhibitor of heat shock protein 90.			
PS	Disclosure; Page 248-249; 389pp; English.			
CC	The invention describes a method of treating genetically-defined disease			
CC	associated with chromosomal aberrations yielding oncogenic fusion			
CC	proteins (I), treating cancerous cells containing (I) in a heterogeneous			
CC	cell population, treating proliferative diseases associated with mutant			
CC	protein or cellular protein isoforms (II) dependent on heat shock protein			
CC	(HSP)-90, or selectively treating cells expressing (II) involving			
CC	administering HSP90-inhibitor. The method is useful for treating			
CC	genetically-defined disease with chromosomal aberration yielding			
CC	oncogenic fusion protein, treating cancerous cells containing fusion			
CC	protein in heterogeneous cell population, treating proliferative disease			
CC	(e.g. rheumatoid arthritis or cancer) associated with mutant protein or			
CC	cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.			
CC	p53), or selectively treating cells expressing mutant protein or cellular			
CC	protein isoform in a patient heterozygous for (II). The method is useful			
CC	for treating a disease, e.g. haematopoietic disorder such as T or B cell			
CC	lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,			
CC	or a disease characterised by a solid tumour such as papillary thyroid			
CC	carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and			
CC	synovial sarcoma. The method is also useful for treating viral			
CC	infections. This represents the DNA sequence of a chromosome aberration			
XX	Sequence 2791 BP; 842 A; 548 C; 625 G; 776 T; 0 U; 0 Other;			
SQ				
Query Match	84.8%; Score 428; DB 6; Length 2791;			
Best Local Similarity	100.0%; Pred. No. 1.4e-59;			
Matches 428; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 GAAAAGTTGAATGCACAACCTGCTTATTATTTTAATCTTATGTACATAAGTTGTAAAAAGAG 60			

Query Match	82.8%	Score 418;	DB 4;	Length 574;
Best Local Similarity	100.0%;	Prod. No. 6.3e-58;		
Matches 418;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GAAGAACTTGAATGCACACAACTGCTCTATTTTAACTTTATTGTACATAAGATTTTGTAAAAAGAG	60	
DB	157	GAAGAACTTGAATGCACAACTGCTCTATTTTAACTTTATTGTACATAAGATTTTGTAAAAAGAG	216	
QY	61	TTAAAAATTTGTTTACCTTCATGTAATTCATTATATATTTTATATATTTTGGCGCTCAATGATTT	120	
DB	217	TTAAAAATTTGTTTACCTTCATGTAATTCATTATATATTTTATATATTTTGGCGCTCAATGATTT	276	
QY	121	TTTATTAACATGATNTTCCTTTTCTTGATATATATGAAATGGAGTCTCAAGACTTCATAAATTT	180	
DB	277	TTTATTAACATGATNTTCCTTTTCTTGATATATGAAATGGAGTCTCAAGACTTCATAAATTT	336	
QY	181	TATAACTTTAGAAATGATTTCTAATAACAAAGTATGTAATTTGAACATTTCCAGTAATGGTG	240	
DB	337	TATAACTTTAGAAATGATTTCTAATAACAAAGTATGTAATTTGAACATTTCCAGTAATGGTG	396	
QY	241	CTACGAAGCCATTTCTCTTTGATTTTGTAGTAAACCTTTTATGCACAGCAAAATTTGCTTCTGCG	300	
DB	397	CTACGAAGCCATTTCTCTTTGATTTTGTAGTAAACCTTTTATGCACAGCAAAATTTGCTTCTGCG	456	
QY	301	TCACCTTCAATCAGTTAAATAAATGATTAATAATTTTGGAAAGCTGTGAAGATAAAATATCC	360	
DB	457	TCACCTTCAATCAGTTAAATAAATGATTAATAATTTTGGAAAGCTGTGAAGATAAAATATCC	516	
QY	361	AAATAAAATTAATAAAAAAGTCATTTATATGAAAGTTAAAAATAAAAAATCATGATGATGG	418	
DB	517	AAATAAAATTAATAAAAAAGTCATTTATGAAAGTTAAAAATAAAAAATCATGATGATGG	574	

RESULT 9	
ADB54251	
ID	ADB54251 standard; DNA; 3000 BP.
XX	
XX	ADB54251;
XX	
XX	
DT	04-DEC-2003 (first entry)
XX	
XX	Pretreated genomic DNA region 175.
DE	
XX	
XX	colon cell proliferative disorder; non methylated CpG dinucleotide;
KW	cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ds.
KW	
XX	
XX	Unidentified.
OS	
XX	WO2003072821-A2.
PN	
XX	
PD	04-SEP-2003.
XX	
XX	
PF	27-FEB-2003; 2003WO-EP002035.
XX	
XX	27-FEB-2002; 2002EP-00004551.
PR	
XX	
XX	(EPIG-) EPIGENOMICS AG.
PA	
XX	
PI	Adorian P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;
PI	Rujan T, Schmitt A;
XX	
XX	WFI; 2003-731620/69.
DR	
XX	
PT	Detecting and differentiating between colon cell proliferative disorders
PT	associated with a gene or its regulatory regions comprises contacting a
PT	target nucleic acid in a biological sample obtained from the subject with
PT	a reagent.
XX	
XX	Claim 32; SEQ ID NO 307; 74pp; English.
PS	
XX	
XX	The invention relates to a novel method for detecting and differentiating
CC	

	CC	between colon cell proliferative disorders associated with at least one
	CC	gene or its regulatory regions. The method comprises contacting a target
	CC	nucleic acid in a biological sample obtained from the subject with at
	CC	least one reagent or a series of reagents, where the reagent or series of
	CC	reagents, distinguishes between methylated and non methylated CpG
	CC	dinucleotides within the target nucleic acid. The molecules of the
	CC	invention demonstrate cytostatic activity whilst the method may be useful
	CC	for detecting and differentiating between colon adenoma and colon carcinoma.
	CC	disorders, including cancers such as colon adenoma and colon carcinoma.
	CC	The PNA (peptide nucleic acid)-oligomers are useful as probes for
	CC	determining cytosine methylation state or single nucleotide
	CC	polymorphisms. The current sequence is that of the preselected genomic DNA
	CC	region of the invention. This sequence is not shown within the
	CC	specification but is taken from Wipoweb.
	XX	
	SQ	Sequence 3000 BP; 679 A; 0 C; 788 G; 1533 T; 0 U; 0 Other;
		Query Match 14.5%; Score 73.2; DB 9; Length 3000;
		Best Local Similarity 48.6%; Pred. No. 0.0031;
		Matches 201; Conservative 0; Mismatches 213; Indels 0; Gaps 0
QY	2	A A A A C T T G A A T G C A A C T G T C T T A T T T T A A T T G T G A C A T A A G T T G T A A A G A G T 61
Db	164	A A A T T T G A G T T T T A G T T T T T T A T A T G T G A A A T G G A G A A A T A A A T T G T A A A A T T A A 223
QY	62	T A A A A A T G T T A C T C A T G T A T C A T T A T T A T T A T T T T T G G T C T A A T G A T T T 121
Db	224	T T A A A T T G T T T A T T A T A T T T T T T T T A G T G T A T A T T A A T T G T A T T T T T G T A G 283
QY	122	T T A T T A A C A T G A T T C C T T T T C T G A T A T A T G A A A T G G A G T C T C A A G C T T C A A A T T T 181
Db	284	T T A G A A T G T G T T T T A A T A T G T T T T A A A T T G T T A A T T T T T T G T T A G T A A T T 343
QY	182	A T A A C T T T T A G A A A T G A T T C T A A T A A C A C G T A T G T A A T T G T A C A T T G C A G T A A T C G T G C 241
Db	344	T T T T T T A T T T T G A G A A T T A G A A A G G A A A A T T A T G T T T G G T A A T G T T A T A T T T T T A A 403
QY	242	T A C G A A G C C A T T C T C T T G A T T T T T A G T A A A C T T T A T G A C A C A A A T T G C T T C T G G C T 301
Db	404	A A T A A A A T T G T A G A A A G A A N A T T T A G T A A G T G A T G A G A G T A G A T G A T T G T T T T A T T 463
QY	302	C A C T T T C A T C A G T T A A A T A A A T C A T A A A A T A A T T T T G A A G A G C T G T C A A G A T A A A A T A C C A 361
Db	464	A T T T T A A A T T A T A A T A T A T T T T T T T T T A G A G T T T T T A A G T A T T G T A G A T A A T T T T T T A 523
QY	362	A A T A A A A T A A T A A A A G T G A T T T A T A T A G A A G T T A A A A T A A A A A T C A G A T A G A 415
Db	524	T T T A T T A A A A A T A A A T T G T A A A T A A T A A G T A T T A A G G T T A T A G G G T T G A T T A T G T T T T T C A 577

RESULT 10	
ADE37774	
ID ADE37774 standard; DNA; 3000 BP.	
XX XX	
AC AC	ADE37774;
XX XX	29-JAN-2004 (first entry)
DT DT	Human chemically treated H-cadherin nucleotide sequence SEQ ID NO:20..
XX XX	XX chemically pretreated genomic DNA; human; versican; TPEF; H-cadherin;
KW KW	calcitonin; EVA4; cytostatic; gene therapy;
KW KW	colon cell proliferative disorder; cytosine methylation state;
KW KW	single nucleotide polymorphism; SNP; disease analysis; CpG dinucleotide;
XX XX	gene; ds.
XX XX	Synthetic.
OS OS	Homo sapiens.
XX XX	WO2003072820-A2.
PD PD	04-SBP-2003.
XX XX	

PF 27-FEB-2003; 2003WO-EP002034.
XX
PR 27-FEB-2002; 2002EP-00004551.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Adorjan P, Burger M, Maier S, Lesche R, Cottrell S, Mooney S;
XX
XX WPI; 2003-731619/69.
DR
XX
XX New nucleic acid comprising a sequence of at least 18 bases in length of
PT a segment of the chemically pretreated genomic DNA, useful for treating
PT colon cell proliferative disorders.
XX
XX Claim 1; SEQ ID NO 20; 147pp; English.
PS
XX
XX The present invention describes a nucleic acid (I) comprising a sequence
CC of at least 18 bases in length of a segment of the chemically pretreated
CC genomic DNA of any of the 5 sequences of 965, 16579, 3000, 1984, or 7833
CC bp, which represent human versican, TPEF, H-cadherin, calcitonin and EYA4
CC respectively (see ADB37755 to ADE37759), or its complement. Also
CC described: (1) an oligomer, in particular an oligonucleotide or peptide
CC nucleic acid (PNA)-oligomer comprising in each case of at least one base
CC sequence having a length of at least 9 nucleotides which is complementary
CC to, or hybridises under moderately stringent or stringent conditions to a
CC pretreated genomic DNA; (2) a set of oligomers comprising at least two of
CC the oligomer of (1); (3) manufacturing an arrangement of different
CC oligomers (array) fixed to a carrier material; (4) an array of different
CC oligonucleotide- and/or PNA-oligomer sequences, which are arranged on a
CC plane solid phase in the form of a rectangular or hexagonal lattice; (5)
CC a composition of matter comprising the nucleic acid and a buffer
CC comprising 1-5 mM magnesium chloride, 100-500 micromole dNTP, 0.5-5 units
CC of taq polymerase, and the oligomer; (6) detecting, differentiating or
CC distinguishing between colon cell proliferative disorders; and (7)
CC detecting a colon cell proliferative disorder. (I) has cytostatic
CC activity, and can be used in gene therapy. The versican, TPEF, H-
CC cadherin, calcitonin and EYA4 genes, and the polypeptides expressed by
CC them, can be used for detecting, differentiating or distinguishing
CC between colon cell proliferative disorders. The oligomers are useful for
CC detecting the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) within nucleic acid sequences. The array is useful
CC for analysing diseases associated with the methylation state of the CpG
CC dinucleotides. The present sequence is used in the exemplification of the
CC present invention.
XX
XX Sequence 3000 BP; 679 A; 0 C; 788 G; 1533 T; 0 U; 0 Other;
SQ
Query Match 14.5%; Score 73.2; DB 9; Length 3000;
Best Local Similarity 48.6%; Pred. No. 0.0031;
Matches 201; Conservative 0; Mismatches 213; Indels 0; Gaps 0;
QY 2 AAAACTGCAATGCAACGCTGCTTATTTTATCTTATTTGTCATCAAGTTCTTAAAGAGT 61
DB 164 AAATTTTGAGTTTGTAGTTTATTTTATATGTCGAAATGGAGAAATAAATTTGTAATAA 223
QY 62 TAAAAATGTTACTTCATGATTCATTATTTATATTTTATTTTTCCTCTCAATGATTTT 121
DB 224 TTAATTTGTTTATTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 283
QY 122 TTATTTAAATGATTTCTTCTTCGATATATTTGAAATGGAGTCTCAAGCTTCATAAATTT 181
DB 284 TTAGAATGGTTTATTAATATGTTTAAATTTTGTGTTTATTTTATTTTATTTTATTT 343
QY 182 ATAACTTTAGAATGATTTCAATCAACAGTATGTAATTTAAATTCAGTCAATGGTGC 241
DB 344 TTTTATTTTTCGAAATAGAAAGGAATATTTATTTGTTGTAATTTTATTTTATTTTAA 403
QY 242 TAGCAAGCATTTCTTCTGATTTTATTTAGTAAATTTTATGACAGCAAAATTTCTTCGCT 301
DB 404 AATAAATTTGTAGGAAGAATAATTTAGTAAGTGTATGATGAGTAGTAATGATTTTATTT 463
QY 302 CACTTTCATCAGTTAAATTAATATGATTAATATTTTGGAGCTGTGAGATAAATACCA 361

Db 464 ATTTTAAATTTATAATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 523
QY 362 AATAAATAATATAAAGTGAATTTATATGAACTTAAATATAAATAAATCAGTATGA 415
Db 524 TTTATTTAAATAAATAATTTGTAATATATTAAGTATTTAGGTGATATTTGTTTGA 577

RESULT 11
ADB37662
ID ADB37662 standard; DNA; 29993 BP.
XX
AC ADB37662;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human chemically pretreated EYA4 gene SEQ ID NO:4.
XX
XX colon cell proliferative disorder; EYA4; cytostatic; gene therapy; human;
XX gene; ds; chromosome 6.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO2003072812-A2.
XX
XX 04-SEP-2003.
XX
XX 13-FEB-2003; 2003WO-EP001457.
XX
XX 27-FEB-2002; 2002EP-00004551.
XX
XX (EPIC-) EPIGENOMICS AG.
XX
XX Adorjan P, Burger M, Maier S, Lesche R, Cottrell S, De Vos T;
XX WPI; 2003-731618/69.
XX
XX Diagnosing a colon cell proliferative disorder in a subject comprises
XX obtaining one or more samples from colon tissue or serum the subject, and
XX detecting a decrease in the amount or expression of a polypeptide
XX expressed from the EYA4 gene.
XX
XX Claim 22; Page 83-91; 101pp; English.
XX
XX The present invention describes a method for diagnosing a colon cell
XX proliferative disorder in a subject. The method comprises obtaining one
XX or more samples from colon tissue or serum or both of the subjects, and
XX detecting a decrease in the amount or expression of a polypeptide
XX expressed from the EYA4 gene. Also described: (1) repressing
XX transformation in a colon cell by contacting the cell with an EYA4
XX polypeptide to inhibit a transformed phenotype; (2) preventing or
XX treating a colon cell proliferative disorder in a subject by
XX administering to the subject a compound that agonises EYA4; (3) a nucleic
XX acid comprising a sequence of at least 18 bases in length of a segment of
XX the chemically pretreated genomic DNA or its complement; (4) an oligomer,
XX in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer,
XX comprising in each case of at least one base sequence having a length of
XX at least 9 nucleotides which is complementary to, or hybridises under
XX moderately stringent or stringent conditions to a pretreated genomic DNA;
XX (5) a set of oligomers comprising at least two of the oligomer described
XX above; (6) manufacturing an arrangement of different oligomers (array)
XX fixed to a carrier material; (7) an arrangement of different oligomers
XX (array) obtainable in (6); (8) an array of different oligonucleotide-
XX and/or PNA-oligomer sequences, which are arranged on a plane solid phase
XX in the form of a rectangular or hexagonal lattice; (9) a composition of
XX matter comprising the nucleic acid and a buffer comprising 1-5 mM
XX magnesium chloride, 100-500 micromole dNTP, 0.5-5 units of taq
XX polymerase, and the oligomer; (10) detecting, differentiating or
XX distinguishing between colon cell proliferative disorders; (11) detecting
XX a colon cell proliferative disorder; and (12) a kit useful for the method
XX in (10) comprising a bisulfite reagent, and at least one of the nucleic
XX acid molecule or peptide described above, or their complements. EYA4 has
XX cytostatic activity, and can be used in gene therapy. The methods, vector

CC and polypeptide from the present invention are useful for treating colon
 CC cell proliferative disorders. The EYA4 gene, the polypeptide expressed
 CC from the EYA4 gene and kit are useful for detecting, differentiating or
 CC distinguishing between colon cell proliferative disorders. The oligomers
 CC are useful for detecting the cytosine methylation state and/or single
 CC nucleotide polymorphisms (SNPs) within nucleic acid sequences. The array
 CC is useful for analyzing diseases associated with the methylation state of
 CC the CpG dinucleotides. The present sequence represents a chemically
 CC pretreated human EYA4 gene, which is given in the exemplification of the
 CC present invention. Human EYA4 is mapped to chromosome 6, more
 CC specifically to 6q22.3.

XX
 SQ Sequence 29993 BP; 8706 A; 0 C; 5856 G; 15431 T; 0 U; 0 Other;
 Query Match 14.5%; Score 73.2; DB 9; Length 29993;
 Best Local Similarity 48.6%; Pred. No. 0.0026;
 Matches 201; Conservative 0; Mismatches 213; Indels 0; Gaps 0;
 QY 2 AAAAAGTGAATGCAACTGCTTATTTTAACTTATTTGACATAAGTTTGTAAAGAGT 61
 DB 1830 AAATTTGAGTTTTAGTTTTTTTATATGTAATGGAATGAGAAATAATTTGTAAATTA 1889
 QY 62 TAAAAATGTTACTTCATGATTCATTTATTTATTTATTTTGGTTCCTAAGATTTT 121
 DB 1890 TTAATTTGTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1949
 QY 122 TTATTAACATGATTTCTTTCTGATATATTGAAATGAGTCTCAAGCTTCATAATTT 181
 DB 1950 TTAGAATGTTTTTAAATTAATTTTAAATTTGTTTGTGTTTAAATTTATTTGTAATTT 2009
 QY 182 ATAACTTTAGAAATGATTTCTTAATACACATGATGTAATTTGACATTTGCGTGC 241
 DB 2010 TTTTATTTTGAATTTAGAAAGGAAATATTTATTTGTTGTAATTTATTTTAA 2069
 QY 242 TACGAAGCCATTTCTCTGATTTTATTTAGTAACTTTTATGACAGCAATTTGCTTGGCT 301
 DB 2070 AATAAATTTGAGAAAGATATTTAGTAAGTGTAGAGTAGTAATGATTTGTTTATTT 2129
 QY 302 CACTTTCAATCAGTTAAATAATGATAATAATTTTGGAAAGCTGTGAAGATAAAATACCA 361
 DB 2130 ATTTAAATTTAATAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2189
 QY 362 AATAAATAATTAAGTGTATTTATGATGATTTAAATTAATAAATCAAGTATGA 415
 DB 2190 TTTATTAATAAATAAATTTGTAATTTAAGTATTTAGGGTTGATATTTGTTTGA 2243

RESULT 12
 ADB54123
 ID ADB54123 standard; DNA; 3000 BP.
 XX
 AC ADB54123;
 XX
 DT 04-DEC-2003 (first entry)
 DE Pretreated genomic DNA region 47.

XX colon cell proliferative disorder; non methylated CpG dinucleotide;
 KW cytosine; cancer; adenoma; carcinoma; cytosine methylation state; ds.
 XX
 OS Unidentified.
 XX
 PN WO2003072821-A2.
 XX
 PD 04-SEP-2003.
 XX
 PF 27-FEB-2003; 2003WO-EP002035.
 XX
 PR 27-FEB-2002; 2002EP-00004551.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX

PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;

PI Rujan T, Schmitt A;
 XX
 DR WPI; 2003-731620/69.
 XX
 PT Detecting and differentiating between colon cell proliferative disorders
 PT associated with a gene or its regulatory regions comprises contacting a
 PT target nucleic acid in a biological sample obtained from the subject with
 PT a reagent.
 XX
 PS Claim 32; SEQ ID NO 179; 74pp; English.
 XX
 CC The invention relates to a novel method for detecting and differentiating
 CC between colon cell proliferative disorders associated with at least one
 CC gene or its regulatory regions. The method comprises contacting a target
 CC nucleic acid in a biological sample obtained from the subject with at
 CC least one reagent or a series of reagents, where the reagent or series of
 CC reagents, distinguishes between methylated and non methylated CpG
 CC dinucleotides within the target nucleic acid. The molecules of the
 CC invention demonstrate cytostatic activity whilst the method may useful
 CC for detecting and differentiating between colon cell proliferative
 CC disorders, including cancers such as colon adenoma and colon carcinoma.
 CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
 CC determining cytosine methylation state or single nucleotide
 CC polymorphisms. The current sequence is that of the pretreated genomic DNA
 CC region of the invention. This sequence is not shown within the
 CC specification but is taken from Wipoweb.
 XX
 SQ Sequence 3000 BP; 679 A; 174 C; 788 G; 1359 T; 0 U; 0 Other;

Query Match 14.2%; Score 71.6; DB 9; Length 3000;
 Best Local Similarity 48.3%; Pred. No. 0.0056;
 Matches 200; Conservative 0; Mismatches 214; Indels 0; Gaps 0;
 QY 2 AAAAAGTGAATGCAACTGCTTATTTTAACTTATTTGACATAAGTTTGTAAAGAGT 61
 DB 164 AAATTTGAGTTTTAGTTTTTTTATATGTAATGGAATGAGAAATAATTTGTAAATTA 223
 QY 62 TAAAAATGTTACTTCATGATTCATTTATTTATTTATTTTATTTTGGTCTCAATGATTTT 121
 DB 224 TTAATTTGTTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 283
 QY 122 TTATTAACATGATTTCTTTCTGATATATTGAAATGAGTCTCAAGCTTCATAATTT 181
 DB 284 TTAGAATGTTTTTAAATTTATTTTAAATTCGTTTGTGTTAAATTTATTTGTTAGATTT 343
 QY 182 ATAACTTTAGAAATGATTTCTAATAACACATGATGTAATTTGACATTTGACAGTATGTCG 241
 DB 344 TTTTATTTTGAAGATTTAGAAAGGAAATATTTATTTTGTGTAATTTATTTTATTTT 403
 QY 242 TACGAAGCCATTTCTCTGATTTTATTTAGTAACTTTTATGACAGCAATTTGCTTGGCT 301
 DB 404 AATAAATTTGAGAAAGATATTTTAGTAAGTGTAGAGTAGTAACGATTTGTTTATTT 463
 QY 302 CACTTTCAATCAGTTAAATAATGATAATAATTTTGGAAAGCTGTGAAGATAAAATACCA 361
 DB 464 ATTTTAAATTTAATAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 523
 QY 362 AATAAATAATTAAGTGTATTTATGATGATTTAAATTAATAAATCAAGTATGA 415
 DB 524 TTTATTAATAAATAAATTTGTAATTTAAGTATTTAGGGTTGATATTTGTTTGA 577

RESULT 13
 ADE37764
 ID ADE37764 standard; DNA; 3000 BP.
 XX
 AC ADE37764;
 XX
 DT 29-JAN-2004 (first entry)
 DE Human chemically treated H-cadherin nucleotide sequence SEQ ID NO:10.
 XX
 KW chemically pretreated genomic DNA; human; versican; TPEF; H-cadherin;

calcitonin; EV4; cytostatic; gene therapy;
colon cell proliferative disorder; cytosine methylation state;
single nucleotide polymorphism; SNP; disease analysis; CpG dinucleotide;
gene; ds.

Synthetic.
Homo sapiens.

WO2003072820-

04-SEP-2003.

27-FEB-2003;

27-FEB-2002; 2002EP-00004551.

(EPIG-) EPIGENOMICS AG.

Adorjan P, Burger M, I

WPI; 2003-731619/69.

New nucleic acid com

a segment of the chemically pretreated genomic DNA, useful for treating colon cell proliferative disorders.

Claim 1; SEQ ID NO 10; 147bp; English.

The present invention describes a nucleic acid (I) comprising a sequence of at least 18 bases in length of a segment of the chemically pretreated genomic DNA of any of the 5 sequences of 965, 16579, 3000, 1984, or 7833 bp, which represent human vesicarin, rPEF, H-cadherin, calcatonin and EVA4 respectively (see ADE37755 to ADE37759), or its complement. Also described: (1) an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer comprising in each case of at least one base sequence having a length of at least 9 nucleotides which is complementary to, or hybridises under moderately stringent or stringent conditions to a pretreated genomic DNA; (2) a set of oligomers comprising at least two of the oligomer of (1); (3) manufacturing an arrangement of different oligomers (array) fixed to a carrier material; (4) an array of different oligonucleotide- and/or PNA-oligomer sequences, which are arranged on a plane solid-phase in the form of a rectangular or hexagonal lattice; (5) a composition of matter comprising the nucleic acid and a buffer comprising 1-5 mM magnesium chloride, 100-500 micromole dNTP, 0.5-5 units of tag polymerase, and the oligomer; (6) detecting, differentiating or distinguishing between colon cell proliferative disorders; and (7) detecting a colon cell proliferative disorder. (I) has cytostatic activity, and can be used in gene therapy. The vesicarin, rPEF, H-cadherin, calcatonin and EVA4 genes, and the polypeptides expressed by them, can be used for detecting, differentiating or distinguishing between colon cell proliferative disorders. The oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within nucleic acid sequences. The array is useful for analysing diseases associated with the methylation state of the CpG dinucleotides. The present sequence is used in the exemplification of the present invention.

Sequence 3000 BP: 679 A; 174 C; 788 G; 1359 T; 0 U; 0 Other;

try Match	14.2%;	Score 71.6;	DB 9;	Length 3000;
t Local Similarity	48.3%;	Pred. No. 0.0056;		

ches 200; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

2 AAACCTGAATGCACAACTGTCTTATTTTAACTTATTGTACATAAGTTTGTAAAGAGT 61
164 AAATTTTGAGTTTTTACGTTTTTTTATGATGTAATGGAGAAAATAAATTTGTAAAAATTAA 223

62 TAAAAATTGTTACCTTCATGTAATTCATTTATATTTATATTTTGGCTCAATGATTTT 121

224 TTTAAATTGTTTATTTTAAATTTTTTTTTTTAGTGATATTAATTCGTATTTTCGTAGG 283

122 TTATTACATGATTTCCTTTCTGATATATTGAATGGAGTCTCAAAGCTTCATAAATTT 181

284	TTAGATGTTGTTTTTAATTATGTTTTAAATTCGTTTTGTGTTAAATTTATTGTTAGAATT	343
Db		
182	ATAACCTTTAGAAATGATTCATAATCAACCGTATGTAAATGTAACATTGCAGTAAATGGTGC	241
Qy		
344	TTTTTTATTTCAGAAATTTAGAAAAGGAAATATTAATGTTTGGTAAATGTTTATTTTTTAA	403
Db		
242	TACGAAGCCATTCCTCTGATTTTTTAGTAAACCTTTTATGACACCAAAATTCGTTCTGGCT	301
Qy		
404	AATAAAATTTAGGAAGAATATTTTAGTAAGTGATGAGAGTAGTAACGATTTGTTTTATT	463
Db		
302	CACCTTCAATCAGTTAAATTAATGTAATAATTTTTTGGAGCTGTGAGAGTAAATAACCA	361
Qy		
464	ATTTAAATTTATAATATTTTTTTTTTAGAGTTTTTTAAGTATGTGAGATAATTTTTTA	523
Db		
362	AATAAAATAATAAAAGTGTATTTATGAAGTTAAATAAAAAATCAGTATGA	415
Qy		
524	TTTTTAAAAAATAAATTTGAATTAAGTATTTAGGTTGATTTGTTTTTGA	577
Db		

RESULT 14

ABL34024
ID ABL34024 standard; DNA; 6375 BP.

XX ABL34024;

XX
DT 26-MAR-2002 (first entry)

DE Human immune system associated gene SEQ ID NO: 1997.

XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; anianaemic; cystostatic; monocytic;
KW neuroprotective; anti-Hiv; anticonvulsant; ophthalmologic;
KW antirheumatic; antiarthritis; antidiabetic; anipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.

XX Homo sapiens.

XX
PN
WC00200928-A2XX
PD 03-JAN-2002

02-III.-2001. 2001WO-EP007537

XX
PR 30-JUN-2000: 2000DE-01032529

PR 01-SEP-2000; 2000DE-01043826.
XX

PA (EPIG-) EPIGENOMICS AG.
XX

Olek A, Piepenbrock C, Berlin K;
PI
yy

WPI; 2002-130909/17.

Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.

XX
XX
PS Claim 1: SEQ ID NO 1997: 32bp + Sequence Listing: German

The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory ulcerative bowel diseases. The present sequence is a gene of the invention.

Sequence 6375 BP: 1795 A: 207 C: 1431 G: 2942 T: 0 U: 0 Other: 0

Query Match 14 2% Score 71 6: DB 6: Length 6375.

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Best Local Similarity	48.3%;	Pred. No. 0.0053;
Matches	200;	Conservative 0; Mismatches 214; Indels 0; Gaps 0;
QY	2	AAAACTGGAATGCAACTGCTTATTTTAACTCTTATTGTACATAAGTTGTAAAGAGT 61
Db	3164	AAATTTTCAGTCTTTTAGTCTTTTATATGTAATCGAAAAATAAATTTGTAAATTA 3223
QY	62	TAAAAATTTGTACTTCATGTATCATTTATATTTTATATTTTTCGCTCAATGATTTT 121
Db	3234	TTAAATTTGTTTATTTATATTTTTTTTTTTTGTAGTGATATTAATGGTATTTTTCGTAGG 3293
QY	122	TTATTAAACATGATTCCTTTTCTGATATATGAAATGGAGTCTCAAGAGCTTCATAAAATTT 181
Db	3284	TTAGAATGTGTTTTTAATATATGTTTTAAATTCGTTTTGTAAATTTTATTGTTAGAAAT 3343
QY	182	ATAACTTTAGAAATGATCTCAATAACAACCTATGTAATTTGTACATTCGAGTAATGGTGC 241
Db	3344	TTTTTTATTTTGAAATAGAAAGGAATATTAATGTTTGGTAATGTTTATATTTTTTAA 3403
QY	242	TACGAAGCCATTTCTCTTGATTTTTTAGTAAACTTTTATGACAGCAAAATTTGTTCTGGCT 301
Db	3404	AATAAAATTTGTAGAAAGAAATATTTTAGTAAGTATGAGAGTAGTAAACGATTTGTTTTATT 3463
QY	302	CACTTTCAATCAGTTAAATAAATGATAAATAAATTTTGGAGCTGTGAAGATAAATAATCCA 361
Db	3464	ATTTTAAATTTATATATATTTTTTTTTTAGAGTTTTTTTAGTATTTGTAGATTAATTTTTTTA 3523
QY	362	AATAAAATATATATAAAGTGTATTTATATGAAGTTAAATAAATAAAATTCAGTATGA 415
Db	3524	TTTATTAATAAAATAAATTTGTAATTTATAGTATTTTAGGGTTGATTTGTTTTTGA 3577

RESULT 15

ADB37660
ID ADB37660 standard; DNA; 29993 BP.

ADB37660:

DT 04-DEC-2003 (first entry)

DE Human chemically pretreated EYA4 gene SEQ ID NO:2.

colon cell proliferative disorder; EYA4; cytostatic; gene therapy; human; gene; ds; chromosome 6.

OS Synthetic.

Homo sapiens.

XX
PN
WO2003072812-A2.

04-SEP-2003.

13-FEB-2003: 2003WO-EP001457.

27-FEB-2002; 2002EP-00004551.

AA (EPIG-) EPIGENOMICS AG.

Adorian P. Burger M. Maier S. Ilesche R. Cottrell S. De Vos T.

XX
DR WPI: 2003-731618/69.

xx Diagnosing a colon cell proliferative disorder in a subject comprises
 PT obtaining one or more samples from colon tissue or serum the subject, and
 PT detecting a decrease in the amount or expression of a polypeptide
 PT expressed from the EYA4 gene.

Claim 22: Page 67-75: 101pp: English.

xx The present invention describes a method for diagnosing a colon cell CC proliferative disorder in a subject. The method comprises obtaining one CC or more samples from colon tissue or serum or both of the subjects, and CC detecting a decrease in the amount or expression of a polypeptide CC

expressed from the EYA4 gene. Also described: (1) repressing transformation in a colon cell by contacting the cell with an EYA4 polypeptide to inhibit a transformed phenotype; (2) preventing or treating a colon cell proliferative disorder in a subject by administering to the subject a compound that agonizes EYA4; (3) a nucleic acid comprising a sequence of at least 18 bases in length of a segment of the chemically pretreated genomic DNA or its complement; (4) an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer, comprising in each case of at least one base sequence having a length of at least 9 nucleotides which is complementary to, or hybridizes under moderately stringent or stringent conditions to, a pretreated genomic DNA; (5) a set of oligomers comprising at least two of the oligomer described above; (6) manufacturing an arrangement of different oligomers (array) fixed to a carrier material; (7) an arrangement of different oligomers (array) obtainable in (6); (8) an array of different oligonucleotide- and/or PNA-oligomer sequences, which are arranged on a plane solid phase in the form of a rectangular or hexagonal lattice; (9) a composition of matter comprising the nucleic acid and a buffer comprising 1-5 mM magnesium chloride, 100-500 micromole dNTP, 0.5-5 units of tag polymerase and the oligomer; (10) detecting, differentiating or distinguishing between colon cell proliferative disorders; (11) detecting in a colon cell proliferative disorder; and (12) a kit useful for the method in (10) comprising a bisulfite reagent, and at least one of the nucleic acid molecule or peptide described above, or their complements. EYA4 has cytosstatic activity, and can be used in gene therapy. The methods, vector and polypeptide from the present invention are useful for treating colon cell proliferative disorders. The EYA4 gene, the polypeptide expressed from the EYA4 gene and kit are useful for detecting, differentiating or distinguishing between colon cell proliferative disorders. The oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within nucleic acid sequences. The array is useful for analysing diseases associated with the methylation state of the CpG dinucleotides. The present sequence represents a chemically pretreated human EYA4 gene, which is given in the exemplification of the present invention. Human EYA4 is mapped to chromosome 6, more specifically to 6q22.3.

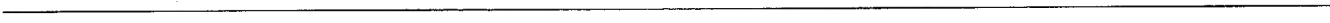
Sequence 29993 BP; 8706 A; 410 C; 5856 G; 15021 T; 0 U; 0 Other;

Query Match 14.2%; Score 71.6; DB 9; Length 29993;
Best Local Similarity 48.3%; Pred. NO. 0.0047;
Matches 200; Conservative 0; Mismatches 214; Indels 0;

Qy	2	AAAACTTGAATGACAACTGCTCTATTATTTAACTCTATTGTACATAAGTTTGTAAAAAGAGT	61
Db	1830	AAATTTTGGAGTTTTTATGTTTTTTTTTATGTGAAATCGAGAAAATAAATTTGTAAAAATTAA	1889
Qy	62	TAAAAAATGTTACTTCATCATGTATTCATTTATATTTATATTTATTTTTCGGTCTAATGATTTT	121
Db	1890	TTAAAAATTTGTTTATTTATATTTTTTTTTTTTTTTAGTGTATATTAATTTGTTATTTTTTCGTAGG	1949
Qy	122	TTATTAACATGATTTCCCTTTTCTGATATATTGAAATGGAGTCTCAAAGCTTCATAAATTT	181
Db	1950	TTAGAATGCTTTTTTAAATTATGTTTTTAAATTCGTTTGTCTAAATTTATTTGTTAGAATTT	2009
Qy	182	ATAACTTTGAATGATCTTAATAACACATGATGTAAATTTGTATCATTCGCAGTAATCGGTGC	241
Db	2010	TTTTTTATTTTTCGAGAATTAGAAAAGAAATATATGTTTGGTAATGTTATATATTTTTTAA	2069
Qy	242	TACGGAAGCCATTTCTCTTGATTTTTTTAGTAAACTTTTATGACAGCAAAATTTGCTCTCGGCT	301
Db	2070	AATTAATTTTGTAGGAAGAAATATTTAGTAGTGATGAGAGTAGTAACGATTTGTTTTTATTT	2129
Qy	302	CACCTTTCAATCAGTTAAATAAATGATAAATAATTTTGGAAAGCTGTGGAAGATAAAATACCA	361
Db	2130	ATTTTTAAATTTATAATATATTTTTTTTTTACAGTTTTTTTAAAGTATTTGAGATAATTTTTTA	2189
Qy	362	AATAAAATAATATAAAGTGAATTTATGAAAGTTAAAAATAAAAAATCAGTATGA	415
Db	2190	TTTTATTAAAAATAAATTCGTAATTAAGATATTTAGGGTTTGAATTTGTTTTTTTCA	2243

Search completed: March 4, 2004, 13:06:23

Job time : 291.715 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 13:06:29 ; Search time 55.9993 Seconds
(without alignments)
5004.527 Million cell updates/sec

Title: US-09-966-880A-35_COPY_10700_11204

Perfect score: 505

Sequence: 1 gaacaactgaatgcacaact.....ggaccattcattggagaaaa 505

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/FCTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	59.6	11.8	20674	4	US-09-641-638-651
C 2	59	11.7	176373	3	US-09-128-155-17
C 3	55.8	11.0	19124	2	US-08-487-826B-13
C 4	55.6	11.0	2614	4	US-09-004-056-1
C 5	55	10.9	6866	4	US-10-204-708-19
C 6	54.4	10.8	615	3	US-08-998-416-186
C 7	52.6	10.4	640681	4	US-09-790-988-1
C 8	52.4	10.4	78431	4	US-09-751-389-3
C 9	52	10.3	11049	4	US-10-204-708-22
C 10	51.8	10.3	20674	4	US-09-641-638-651
C 11	51.6	10.2	832	4	US-09-621-976-2813
C 12	51.6	10.2	22067	4	US-09-820-001-3
C 13	51.4	10.2	1218	2	US-08-731-722-4
C 14	51.4	10.2	11049	4	US-10-204-708-22
C 15	50.8	10.1	10640	4	US-09-417-485D-5
C 16	50.6	10.0	1200	3	US-09-018-584A-37
C 17	50.2	9.9	658	3	US-08-998-416-595
C 18	50	9.9	636	3	US-08-998-416-1137
C 19	50	9.9	32042	4	US-09-245-281-44
C 20	50	9.9	32042	4	US-09-340-620A-63
C 21	49.8	9.9	116592	4	US-09-818-512-3
C 22	49.8	9.9	392000	4	US-10-027-983-11
C 23	49.6	9.8	98844	4	US-09-791-211-10
C 24	49.2	9.7	51952	3	US-08-947-823-1
C 25	49	9.7	10409	3	US-08-772-440-33
C 26	48.8	9.7	3926	2	US-08-731-722-1
C 27	48.8	9.7	3926	2	US-08-731-722-1

C 28	48.8	9.7	3926	2	US-08-731-722-2
C 29	48.8	9.7	3926	2	US-08-731-722-2
C 30	48.8	9.7	8093	4	US-10-204-708-32
C 31	48.4	9.6	5666	4	US-10-204-708-29
C 32	48.4	9.6	8920	2	US-08-446-855A-1
C 33	48.4	9.6	8920	3	US-09-150-741-1
C 34	48.2	9.5	6866	4	US-10-204-708-20
C 35	48	9.5	832	4	US-09-621-976-2813
C 36	48	9.5	53332	4	US-09-801-861-3
C 37	48	9.5	246240	2	US-08-724-394A-20
C 38	48	9.5	246240	2	US-08-724-394A-21
C 39	48	9.5	246240	2	US-08-724-394A-22
C 40	47.8	9.4	6243	2	US-09-056-075-1
C 41	47.6	9.4	6866	4	US-10-204-708-20
C 42	47.4	9.4	516	4	US-09-621-976-2344
C 43	47.4	9.4	29604	3	US-08-781-891-207
C 44	47.4	9.4	29604	4	US-09-618-166-207
C 45	47.2	9.3	2251	3	US-08-991-677-11

ALIGNMENTS

RESULT 1

US-09-641-638-651/c
; Sequence 651, Application US/09641638
; Patent No. 6432646
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GENSET.051CPI
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 651
; LENGTH: 20674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1123..3123
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 3124..3297
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 3871..4072
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 5552..5633
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 5758..5880
; OTHER INFORMATION: exon 4
; NAME/KEY: exon
; LOCATION: 5996..6099
; OTHER INFORMATION: exon 5
; NAME/KEY: exon
; LOCATION: 6349..6509
; OTHER INFORMATION: exon 6

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, NAME/KEY: exon
, LOCATION: 7379..7522
, OTHER INFORMATION: exon 7
, NAME/KEY: exon
, LOCATION: 8645..8854
, OTHER INFORMATION: exon 8
, NAME/KEY: exon
, LOCATION: 12254..12340
, OTHER INFORMATION: exon 9
, NAME/KEY: exon
, LOCATION: 12854..13023
, OTHER INFORMATION: exon 10
, NAME/KEY: exon
, LOCATION: 13308..13429
, OTHER INFORMATION: exon 11
, NAME/KEY: exon
, LOCATION: 16567..16667
, OTHER INFORMATION: exon 12
, NAME/KEY: exon
, LOCATION: 16775..16945
, OTHER INFORMATION: exon 13
, NAME/KEY: exon
, LOCATION: 17063..17554
, OTHER INFORMATION: exon 14
, NAME/KEY: misc.feature
, LOCATION: 17555..20674
, OTHER INFORMATION: 3'regulatory region
, NAME/KEY: allele
, LOCATION: 1128
, OTHER INFORMATION: 10-508-191 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 1182
, OTHER INFORMATION: 10-508-245 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 1559
, OTHER INFORMATION: 10-509-284 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 1570
, OTHER INFORMATION: 10-509-295 : deletion of C
, NAME/KEY: allele
, LOCATION: 1827
, OTHER INFORMATION: 10-510-173 : variable motif ATTAA or TTTT
, NAME/KEY: allele
, LOCATION: 2048
, OTHER INFORMATION: 10-511-62 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 2323
, OTHER INFORMATION: 10-511-337 : insertion of T
, NAME/KEY: allele
, LOCATION: 2341
, OTHER INFORMATION: 10-512-36 : polymorphic base G or C
, NAME/KEY: allele
, LOCATION: 2623
, OTHER INFORMATION: 10-512-318 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 2832
, OTHER INFORMATION: 10-513-250 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 2844
, OTHER INFORMATION: 10-513-262 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 2934
, OTHER INFORMATION: 10-513-352 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 2947
, OTHER INFORMATION: 10-513-365 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 3802
, OTHER INFORMATION: 12-206-81 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 4062
, OTHER INFORMATION: 10-343-231 : deletion of C
, NAME/KEY: allele
, LOCATION: 4088
, OTHER INFORMATION: 12-206-366 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 4109
, OTHER INFORMATION: 10-343-278 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 4170
, OTHER INFORMATION: 10-343-339 : polymorphic base G or T
, NAME/KEY: allele
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, OTHER INFORMATION: 10-346-23 : polymorphic base A or G
, NAME/KEY: allele
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, OTHER INFORMATION: 10-346-141 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 6141
, OTHER INFORMATION: 10-346-263 : polymorphic base G or C
, NAME/KEY: allele
, LOCATION: 6183
, OTHER INFORMATION: 10-346-305 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 6338
, OTHER INFORMATION: 10-347-74 : polymorphic base A or G
, NAME/KEY: allele
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, OTHER INFORMATION: 10-347-165 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 6467
, OTHER INFORMATION: 10-347-203 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 6484
, OTHER INFORMATION: 10-347-220 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 6534
, OTHER INFORMATION: 10-347-271 : polymorphic base A or T
, NAME/KEY: allele
, LOCATION: 6611
, OTHER INFORMATION: 10-347-348 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 7668
, OTHER INFORMATION: 10-348-391 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 8608
, OTHER INFORMATION: 10-349-47 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 8658
, OTHER INFORMATION: 10-349-97 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 8703
, OTHER INFORMATION: 10-349-142 : polymorphic base G or C
, NAME/KEY: allele
, LOCATION: 8777
, OTHER INFORMATION: 10-349-216 : deletion of CTG
, NAME/KEY: allele
, LOCATION: 8785
, OTHER INFORMATION: 10-349-224 : polymorphic base G or T
, NAME/KEY: allele
, LOCATION: 8926
, OTHER INFORMATION: 10-349-368 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 12171
, OTHER INFORMATION: 10-350-72 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 12429
, OTHER INFORMATION: 10-350-332 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 13341
, OTHER INFORMATION: 10-507-170 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 13492
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; ; OTHER INFORMATION: 10-507-321 : polymorphic base A or C
; NAME/KEY: allele
; LOCATION: 13524
; ; OTHER INFORMATION: 10-507-353 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 13535

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Query Match	11.8%; Score 59.6; DB 4; Length 20674;
Best Local Similarity	49.1%; Pred. No. 0.0011;
Matches 158; Conservative	0; Mismatches 164; Indels 0; Gaps 0;
101	TATTTTGGCTCAAGATTTTTTATACATGATTCCTTTCTCGATATATTTGAAATCGA 160
11560	TTTTTTTAAATATAAAATATTTCTTACGTATTAATAATTTAAATTTAAATTAA 11501
161	GTCTCAAAAGCTTCATAAAATTTATACTTTAGAAATGATTCCTAATAACACGTATGTAAAT 220
11500	TTTATAATTAAATATTTTAAATTTAAATTTTAAATTTAAATTTAAATAAAAAATAT 11441
221	GTAAACATTCGCAGTAAATGGTGGCTACGAAGCCATTTCTCTGTATTTTTAGTAAACTTTTATG 280
11440	TAAAAATTTAAATTTAAATTTTGGAGCAATTAATAATTAATAATTTAAATTTAAATTTAAATTT 11381
281	ACAGCAAAATTTGGCTTCGCTGCCTCACATTCCTCAATCAGTTAAATAAATGATAAATAATTTTGG 340
11380	AAATTTAAATTTAAATTTAAATTTAAATTTAAATAATTTAAATAATTTAAATTTAAATTTAAATTT 11321
341	AGCTGTGAAGATAAAAAATACCAAAATAAAATAATATAAAAAAGTCATTTATATGAAAGTTAAAAAT 400
11320	ATTAAATTAAGTTAAATTAATTAATTAATTAATTAAGTTAAATTAATTAATTTAAATTTAAATTT 11261
401	AAAAAATCAGTATGATGGAATA 422
11260	AAATTTAAATTTAAATTTAAATA 11239

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RESULT 2
US-09-128-155-17
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

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	Query Match	11.7%	Score 59	DB 3	Length 176373
	Best Local Similarity	78.0%	Pred. No. 0.0018		
	Matches 71	Conservative	0	Mismatches 20	Indels 0
	Gaps	0			
QY	415	ATGGAAATAAATTGAGAGTCCAGAGTTATCCCATACATCTGTAATCAACTAATTCTCA	474		
Ddb	167654	ATGGAAATAGAAATTGAGAGTCCAGAAATAATCTCATCTCTATGAICAAATTGATTTTCAG	167713		
QY	475	CAAGGGTGTAAAGGACCATTCAATGAGAAA	505		

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DB      167714 CAAGGTGCCAGACCAATTCATGAGGAAA 16774A
RESULT 3
US-08-487-826B-13/c
; Sequence 13, Application US/08457826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487.826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

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Query Match	11.0%;	Score 55.8;	DB 2;	Length 19124;
Best Local Similarity	48.6%;	Pred. No. 0.0061;		
Matches 153;	Conservative 0;	Mismatches 162;	Indels 0;	Gaps 0;
QY	17	AACCTGCTTATTTTAACTTATTTGACATAAGTTTGTAAAAGAGCTTAAAAATGTTTACTT	76	
DB	15885	AATTAATAATTTTTTATTTTATTTATTTTATTTTATTTAATTAATTTTTTATTTATTTATTT	15826	
QY	77	CATGTATTCATTTATATTTTATTTATTTTTCGGCTCAATGATTTTTTTTATTAACATGATTT	136	
DB	15825	TTTTTTTATTAATAATAATTTTTTTTATTTTATGTATATATTTTTTTTTTTTACATTTTTTT	15766	
QY	137	CTTTTCTGATATATGTAAATGGAGCTCAAGCTTCATTAATTTTAACTTTTAGAAGT	196	
DB	15765	AAATTTTTTTTTTATTTTATGATATATATTTTATTTTAAATATATTTTTTCTTTTTTTTTT	15706	
QY	197	ATTCTAAATAACAAGTATGTAAATTTGTAACATTCGAGTAATGGTGCTACGAAGCCATTTCT	256	
DB	15705	GTATTTATGATATATATTTTTTTTTTTTTTAAATGTTTTTTTTTTTTCTCTCTTGTTTTAT	15646	
QY	257	CTTGATTTTTTAGTAACCTTTTATGACGCAAAATTTGCTTCCTGGCTCACTTTTCAATCAGTT	316	

Db 15645 TTTTATTATATCAATTTTTTTTTTATATAAAATTTTTTTTAAATTTTTTTTGTGATAATCT 15586
 QY 317 AAATAAATGATAAAT 331
 Db 15585 TTTTCATTTTTTATT 15571

RESULT 4

US-09-004-056-1/c
 ; Sequence 1, Application US/09004056A
 ; Patent No. 656586
 ; GENERAL INFORMATION:
 ; APPLICANT: Calgene LLC
 ; TITLE OF INVENTION: Plant Expansin Promoter Sequences
 ; FILE REFERENCE: 125
 ; CURRENT APPLICATION NUMBER: US/09/004,056A
 ; CURRENT FILING DATE: 1998-01-07
 ; EARLIER APPLICATION NUMBER: 60034914
 ; EARLIER FILING DATE: 1997-07-01
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 2614
 ; TYPE: DNA
 ; ORGANISM: Gossypium hirsutum
 ; FEATURE:
 ; NAME/KEY: promoter
 ; LOCATION: (930)
 ; OTHER INFORMATION: unknown nucleotide
 ; FEATURE:
 ; NAME/KEY: promoter
 ; LOCATION: (947)
 ; OTHER INFORMATION: unknown nucleotide
 ; FEATURE:
 ; NAME/KEY: promoter
 ; LOCATION: (956)
 ; OTHER INFORMATION: unknown nucleotide
 US-09-004-056-1

Query Match 11.0%; Score 55.6; DB 4; Length 2614;

Best Local Similarity 47.9%; Pred. No. 0.0053; Mismatches 160; Conservative 0; Indels 0; Gaps 0;

QY 83 TTCAATTATATTTTATATTTTTCGGCTAAATGATTTTTTTTAAATGATTTTCTTTT 142
 Db 461 TTTAATTATTAATTTAGTTAGTTTGGTTATCAATTTTTTTTCATATTAATTTTAGTTT 402
 QY 143 CTGATATATTGAATGGAGTCTCAAGCTTCATAATTTATAACTTTAGAAATGATCTTA 202
 Db 401 TATTTCTAAATTTATGTTGACAAATGAACCTTTATTTTATATATTTTAAATATTATTGA 342
 QY 203 ATAACAACGTATGTAATTTGAATGCAATGCGTGTGAGTAAATGCTAGCAAGCCATTTCTTTGAT 262
 Db 341 TAAATTTTAAAGTATTTTTCATATATATTTTCAGGAACAATAATTTTCGAATACG 282
 QY 263 TTTTGTAAACTTTTATGACAGCAATTTGCTTCTGGCTCAGCTTTCAATCAGTTAAATAA 322
 Db 281 AATTTTGTAGATTTTAAATCTTATGATTTTAAATTTTAAATTTTAAATTTTAAATTTAATA 222
 QY 323 ATGATAAATAATTTTGGAGCTGTGAAGATAAAATACCAATATAAATAATAATAAAGTGA 382
 Db 221 TTTAGAAAATAATTTAGTTAAATGGAATTTTAAATTTTAAATTTTAAATTTTAAATTTAATA 162
 QY 383 TTTATATGAAGTTAAATTAATAAATAATCAATCAGTATGAT 416
 Db 161 ATTATATTAATAATAATAATAATAATAAATGGAAT 128

RESULT 5

US-10-204-708-19
 ; Sequence 19, Application US/10204708
 ; Patent No. 667731
 ; GENERAL INFORMATION:

; APPLICANT: OLEK, Alexander
 ; APPLICANT: PIEPENROCK, Christian
 ; APPLICANT: BERLIN, Kurt
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
 ; TITLE OF INVENTION: by Assessing DNA Methylation
 ; FILE REFERENCE: 5013.1012
 ; CURRENT APPLICATION NUMBER: US/10/204,708
 ; CURRENT FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03971
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: DE 10019058.8
 ; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: DE 10032529.7
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: DE 10043826.1
 ; PRIOR FILING DATE: 2000-09-01
 ; NUMBER OF SEQ ID NOS: 98
 ; SEQ ID NO 19
 ; LENGTH: 6866
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-204-708-19

Query Match 10.9%; Score 55; DB 4; Length 6866;

Best Local Similarity 49.6%; Pred. No. 0.0079; Mismatches 196; Conservative 0; Mismatches 195; Indels 4; Gaps 2;

QY 27 TTTTATCTTTTGTACATAAGTTTGTAAAGAGTTAAATAATTTGTTACTTCATGTATTTCA 86
 Db 910 TTTAGTAGAATTTGGGAAATTTTAAATAAATTTAATTTTAAATTTTAAATTTAATA 969
 QY 87 TTTATATTTTATATTATTGCGTCTAATGATTTTTTAAATGATTTTCAATGATTTCTCTGTA 146
 Db 970 TTTTGTGTTGTTATTTATTTTAAATTTGTTTTTTTTCGATTTTAAATTTATAG 1029
 QY 147 TATATTGAATCGAGTCTCAAGCTTCATAAATTTTATACTTTAGAAATGATTTCTAATAA 206
 Db 1030 TTGGTTGGATTTTATAGATGATGAATTTATAGAGGTTAATGTAGTTTATTTATTTA 1089
 QY 207 CACGATGATTAATTTGAACATTTGCAGTA-ATGCTGCTACGAAGCCATTTCTTGAATTT 265
 Db 1090 TATTTATAGTTTAGGTAAAGATAATGTTGTTATTTATATTTAAATATATTTAGGTAGATATA 1149
 QY 266 TAGTAACTTTTATGACAGCAATTTGCTTCTGGCTCACTTTCAATCAGTTAAATAAATG 325
 Db 1150 TAGAAAATTTGTATATATTTTAAATTTTATGTAGATAGAT---AGAGAAATTAATAAAA 1206
 QY 326 ATAAATAATTTTGGAGCTGTGAAGATAAAATACCAATAAATAATAATAATAAAGTGAATTT 385
 Db 1207 ATTAAGAAGTTTATGAAATAAAAGTAGGGAGTTATAAGGTAAGATAGAAATGTAGA 1266
 QY 386 ATATGAAGTTAAATAAATAAATAATCAGTATGATGAA 420
 Db 1267 ATAAAAGTTAAATTAAGAAAGAAATATGAGGAA 1301

RESULT 6

US-08-998-416-186
 ; Sequence 186, Application US/08998416
 ; Patent No. 6239284
 ; GENERAL INFORMATION:
 ; APPLICANT: Philippsen, Peter
 ; APPLICANT: Pohlmann, Rainer
 ; APPLICANT: Steiner, Sabine
 ; APPLICANT: Mohr, Christine
 ; APPLICANT: Wendland, Jürgen
 ; APPLICANT: Knechtle, Philipp
 ; APPLICANT: Rebschung, Corinne
 ; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSIPII

;; TITLE OF INVENTION: AND USES THEREOF
;; NUMBER OF SEQUENCES: 1152
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 6239264artis Corporation
;; STREET: 3054 Cornwallis Road
;; CITY: Research Triangle Park
;; STATE: No. 6239264th Carolina
;; COUNTRY: USA
;; ZIP: 27709
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/998,416
;; FILING DATE: 24-DEC-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: CH 0016/97
;; FILING DATE: 31-DEC-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meigs, J. Timothy
;; REGISTRATION NUMBER: 38,241
;; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 919-541-8587
;; TELEFAX: 919-541-8689
;; INFORMATION FOR SEQ ID NO: 186:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 615 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: PAG1074RP
;; US-08-998-416-186

Query Match 10.8%; Score 54.4; DB 3; Length 615;
Best Local Similarity 48.2%; Pred. No. 0.0079;
Matches 184; Conservative 0; Mismatches 196; Indels 2; Gaps 1;

QY 28 TTATATCTTATTTGCTACATAAGTTTGTAAAGAGTTTAAAGATTTGTTTCTCATGTTTCAT 87
DB 220 TAGTTTCAAAATTTTAAATTTAGTTTATTAATATTTAGATATTTATTTTCTTTAATA 279

QY 88 TTATATTTTATATTTTTCGCTCTAATGATTTTATTAACATGATTTTCTCTGAT 147
DB 280 AATTATTAATAGATTATCAATAATTAATATATTTATTTATTTATTTTAAATTAAT 339

QY 148 ATATTGAATGGTCTCAAGCTTCATTAATTTTATACCTTTAGAAATGATTTCTAATAAC 207
DB 340 ATATTTTATTTATTAAGATTTAATTTATTTTAAATATTTGTAATATTTATTTTATAT 399

QY 208 AACGTATGTAATTTGAACATTTGAGT--AATGGTCTACGAAGCCATTTCTCTGATTTT 265
DB 400 AATATCTATTTTATTAATATTTATTTGATTTATTTATTTTAACTTTTATTAAGATTTAT 459

QY 266 TAGTAACATTTTATGACAGCAATTTGCTTCGCTCCTCAATCAGTTTAAATGATG 325
DB 460 TATTAATTAATTTTAACTTTTAACTTTTATTTATTTATTTATTTTAAATTT 519

QY 326 ATAAATTAATTTTGAAGCTGTGAAGATAAAATACCAATTAATTAATTAATTAATTTATCA 385
DB 520 ATATTCATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATCA 579

QY 386 ATATGAAGTTAAATTAATAAT 407
DB 580 TTATTTTAATTAATTAATAAT 601

RESULT 7

US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 10.4%; Score 52.6; DB 4; Length 640681;
Best Local Similarity 47.7%; Pred. No. 0.041;
Matches 195; Conservative 0; Mismatches 204; Indels 10; Gaps 1;

QY 26 ATTTTAACTTATTTGTACATAAGTTTGTAAAGAGTTAAAGATTTGTTTCTCATGTTTC 85
DB 527077 ATGTTATATTTTGTAGAGTTAAATATTTTAACTCTATTTTGTAGTATTTTAAATGAATA 527018

QY 86 ATTTATATTTTATTTTGGTCTAATGATTTTATTAACATGATTTCTTTCTG 145
DB 527017 TTGTTATTTAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTCTTTT 526958

QY 146 ATATTTGAATGGAGTCTCAAGCTTCATAATTTTATAACTTTAGAAATGA----- 197
DB 526957 TAATATTTTATTTTAACTTTTATTTATATATGATCATGAAATAATAGATCTACT 526898

QY 198 --TTCTAATAACCAACGTTGTTTAACTTTGAGTAAATGCTGCTACGAGCCATTT 255
DB 526897 TTTTGTAGTATGAAATTAATGTTTCTTTATTTTAAATTTAGAAATTAATTT 526838

QY 256 TCTTGATTTTGTAACTTTTATGACAGCAATTTGCTTCTGCTCAGTTTCAATCAGT 315
DB 526837 TTAATATGTAACCAATTTTAAATTTAGATTTATTAAGAAATATTTTAAATATTT 526778

QY 316 TAAATTAATGATAAATTTTGTGAAGCTGTGAAGATTAATTAACCAATTAATTAATA 375
DB 526777 TAAACTTACTTTAAATTTAGAAATATGTTTATCAGACTAATAGAAATATATTT 526718

QY 376 AATGATGATTTTATGAGTTAAATTAATAATCAAGTATGATGGAATAA 424
DB 526717 AATATAATTTTAAATCAGTATTTTATTTTATTTTATTTTGAATAA 526669

RESULT 8
US-09-751-389-3/c
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUGLIER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001067
; CURRENT APPLICATION NUMBER: US/09/751,389
; CURRENT FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 786431
; TYPE: DNA
; ORGANISM: Human

[illegible]

```

OTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12854..13023
OTHER INFORMATION: exon 10
NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTTT
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2844
OTHER INFORMATION: 10-513-262 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2934
OTHER INFORMATION: 10-513-352 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 : deletion of C
NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 12-206-366 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-363 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6338
OTHER INFORMATION: 10-347-74 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6429
OTHER INFORMATION: 10-347-165 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6467
OTHER INFORMATION: 10-347-203 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6534
OTHER INFORMATION: 10-347-271 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 6611
OTHER INFORMATION: 10-347-348 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 10-348-391 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 8658
OTHER INFORMATION: 10-349-97 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 8777
OTHER INFORMATION: 10-349-216 : deletion of CTG
NAME/KEY: allele
LOCATION: 8785
OTHER INFORMATION: 10-349-224 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 8926
OTHER INFORMATION: 10-349-368 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12171
OTHER INFORMATION: 10-350-72 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12429
OTHER INFORMATION: 10-350-332 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 13341
OTHER INFORMATION: 10-507-170 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 13492
OTHER INFORMATION: 10-507-321 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 13524
OTHER INFORMATION: 10-507-353 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 13535

```

Query Match

10.3%; Score 51.8; DB 4; Length 20674;

[illegible]

```

RESULT 11
US-09-621-976-2813/c
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; FEATURE:
; LOCATION: 235..399
; US-09-621-976-2813

```

	Query Match	10.2%	Score 51.6;	DB 4;	Length 832;
	Best Local Similarity	12.4%;	Pred. No. 0.03;		
	Matches	39;	Conservative 148;	Mismatches 127;	Indels 0; Gaps 0;
Qy	12	TGCACAACTCGTCTATTTTTAATCTTATTGTACATAGAAGTTGTAAAGAGCTTAAAAATTGT	71		
Db	314	WGHHYMKEMSTRWYCYMKCKMYRGRCAWYTAERGWSYANGKWSRGSMSNC	255		
Qy	72	TACTCANGTATTCATTTATTTATTTATTTTTCGGTCTAATGATTTTTTTTATTAAACAT	131		
Db	254	TRWYFKGGSTYWTMKTCATWCYWKYKRWMSKTCWSGSGGYNTSYSTRSYSMYWA	195		
Qy	132	GAU TTCCTTTCTGATATTTGAATGGAGCTCTCAAAGCTTCATATAATTTATAACTTTAG	191		

```

RESULT 12
US-09-820-001-3/c
; Sequence 3, Application US/09820001
; Patent No. 6387680
;
; GENERAL INFORMATION:
;
; APPLICANT: MERKULOV, Gennady et al
;
; TITLE OF INVENTION: ISOLATED MOLECULES ENCODING HUMAN LIPASE PROTEINS, NUCLEIC
; AND USES
;
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; THEREOF
;
; FILE REFERENCE: CL001186
;
; CURRENT APPLICATION NUMBER: US/09/820,001
;
; CURRENT FILING DATE: 2001-03-29
;
; NUMBER OF SEQ ID NOS: 4
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 3
;
; LENGTH: 22067
;
; TYPE: DNA
;
; ORGANISM: Human
;
US-09-820-001-3

```

	Query Match	10.2%;	Score 51.6;	DB 4;	Length 22067;
	Best Local Similarity	60.9%;	Pred. No. 0.044;		
	Matches	84;	Conservative	0;	Mismatches 54; Indels 0; Gaps 0;
Qy	367	ATAATAATAAAAGTCATTATATGTAAGTTAAAAATAAAAAATCAGTATGATGGATAAACT	426		
Db	14591	ATAATACAAACTCGCATGATCTGGCATAAATAACAGACACATAGACCANTGGACAGAT	14532		
Qy	427	TGAGAGTCACGAAGTTATCCCATACATCTGTAATCAACTAATTTTCTCACAGGGTGTAAG	486		
Db	14531	AANGACCCACAAATATATCCACACATTTATAGTCAACTAATTTTCAACAAAGCATCAA	14472		
Qy	487	GACCATTCAATCGAGAAA	504		
Db	14471	GAACATACATTGGGAAA	14454		

RESULT 13
US-08-731-722-4/c
; Sequence 4, Application US/08731722
; Patent No. 5961971
; GENERAL INFORMATION:
; APPLICANT: Martin, Frank N.
; TITLE OF INVENTION: Biocontrol of Fungal Soilborne Pathogens
; TITLE OF INVENTION: by Pythium oligandrum
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Salivanchik & Salivanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/731,722
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Whittlock, Ted W.
 REGISTRATION NUMBER: 36,965
 REFERENCE/DOCKET NUMBER: UF-161
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 352-375-8100
 TELEFAX: 352-372-5800
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: 17-1
 US-08-731-722-4

Query Match	10.2%	Score 51.4;	DB 2;	Length 1218;
Best local similarity	45.4%;	Pred. No. 0.034;		
Matches 184;	Conservative 0;	Mismatches 221;	Indels 0;	Gaps 0;
QY	17	AACGTGCTCTATTTAATCTTATTGTCATCAAGTTTGTAAAAGAGTGTAAAAAATGTTACTT	76	
Db	807	AATTAATTATATCTTTTAAAGNATATATACCTTTAAAAAANAATTTAAATGAAATAC	748	
QY	77	CATGTATTCATTATATATTTTATATATATTTTGGCGTCTAATGATTTTTTTTATTAAACATGATTT	136	
Db	747	TTCTAATAAGATATATATTTTATTATAAATATTAATTAATTTATTTCTTTATTAAAGTAAAT	688	
QY	137	CCTTTTCTGATATATCGAATGGAGTCTCAAGGCTTCATAAACTTATAAATCTTTAGAAATG	196	
Db	687	AAGATTCACATTTTCTATTAAAAAATAAACCCTTTCTCTATTGAAAAATTTCTTTATAG	628	
QY	197	ATTCTAATAACAAGTATGTAAATGTAACTATGCAGTAATGGTGCTACGAAGCATTTCT	256	
Db	627	CTATTATTAAGGTTTCATAGGCTCTACTGTTTAAATTCAGATTTATTTATTAGAAATATAA	568	
QY	257	CTTGATTTTTAGTAAACTTTTATGACAGCAAAATTTGCTTCTGGGCTCACTTTCATCAGTT	316	
Db	567	GTAAGCTTCTTCAATATTTATATAATGTTAAAAATTTCTGGTGGATTTACACAATTTAAAT	508	
QY	317	AAATAAATGATAATAATTTTTGGAGCTGTGAAGATAAAATACCAAATAAATAATAATAA	376	
Db	507	AAUTTAATTTATAATAAATAATATCTTATTAGAAGTATTTTCATTTTAATTTTTTTTT	448	
QY	377	AAGTGATTTATGAAGTTTAAAAATAAAAAATCAGTATGATGGAT	421	
Db	447	AAAAGTTATATATCTTTTAAAAAGATATATAATTAATTAATTCATATAATAT	403	

```

RESULT 14
US-10-204-708-22
; Sequence 22, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8

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; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 22
; LENGTH: 11049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-22

      Query Match      10.2%; Score 51.4; DB 4; Length 11049;
      Best Local Similarity 48.1%; Pred. No. 0.044;
      Matches 210; Conservative 0; Mismatches 221; Indels 6; Gaps 2;

QY 75 TTCATGATTCATTTATATATTTTATATATTTTGGTCTAATGATTTTATTTTAATTAACATGAT 134
Db 10219 TTTTCTTATTTTAAATTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 10278

QY 135 TTCCTCTTCTGATATATTGAATGGAGTCTCAAGAGTTCATAAATTTTATAACTTTAGAAA 194
Db 10279 TTTATTTTACGTTTTTTTTTGAAATATTAGTTGAATGCTATGCAATTTGTTAATATTAAAT 10338

QY 195 TGATTTCTAATAACACGATGTAATGTGACAA---TTGCGAGTAATGTGTGTACGAAGCCA 251
Db 10339 ATTTTTGATTTATAAGATGATAATTTTATTTGGTTTTAAGTTAATAAAGAATTTAAATTT 10398

QY 252 TTTCTCTTGATTTTTTAGTAAACTTTTATGACAGCAAAATTTGCTCTCGCTCACTTTCAAT 311
Db 10399 TTTTATTTTATTAATTTAGAAATTTAAATATTAGTATTATTAATGATATTATGTTTTAT 10458

QY 312 CAGTTAAATAATGATAAATAA---TTTTGGAGCTGTGAAGATATAAATTCAAAATAAAA 368
Db 10459 TAATTATAAAGGTTTTAAGATGGTTTTTTTATAATGATATTAGTTGAGTAGAATTCATAAT 10518

QY 369 TAATATAAAGTGATTTTATATGAAGTTAAAAATAAAAAATCAGTATGATGAAATAAACTTG 428
Db 10519 TATTATGTTATTTTAAAGATATAATGGTATTTTTTTATTTAAATATAAGTTTTAAAAATATT 10578

QY 429 AGAGTCCGAAGTTATCCCATACATCTGTAACTCAACTTAATTTCTCACAAGGGTGTAGGA 488
Db 10579 ATATAATTAAGAGTAGAAAAATAAATTTATTTTCATGAAAAATTTTTTTTAAAGTTTTAGTA 10638

QY 489 CCATTCATGGAGAAA 505
Db 10639 TGAAGTAAATAAATTAA 10655

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RESULT 15
US-09-417-485D-5
; Sequence 5, Application US/09417485D
; Patent No. 6541202
; GENERAL INFORMATION:
; APPLICANT: Long, David M.
; APPLICANT: Metz, Anneke M.
; APPLICANT: Love, Ruschelle A.
; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
; FILE REFERENCE: 47714-5009-US
; CURRENT APPLICATION NUMBER: US/09/417,485D
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10640
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (834)..(7385)
; OTHER INFORMATION: TERT gene

```

Search completed: March 4, 2004, 16:42:05
Job time : 59.9993 secs

1	GAAAACCTTGAATGCACACCTGCTTATTTTAACTTATTGACATACAGTTGTGTAAGAG	60
QY		
5485	GAAAACCTTGAATGCACACCTGCTTATTTTAACTTATTGACATACAGTTGTGTAAGAG	5544
Db		
61	TTAAAAATCTTACTTCATGATTCATTTATATTTTATATTTATTTTGGCTCAATGATTT	120
QY		
5545	TTAAAAATCTTACTTCATGATTCATTTATATTTTATATTTTGGTCAATGATTT	5604
Db		

Qy	121	TTTATTAAACATGATTTCTCTTTCTGATATATTTGAAATGGAGTCTCAAGGCTTCATAAATT	180
Db	5605	TTTATTAAACATGATTTCTCTTTCTGATATATTTGAAATGGAGTCTCAAGGCTTCATAAATT	5664
Qy	181	TATAACCTTTAGAAATGATTTCTAAATAACAAACGTATGTAATTTGAACATTCAGAGTAATGGTG	240
Db	5665	TATAACCTTTAGAAATGATTTCTAAATAACAAACGTATGTAATTTGAACATTCAGAGTAATGGTG	5724
Qy	241	CTACGAAGCCATTCTCTCGATTTTGTAGTAAACCTTTTATGACAGCAAAATTTGCTTCTGGC	300
Db	5725	CTACGAAGCCATTCTCTCGATTTTGTAGTAAACCTTTTATGACAGCAAAATTTGCTTCTGGC	5784
Qy	301	TCACCTTTCAATCAGTTAAATAAATGATAAATAATTTTGGAGCTGTGGAAGATAAAATACC	360
Db	5785	TCACCTTTCAATCAGTTAAATAAATGATAAATAATTTTGGAGCTGTGGAAGATAAAATACC	5844
Qy	361	AAATATAAATAATATAAAAGTGATTTTATGAAAGTTTAAAAATAAAAAATCAGTATGATGGAA	420
Db	5845	AAATATAAATAATATAAAAGTGATTTTATGAAAGTTTAAAAATAAAAAATCAGTATGATGGAA	5904
Qy	421	TAAACTTTGAGAGTCAGAAGTTATCCCATACATCTCTGTAATCAACTAATTTCTCACAAAGG	480
Db	5905	TAAACTTTGAGAGTCAGAAGTTATCCCATACATCTCTGTAATCAACTAATTTCTCACAAAGG	5964
Qy	481	TGTAAGGACCATTCATGGAGAAAA	505
Db	5965	TGTGAAGGACCATTCATGGAGAAAA	5989

```

RESULT 2
US-09-966-880A-35
; Sequence 35, Application US/09966880A
; Patent No. US20020164743A1
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Muramatsu, Masanichi
; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
; FILE REFERENCE: 08501-088001
; CURRENT APPLICATION NUMBER: US/09/966;880A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: PCT/JPC0/01918
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: JP 11-371382
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: JP 11-178999
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: JP 11-87192
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 11204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-966-880A-35

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Query Match	100.0%	Score 505;	DB 9;	Length 11204;
Best Local Similarity	100.0%;	Pred. No. 8.3e-82;		
Matches 505;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	GAAACCTTGAATGCACAACTGCTCTTATTTTATCTTATTGTACATAAGTTTGTAAAGAG	60		
DB				
10700	GAAACCTTGAATGCACAACTGCTCTTATTTTAACTCTTATTGTACATAAGTTTGTAAAGAG	10759		
QY 61	TTAAAAATCTGTACTTTCATGCTATTCTATTTATATTTTATATTTTGGCTCTAAATGATT	120		
DB				
10760	TTAAAAATCTGTACTTTCATGCTATTCTATTTATATTTTATATTTTGGCTCTAAATGATT	10819		
QY 121	TTTATTAAACATGATTTTCCCTTTTCGTATATATTGAAATGGAGTCTCAAAGCTTCATAAAATT	180		
DB				
10820	TTTATTAAACATGATTTTCCCTTTTCGTATATATTGAAATGGAGTCTCAAAGCTTCATAAAATT	10879		

Qy	181	TATACTTTAGAAATGATCTCTAATAACAACGTAATGTAATTGTAAACATTGCGATATGGTG	240
Db	10880	TATACTTTTAGAAATGATCTCTAATAACAACGTAATGTAATTGTAAACATTGCGATATGGTG	10939
Qy	241	CTACGAAGCCATTCTCTTGGATTTTATGAACTTTTATGACAGCAAAATTTGCTTCTGGC	300
Db	10940	CTACGAAGCCATTCTCTTGGATTTTATGAACTTTTATGACAGCAAAATTTGCTTCTGGC	10999
Qy	301	TCACTTTCAATCAGTTTAAATAATGATAAATAATTTTGGAACTGTGGAATATAAATACC	360
Db	11000	TCACTTTCAATCAGTTTAAATAATGATAAATAATTTTGGAACTGTGGAATATAAATACC	11059
Qy	361	AAATAAAATAATATAAAAGTGATTTATATGAGTTTAAATAATAAAATCAGTATGATGAA	420
Db	11060	AAATAAAATAATATAAAAGTGATTTATATGAGTTTAAATAATAAAATCAGTATGATGAA	11119
Qy	421	TAACTTGGAGTCCAGAGTATCCCATACATCTGTAATCAACTAAATTTCTCCACAGGG	480
Db	11120	TAACTTGGAGTCCAGAGTATCCCATACATCTGTAATCAACTAAATTTCTCCACAGGG	11179
Qy	481	TGTAAGGACCATTCAATGGAGAAA	505
Db	11180	TGTAAGGACCATTCAATGGAGAAA	11204

```

RESULT 3
US-09-966-880A-7
; Sequence 7, Application US/09966880A
; Patent No. US2002016473A1
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Muramatsu, Masamichi
; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
; FILE REFERENCE: 08501-088001
; CURRENT APPLICATION NUMBER: US/09/966,880A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: PCT/JP00/01918
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: JP 11-371382
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: JP 11-178999
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: JP 11-87192
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2818
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)...(673)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(79)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (677)...(2818)
; US-09-966-880A-7

```

	Query Match	85.0%	Score 429.4;	DB 9;	Length 2818;
	Best Local Similarity	99.8%;	Pred. No. 2.5e-68;		
	Matches 430;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	GAAACTTGATGACCAAC	GTCTTATTTTAAATCTTATTGTACATAAGTTGTGAAAGAG	60	
Db	2367	GAAACTTGATGACCAAC	GTCTTATTTTAAATCTTATTGTACATAAGTTGTGAAAGAG	2426	
Qy	61	TTAAAAATCTGCTACTTCATGCTATTCATTTATATTTTATTTTTCGCGCTCAATCATTT		120	
Db	2427	TTAAAAATCTGCTACTTCATGCTATTCATTTATATTTTATTTTTCGCGCTCAATCATTT		2486	

QY 121 TTTATTACATGATTTCTTTCTGATATATTGAAATGGAGTCTCAAGCTTCATAAATT 180
 DB 2487 TTTATTACATGATTTCTTTCTGATATATTGAAATGGAGTCTCAAGCTTCATAAATT 2546
 QY 181 TATAACTTTAGAAATGATTTCTTAATAACACGATGTAATTTGTAACATTTGCAGTAATGGTG 240
 DB 2547 TATAACTTTAGAAATGATTTCTTAATAACACGATGTAATTTGTAACATTTGCAGTAATGGTG 2606
 QY 241 CTACGAAGCCATTTCTCTGATTTTCTAGTAACCTTTTATGACACGAAATTTGCTTCGGC 300
 DB 2607 CTACGAAGCCATTTCTCTGATTTTCTAGTAACCTTTTATGACACGAAATTTGCTTCGGC 2666
 QY 301 TCACCTTTCAATCAGTTAAATAAATGATAAATAAATTTTGGAGCTGTGAAGATAAAATACC 360
 DB 2667 TCACCTTTCAATCAGTTAAATAAATGATAAATAAATTTTGGAGCTGTGAAGATAAAATACC 2726
 QY 361 AAATAAAATATATAAAGTGAATTTATATGAAGTTAAATAAATAAATCAGTATGATGAA 420
 DB 2727 AAATAAAATATATAAAGTGAATTTATATGAAGTTAAATAAATAAATCAGTATGATGAA 2786
 QY 421 TAAACTTGGGA 431
 DB 2787 TAAACTTGGAA 2797

RESULT 4
 US-09-966-880A-15
 ; Sequence 15, Application US/09966880A
 ; Patent No. US20020164743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Honjo, Tasuku
 ; APPLICANT: Muramatsu, Masamichi
 ; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
 ; FILE REFERENCE: 06501-088001
 ; CURRENT APPLICATION NUMBER: US/09/966, 880A
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: PCT/JP00/01918
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: JP 11-371382
 ; PRIOR FILING DATE: 1999-12-27
 ; PRIOR APPLICATION NUMBER: JP 11-178999
 ; PRIOR FILING DATE: 1999-06-24
 ; PRIOR APPLICATION NUMBER: JP 11-87192
 ; PRIOR FILING DATE: 1999-03-29
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 2172
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-966-880A-15

Query Match 84.8%; Score 428; DB 9; Length 2172;
 Best Local Similarity 100.0%; Pred. No. 4.1e-68;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAAACTTGAATGCACAACTGCTTATTTTAACTTTATGACATAGCTTTGTAAGAG 60
 DB 1745 GAAAACTTGAATGCACAACTGCTTATTTTAACTTTATGACATAGCTTTGTAAGAG 1804
 QY 61 TTAAAAATTTGTTACTTCATGATTCATTTATATTTTATTTTATTTTGGCTCTAATGATTT 120
 DB 1805 TTAAAAATTTGTTACTTCATGATTCATTTATATTTTATTTTATTTTGGCTCTAATGATTT 1864
 QY 121 TTTATTACATGATTTCTTTCTGATATATTGAAATGGAGTCTCAAGCTTCATAAATT 180
 DB 1865 TTTATTACATGATTTCTTTCTGATATATTGAAATGGAGTCTCAAGCTTCATAAATT 1924
 QY 181 TATAACTTTAGAAATGATTTCTTAATAACACGATGTAATTTGTAACATTTGCAGTAATGGTG 240
 DB 1925 TATAACTTTAGAAATGATTTCTTAATAACACGATGTAATTTGTAACATTTGCAGTAATGGTG 1984
 QY 241 CTACGAAGCCATTTCTCTGATTTTCTAGTAACCTTTTATGACACGAAATTTGCTTCGGC 300

DB 1985 CTACGAAGCCATTTCTTTCTGATATATTGAAATGGAGTCTCAAGCTTCATAAATT 2044
 QY 301 TCACCTTTCAATCAGTTAAATAAATGATAAATAAATTTTGGAGCTGTGAAGATAAAATACC 360
 DB 2045 TCACCTTTCAATCAGTTAAATAAATGATAAATAAATTTTGGAGCTGTGAAGATAAAATACC 2104
 QY 361 AAATAAAATATATAAAGTGAATTTATATGAAGTTAAATAAATAAATCAGTATGATGAA 420
 DB 2105 AAATAAAATATATAAAGTGAATTTATATGAAGTTAAATAAATAAATCAGTATGATGAA 2164
 QY 421 TAAACTTGG 428
 DB 2165 TAAACTTGG 2172

RESULT 5
 US-10-311-455-1997
 ; Sequence 1997, Application US/10311455
 ; Publication No. US20030143606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OLEK, Alexander
 ; APPLICANT: FIEPENBROCK, Christian
 ; APPLICANT: BERLIN, Kurt
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete
 ; TITLE OF INVENTION: cytosine methylation
 ; FILE REFERENCE: 5013.1014
 ; CURRENT APPLICATION NUMBER: US/10/311,455
 ; PRIOR FILING DATE: 2002-12-16
 ; PRIOR APPLICATION NUMBER: PCT/EP01/07537
 ; PRIOR FILING DATE: 2001-07-02
 ; PRIOR APPLICATION NUMBER: DE 10032529.7
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: DE 10043826.1
 ; PRIOR FILING DATE: 2000-09-01
 ; NUMBER OF SEQ ID NOS: 2424
 ; SEQ ID NO 1997
 ; LENGTH: 6375
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-311-455-1997

Query Match 14.2%; Score 71.6; DB 14; Length 6375;
 Best Local Similarity 48.3%; Pred. No. 0.0019;
 Matches 200; Conservative 0; Mismatches 214; Indels 0; Gaps 0;
 QY 2 AAAAACTTGAATGCACAACTGCTTATTTTAACTTTATGACATAGCTTTGTAAGAGT 61
 DB 3164 AAAAACTTGAATGCACAACTGCTTATTTTAACTTTATGACATAGCTTTGTAAGAGT 3223
 QY 62 TAAAAATTTGTTACTTCATGATTCATTTATATTTTATATTTTTCGGCTCTAATGATTTT 121
 DB 3224 TAAAAATTTGTTACTTCATGATTCATTTATATTTTATATTTTTCGGCTCTAATGATTTT 3283
 QY 122 TTATTAACATGATTTCTTTCTGATATATTGAAATGGAGTCTCAAGCTTCATAAATT 181
 DB 3284 TTAAATGTTGTTTAAATTAATGTTTAAATGTTTAAATGTTTAAATTAATTTAGTAAT 3343
 QY 182 ATAACCTTTGAATGATTTCTTAATAACACGATGTAATTTGTAACATTTGCAGTAATGGTGC 241
 DB 3344 TTTTATTTTGAATGATTTAGAAAAGGAAATATTATGTTTGGTAAATGTTTATATTTTAA 3403
 QY 242 TAGGAAGCCATTTCTTTCTGATATTTTATGTAACCTTTTATGACACGAAATTTGCTTCGGCT 301
 DB 3404 AATAAATTTGTGGAAGAAGATATTATGTAAGTGAATGAGTAGTAGTAACGATTTGTTTATT 3463
 QY 302 CACTTTCAATCAGTTAAATAAATGATAAATAAATTTTGGAGCTGTGAAGATAAAATACC 361
 DB 3464 ATTTTAAATTTAATAATTTATTTTATGAGTTTTTTTAAAGTATTGAGATAATTTTAA 3523
 QY 362 AATAAATAATATAAAGTGAATTTATATGAACTTAAATAAATAAATCAGTATGA 415

Db 3524 TTTATTAAAAATAAATGTAATTATTAAGTATTTAGGGTTGATATTCTTTTGA 3577

RESULT 6
US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MGC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312.841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match 13.0%; Score 65.4; DB 14; Length 3673778;
Best Local Similarity 46.9%; Pred. No. 0.21; 231; Indels 0; Gaps 0;
Matches 204; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

Qy 42 ACATAAGTTGTGTAAGAGATTAAAAATGTTTACTTCATGATTTCATTTATATTTATATT 101
Db 730168 ATATTATAAAAAAATACTTAAACAAAAATTATAAAATATCTTATATTTCTCTCACTTA 730109
Qy 102 ATTTTGGTCTAATGATTTTTTATTACATGATTTCTTTCTGATATATGAAATGGAG 161
Db 730108 TCATCATCTCAAAATAAACTTCTTAATTAATATTTATAATAATTTATATCCCAATAA 730049
Qy 162 TCTCAAGCTTCATAAAATTTTATACTTTAGAAATGATCTTAATAACCAACGATGTAATTG 221
Db 730048 AAAATAACATAAATTAACAATAAACAATTAAACCAACTTCATATAACAAAAATCCCAACC 729989
Qy 222 TAACATTCGAGTAATGTGCTACGAGCCATTTCTTGATTTTCTAGTAACTTTTATGA 281
Db 729988 ATAATATCAATCAATCTCTTAAATATCAAAACTCTCTATTTCTTTCTTTAAATTCAC 729929
Qy 282 CAGCAAAATTTGCTTCTGGCTCACCTTCATCAGTAAATAAATGATAAATAATTTTGGAA 341
Db 729928 ATTTAAAAATATCTACGTCCCATTTAAAAAATAAATAAATAATTAACACATAATTTAA 729869
Qy 342 GCTGTGAGATAAATAACCAATAAATAATAATAAAGTGATTTATATGAGTTAAATA 401
Db 729868 CATAAAAATACAAATATCAATATAATAATAATAATAATAATAATAATAATAATAATA 729809
Qy 402 AAAAATCAGTATGATGGAATAAATCTCAGAGTCGAGAGTCCAGAGTTATCCCATACATCTGTAATC 461
Db 729808 TAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 729749
Qy 462 AACTAATTTCTCACA 476
Db 729748 AATAATAATATAA 729734

RESULT 7
US-09-796-692-8856/c
; Sequence 8856, Application US/09796692
; Publication No. US20020195362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8856
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (443)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (463)
; OTHER INFORMATION: n=A,T,C or G
US-10-040-862-8856

Query Match 12.7%; Score 64; DB 14; Length 469;
Best Local Similarity 65.3%; Pred. No. 0.019; Indels 0; Gaps 0;
Matches 94; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 361 AATAAATAATATAAAGTGTATATGAAGTTAAATAAAAAATCAGTATGATGAA 420
Db 278 AACTAAATAACCAAAACAGGCTGGTACTGGCATAAAGATAACATTAGACCAATAGAA 219
QY 421 TAACTTCAGAGTCGAGAGTATCCCATACATCTGTAATCAACTAATTTCTCACAAGG 480
Db 218 TAGAATTGAGAGTCGAGAGTAACTCATACATATCTTCAATTGAATTTCTCACAAGG 159
QY 481 TGTAGGACCATTCATCGAGAAA 504
Db 158 TGTACGAGCATACCATCAGAAA 135

RESULT 9
US-10-057-475B-8856/c
; Sequence 8856, Application US/10057475B
; Publication No. US2004002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne

; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Thera
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8856
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(469)
; OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-8856

Query Match 12.7%; Score 64; DB 15; Length 469;
Best Local Similarity 65.3%; Pred. No. 0.019; Indels 0; Gaps 0;
Matches 94; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 361 AATAAATAATATAAAGTGTATATGAAGTTAAATAAAAAATCAGTATGATGAA 420
Db 278 AACTAAATAACCAAAACAGGCTGGTACTGGCATAAAGATAACATTAGACCAATAGAA 219
QY 421 TAACTTCAGAGTCGAGAGTATCCCATACATCTGTAATCAACTAATTTCTCACAAGG 480
Db 218 TAGAATTGAGAGTCGAGAGTAACTCATACATATCTTCAATTGAATTTCTCACAAGG 159
QY 481 TGTAGGACCATTCATCGAGAAA 504
Db 158 TGTACGAGCATACCATCAGAAA 135

RESULT 10
US-10-154-884B-8856/c
; Sequence 8856, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Better, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Thera
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 8856
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(469)
; OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-8856

Query Match 12.7%; Score 64; DB 15; Length 469;
Best Local Similarity 65.3%; Pred. No. 0.019;
Matches 94; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 361 AAATAAAATAATAAAGTGATTATATGAACTTAAATAAATAAATAAATCAGTATGATGAA 420
Db 278 AACTAAATAACCAAAACAGGCTGGTACTGGCATAAAGATAAATTTAGACCAATAGAA 219

QY 421 TAAACTTGAGTCCAGAGTTATCCATACATCTGTATCAACTAATTTCTCACAAGG 480
Db 218 TAGAATTGAGCTGCAGAGTAACTCATACATATCTTCAATTGAATTTCTACAAGG 159

QY 481 TGTAAGGACCAATCAATGGAGAA 504
Db 158 TGTGAGGACCAATCAATGGAGAA 135

RESULT 11
US-10-001-843-11
; Sequence 11, Application US/10001843
; Publication No. US20020132255A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
; FILE REFERENCE: DEX-0267
; CURRENT APPLICATION NUMBER: US/10/001,843
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,992
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-843-11

Query Match 12.7%; Score 64; DB 13; Length 1925;
Best Local Similarity 65.3%; Pred. No. 0.03;
Matches 94; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 361 AAATAAAATAATAAAGTGATTATATGAACTTAAATAAATAAATAAATCAGTATGATGAA 420
Db 972 AACTAAATAACCAAAACAGGCTGGTACTGGCATAAAGATAAATTTAGACCAATAGAA 1031

QY 421 TAAACTTGAGTCCAGAGTTATCCATACATCTGTATCAACTAATTTCTCACAAGG 480
Db 1032 TAGAATTGAGCTGCAGAGTAACTCATACATATCTTCAATTGAATTTCTACAAGG 1091

QY 481 TGTAAGGACCAATCAATGGAGAA 504
Db 1092 TGTGAGGACCAATCAATGGAGAA 1115

RESULT 12
US-09-835-232-6
; Sequence 6, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(180216)
; OTHER INFORMATION: n = A,T,C or G
US-09-835-232-6

Query Match 12.7%; Score 64; DB 9; Length 180216;
Best Local Similarity 56.6%; Pred. No. 0.14;
Matches 138; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

QY 262 TTTTGTAGTAACTTTTATGACAGCAAAATTTGCTTCTGCTCACTTTCAATCAGTTAAATA 321
Db 56089 TTATTTGAACCAACCAAAACCAATAGCCCAAGTAATCTTGATCAAAAGACAAA 56148

QY 322 AATGATAAATAATTTTGGAGCTGTGAAGATAAATAACCA-ATAAATAATATAAAGT 380
Db 56149 CCAGAGAAATCACACAACCCAGATTGAAAATATATTACAAAGCTATAGTAATCAAAACAG 56208

QY 381 GATTTATATCAAGTTAAATATAAATAAATCAGTATGATGGAATAAATTTGAGAGTCCAGAAG 440
Db 56209 TATGTTGTTGGCATAAATAATAGACATGTCAGTGGGATAAGATGGAGTCCAGAA 56268

QY 441 TTATCCCATACATCTGTATCAACTAATTTCTCACAAGGCTGAAGACCAATTTCAATGGA 500
Db 56269 TAAACCCAGCTAACTACAGTCAATTTGATTGCAACAAAGGTGTCAAGAACACACAGAATGGG 56328

QY 501 GAAA 504
Db 56329 GAAA 56332

RESULT 13
US-10-308-485-6
; Sequence 6, Application US/10308485
; Publication No. US20030170683A1

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; GENERAL INFORMATION:
; APPLICANT: Leder, Phillip
; APPLICANT: Leder, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(180216)
; OTHER INFORMATION: n = A,T,C or G
US-10-308-485-6

Query Match      12.7%; Score 64; DB 14; Length 180216;
Best Local Similarity 56.6%; Pred. No. 0.14;
Matches 138; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

QY 262 TTTTATGTAACCTTTTATGACGACAAATTTCTTCTGGCTCACTTTCAATCAGTTAAATA 321
DB 56089 TTATTTGAACCAACAAAAAATAGCCAAAGTAATCTTGATCAAAAAGGACAAAA 56148

QY 322 AATGATAAATAATTTTGGAGCTGTGAAGATAAAATACCAA-ATAAATAATATAAAGT 380
DB 56149 CCAGAGAAATCACACACACAGATTTGAAATATATTACAAAGCTAGTAATCAAAAACAG 56208

QY 381 GATTTATATGAGTTAAATAAATAATCAGTATGATGGAATAAATCTTGAGAGTCCAGAG 440
DB 56209 TATGGTGGTGCATAAAATAGACACATCTCCAGTGGATAGATGGAGTCCAGAAA 56268

QY 441 TTATCCATACATCTGTAATCACTAATTTCTCAGAGGTTGAAGGACCATTCATGGA 500
DB 56269 TAAACCCAGCTAACTACAGTCAATGTTTGGCAACAAAGGTGTGCAAGAACACAGAAATGGG 56328

QY 501 GAAA 504
DB 56329 GAAA 56332

RESULT 14
US-10-027-632-311405
; Sequence 311405, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67377
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-67377

Query Match      12.2%; Score 61.8; DB 15; Length 505;
Best Local Similarity 62.7%; Pred. No. 0.048;
Matches 96; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 352 TAAATACCAATAAATAATAATAAAGTGAATTTATATGAAGTTAAATAAATAAATCAGT 411
DB 238 TACAATGCGATAGCAATCAATCAAGACAGTGTGCTACTGCGATAAAGATAGAAATACAAA 297

QY 412 ATGATGGAATAAATCTGAGAGTCCAGAGTTATCCCATACATCTGTAATCAACTAATTC 471
DB 298 TCAATGGAATGGAATGAGAGTCTGGAAGTATATCCATACATCTGTGCTCACTGAGTTT 357

QY 472 TCACAAGGGTGAAGGACCATTCATCGGAGAAA 504
DB 351 TGAATAAGGCTCCAGGACCGTTCAATGGGAAA 383

RESULT 15
US-10-027-632-67377
; Sequence 67377, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67377
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-67377

Query Match      12.2%; Score 61.8; DB 15; Length 505;
Best Local Similarity 62.7%; Pred. No. 0.048;
Matches 96; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 352 TAAATACCAATAAATAATAATAAAGTGAATTTATATGAAGTTAAATAAATAAATCAGT 411
DB 238 TACAATGCGATAGCAATCAATCAAGACAGTGTGCTACTGCGATAAAGATAGAAATACAAA 297

QY 412 ATGATGGAATAAATCTGAGAGTCCAGAGTTATCCCATACATCTGTAATCAACTAATTC 471
DB 298 TCAATGGAATGGAATGAGAGTCTGGAAGTATATCCATACATCTGTGCTCACTGAGTTT 357

QY 472 TCACAAGGGTGAAGGACCATTCATCGGAGAAA 504
DB 351 TGAATAAGGCTCCAGGACCGTTCAATGGGAAA 383
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Db 358 TGAAGAGGCTCCAGGACCGTTCAATGGGAAA 390

Search completed: March 4, 2004, 19:00:27
Job time : 258.462 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:54:45 ; Search time 1974.73 Seconds
(without alignments)
7636.686 Million cell updates/sec

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Perfect score: 505
Sequence: 1 gaaacttgatgcacact.....ggaccattcaatggagaaaa 505

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513299 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
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8: em_hic:*
9: gb_est1:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pig:*
27: em_gss_vrl:*
28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	286	56.6	442	9	AI016902 ou3id03.x
C 2	256	50.7	268	9	AA879422 oJ9ic11.s
C 3	78.2	15.5	1201	13	BX439779 BX439779
C 4	76	15.0	1013	29	AL412260 T7 end of

C 5	75.6	15.0	1201	9	AL532464
C 6	75.6	15.0	1201	13	BX424465
C 7	75.2	14.9	1200	13	BX437758
C 8	74.8	14.8	1201	9	AL536104
C 9	74.6	14.8	1101	29	CNS00021J
C 10	73.6	14.6	1101	29	CNS000F1G
C 11	73.4	14.5	1056	13	BX415058
C 12	73.4	14.5	1101	29	CNS000RVL
C 13	72.8	14.4	1064	13	BX361825
C 14	72.6	14.4	1056	13	BX415058
C 15	72.6	14.4	1101	29	CNS000R07
C 16	72.6	14.4	1201	13	BX424465
C 17	72.2	14.3	1098	13	BX377526
C 18	72	14.3	1200	13	BX437739
C 19	71.6	14.2	1133	13	BX444099
C 20	71.2	14.1	1201	9	AL536104
C 21	71	14.1	843	29	CNS000CS1
C 22	70.4	13.9	887	13	BX441520
C 23	70.4	13.9	1043	29	CNS0145P
C 24	70.4	13.9	1201	13	BX439779
C 25	70.2	13.9	1200	13	BX436510
C 26	70	13.9	793	28	BZ882481
C 27	70	13.9	1200	13	BX415878
C 28	70	13.9	1200	13	BX437739
C 29	70	13.9	1201	13	BX336467
C 30	69.8	13.8	1101	29	CNS0003DQ
C 31	69.6	13.8	483	14	CA389449
C 32	69.6	13.8	899	13	BX453223
C 33	69.6	13.8	1061	13	BX437039
C 34	69.6	13.8	1200	13	BX436510
C 35	69.4	13.7	843	29	CNS00031L
C 36	69.4	13.7	945	29	CNS040DOK
C 37	69.4	13.7	1201	13	BX446296
C 38	69.2	13.7	1098	13	BX377526
C 39	69.2	13.7	1200	13	BX415878
C 40	68.8	13.6	691	13	BX436603
C 41	68.6	13.6	1101	29	CNS000EVL
C 42	68.6	13.6	1563	28	CC206942
C 43	68.4	13.5	734	29	CNS010MP
C 44	68.4	13.5	964	13	BX341256
C 45	68.4	13.5	1101	29	CNS000EQL

ALIGNMENTS

RESULT 1
AI016902/c
LOCUS AI016902 442 bp mRNA linear EST 17-MAR-1999
DEFINITION ou3id03.x1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone
IMAGE:1627877 3', mRNA sequence.
ACCESSION AI016902
VERSION AI016902.1 GI:3231238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 442)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 426 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 433.
Location/Qualifiers
1. .442
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1627877"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
```

ORIGIN

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Query Match      56.6%; Score 286; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.5e-32;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAACTTGAATGACCAACTGCTTATTTTAACTTATTTGATACATAAGTTTGTAAAGAG 60
DB 286 GAAACTTGAATGACCAACTGCTTATTTTAACTTATTTGATACATAAGTTTGTAAAGAG 227
QY 61 TTTAAATTTGATCTTCAATGATTCATTTATTTATTTATTTTTCGCTTAATGATTT 120
DB 226 TTTAAATTTGATCTTCAATGATTCATTTATTTATTTATTTTTCGCTTAATGATTT 167
QY 121 TTTATTAACATGATTTCTTCTTGATATATTGAATGGAGTCTCAAGCTTCATAAAT 180
DB 166 TTTATTAACATGATTTCTTCTTGATATATTGAATGGAGTCTCAAGCTTCATAAAT 107
QY 181 TATAACTTTAGAAATGATTTCAATAACACGATGTAATTTGTAACATTCAGTAATGGTG 240
DB 106 TATAACTTTAGAAATGATTTCAATAACACGATGTAATTTGTAACATTCAGTAATGGTG 47
QY 241 CTACGAAGCCATTTCTCTTGATTTTATGTAACATTTTATGACAGCA 286
DB 46 CTACGAAGCCATTTCTCTTGATTTTATGTAACATTTTATGACAGCA 1
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RESULT 2
AA879422/c
LOCUS      AA879422      268 bp      mRNA      linear      EST 19-MAY-1998
DEFINITION oJ91c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1505684 3', mRNA sequence.
ACCESSION  AA879422
VERSION    AA879422
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 268)
AUTHORS   NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL   Tumor Gene Index
COMMENT   Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 685 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 252.
Location/Qualifiers
1..268
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone="IMAGE:1505684"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
```

ORIGIN

```
Query Match      50.7%; Score 256; DB 9; Length 268;
Best Local Similarity 99.6%; Pred. No. 7.4e-28;
Matches 267; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 152 TGAATGAGAGTCTCAAGCTTCATAAAATTTATACTTTAGAAATGATTTCTTAATAACAAG 211
DB 268 TGAATGAGAGTCTCAAGCTTCATAAAATTTATACTTTAGAAATGATTTCTTAATAACAAG 209
QY 212 TATGTAATTTGTAACATTCAGTAATGGTGTACGAAGCCATTTCTTGAATTTTAGTAA 271
DB 208 TATGTAATTTGTAACATTCAGTAATGGTGTACGAAGCCATTTCTTGAATTTTAGTAA 149
QY 272 ACTTTTA-TGACAGCAAAATTTGCTTCTGGCTCACCTTCATTCAGTAAATAAATGATATAA 330
DB 148 ACTTTTATGACAGCAAAATTTGCTTCTGGCTCACCTTCATTCAGTAAATAAATGATATAA 89
QY 331 TAAATTTGGAAGCTGTGAAGATAAAATACCAATAAATAATAATAAATGATTTATATG 390
DB 88 TAAATTTGGAAGCTGTGAAGATAAAATACCAATAAATAATAATAAATGATTTATATG 29
QY 391 AAGTTAAATAAATAAATCAGTATGATGG 418
DB 28 AAGTTAAATAAATAAATCAGTATGATGG 1
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RESULT 3
BX439779
LOCUS      BX439779      1201 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION BX439779 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE014YF05
3-PRIME mRNA sequence.
ACCESSION  BX439779
VERSION    BX439779.1 GI:30771778
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1201)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3370.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE014CC03NP1&cluster=3370.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE014CC03NP1.
Location/Qualifiers
1..1201
/organism="Homo sapiens"
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[illegible][illegible]

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1200)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP008CA01QF1.
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1..1200
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP008YB01"
/tissue_type="THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 14.9%; Score 75.2; DB 13; Length 1200;
Best Local Similarity 34.6%; Pred. No. 0.032;
Matches 158; Conservative 91; Mismatches 202; Indels 5; Gaps 1;
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DB 937 TTYWTTWAAATWTTTTTATATAAAWTTTTTATTTTCWYTTTATTTTATTTT 878
QY 82 ATTCATTTATATTTATATTTTTCGCTCAATGATTTTTTATTAACATGATTTCCCTT 141
DB 877 ATTITTYTWTATATAAATAATATATTTTWTWTTTTTTTTTTTWTWAAWTTTTCW 818
QY 142 TCTGATATATGAATGGAGTCTCAAGCTTCATATAATTTATTAACATGATTTCT 201
DB 817 WNAATTTTTTTTAAWAAWTTTTTTTTHAATCTTTWTAATAAATAATWTTATAAAAAAHTCYT 758
QY 202 AATAACAAGCTATGTAATTTGAACATTCGAGTAATGCTGACGAAGCATTTCTCTGA 261
DB 757 CYYATATWTTTAAWATCYTCTMATATAAATAAATW-----TCTCTCTCTTCTWTT 703
QY 262 TTTTATGTAACCTTTTATGACGCAAAATTTGCTCTGCTCACTTTCAATCAGTTAATA 321
DB 702 TTWAAWATYTYMYTTCCTTWTAWAAWAAWMTATWTTAYTTCYWWAAACAAWAAAAA 643
QY 322 AATGATAAATAATTTTGAAGCTGTGAAGATAAATAACCAATAAATAATAATAAAGTG 381
DB 642 AAWAAAAAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 583
QY 382 ATTATATGAAGTAAAAATAAATAATCAATGATGGAATAAATACTTGAGAGTCCAGAAGT 441
DB 582 CTSTTTTTTAAWAAAAATAATATATWTTAAAAAATAAATAAATAAATAAATAAATAA 523
QY 442 TATCCATACATCTGTAATCAACTAATTTCTCACA 477
DB 522 WTTAAAAAAATCTTCYTTTWWAAWTTTTTTTTTTTWW 487
RESULT 8
AL536104 1201 bp mRNA linear EST 31-MAY-2003
LOCUS AL536104 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF022YC18 5-PRIME, mRNA sequence.
ACCESSION AL536104

AL536104.2 GI:13260974
EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:12799597.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF022BB09QP1.
FEATURES
source
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF022YC18"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
ORIGIN
Query Match 14.8%; Score 74.8; DB 9; Length 1201;
Best Local Similarity 33.1%; Pred. No. 0.036;
Matches 127; Conservative 86; Mismatches 171; Indels 0; Gaps 0;
QY 24 TTATTTTAACTTATTTGTACATAAGTTTGTAAAGAGTTTAAAGATTTGTTACTTCATGTAT 83
DB 775 TTTATRWATWATWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTW 834
QY 84 TCATTTATATTTTATTTATTTTTCGCTCAATGATTTTTTATTAACATGATTTCTCTTTC 143
DB 835 TAWAAAWTTTWTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 894
QY 144 TGATATATTCAAATGAGTCTCAAGCTTCATAAATTTATTAACATTTAGAAATGATTTCTAA 203
DB 895 TTTTATTTATTAATTTTATWAAWATTTTWWAAWATTTAGTAWAAWAAATATATAW 954
QY 204 TAACAAGTATGTAATTTGTAACATTTGCAATGCTGCTACGAAGCATTTCTCTGATTT 263
DB 955 TAWGRTAAATATWTTAAWAAWATTTATWTAATAAATAAATAAATAAATAAATAAATAA 1014
QY 264 TTTTATGTAACCTTTTATGACAGCAAAATTTGCTTCTGCTCACTTTCAATCAGTTTAAATAA 323
DB 1015 TTTTWTWTTWATWTTATWATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1074
QY 324 TGATAAATAAATTTTGAAGCTGTGAAGATAAATAAATAAATAAATAAATAAATAAATAA 383
DB 1075 WRTWTTTWTAAWAAWAAWATTTTWTWTAATAAATAAATAAATAAATAAATAAATAA 1134
QY 384 TTATATCAAGCTTAAATAAATAAAT 407
DB 1135 TATTATTATWATWTTTADAWDAT 1158
RESULT 9
CNS0021J/c 1101 bp DNA linear GSS 03-JUN-1999
LOCUS CNS0021J melanogaster genome survey sequence FET3 end of BAC #
DEFINITION Drosophila melanogaster library from Drosophila melanogaster (fruit
BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit


```

QY 386 ATATGAAGTTAAATAAATAAATCAGTAT 413
Db 707 AAAATAAATTAATTAATATAATAAAT 680

RESULT 11
BX415058 1056 bp mRNA linear EST 15-MAY-2003
LOCUS BX415058 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP004YG19
DEFINITION 3-PRIME, mRNA sequence.
ACCESSION BX415058
VERSION BX415058.1 GI:30767520
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/InvitrogenCorporation.1600
Faraday Avenue Genoscope sequence ID: CSOCAP004AD10NP1.
Location/Qualifiers
FEATURES
source
1..1056
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP004YG19"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched
double-strand cDNA was digested with NotI and cloned into
the NotI and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 14.5%; Score 73.4; DB 13; Length 1056;
Best Local Similarity 34.2%; Pred. No. 0.063;
Matches 163; Conservative 82; Mismatches 232; Indels 0; Gaps 0;

QY 2 AAAACTGATGCAACAGTCTTATTTTAACTTATGTCATCAAGTTGTAAGAGT 61
Db 531 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 590

QY 62 TAAAAATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 121
Db 591 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 650

QY 122 TTATTAACATGATTTCCCTTTCTGATATATTGAATGAGTCTCAAGCTTCATAAATTT 181
Db 651 KTTTTTATADWDATWAATAATATWTGTCAGWAAAAAAATKATAKTKTKTAAWAAA 710

QY 182 ATAACTTTAGATGATCTTATACACAGTATGTAATGTAACATTCGACGATGTCG 241
Db 711 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 770

QY 242 TACGAAGCATTCTCTGATTTTATGTAAGCTTTTATGACAGCAAAATTCGCTTCGCT 301
Db 771 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 830

QY 302 CACTTTCATCAATGATTAATGATTAATTAATTTTGAAGCTGTGAAGATAAATACCA 361
Db 831 WAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 890

QY 362 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 421

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Db 891 RWAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 950
QY 422 AAACCTTGAGAGTCCAGAGTTATCCATCATCTGTAATCAACTTAATTTCTCACAAG 478
Db 951 AAAAATTTTATAGGAGCGTTTAAATAAATAAATAAATAAATAAATAAATAAATAA 1007

RESULT 12
CNS00EVL/c 1101 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL069706
VERSION AL069706.1 GI:4949849
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
FEATURES
source
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29B23"
/clone_lib="RPCI-98"
/note="end : T7"

ORIGIN
Query Match 14.5%; Score 73.4; DB 29; Length 1101;
Best Local Similarity 39.3%; Pred. No. 0.061;
Matches 160; Conservative 69; Mismatches 175; Indels 3; Gaps 2;

QY 3 AAACCTTGAATGCAACACTGCTCTTATTTTAACTTATGTCATCAAGTTGTAAGAGT 62
Db 988 AWATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 929

QY 63 AAAAAATGTTACTTCATGATTCATTTATATTTATTTTGGCTCTAATGATTTT 122
Db 928 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 869

QY 123 TATTAACATGATTTCTCTTCTGATATATTGAAATGAGCTCTCAAGCTTCATAAATTTA 182
Db 868 WATTAATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 810

QY 183 TAACTTTAGAAATGATCTTAATAACACAGTATGTAATTTGTAACATTCGAGTAATGGTGT 242
Db 809 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 750

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 22:01:47 ; Search time 78 Seconds
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Title: US-09-966-880A-7_COPY_80_676

Perfect score: 597

Sequence: 1 atggacagcctcttgatgaa.....ttcgtaatttgggactttga 597

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 353258

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/2/ina/5B-COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A-COMB.seq:*
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- 5: /cgn2_6/ptodata/2/ina/PTCUS-COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	2.5	20	4	US-09-422-978-10030
C 2	14	2.3	20	2	US-08-651-692-1
C 3	14	2.3	20	2	US-08-651-692-2
C 4	13	2.2	18	3	US-09-357-072-30
C 5	13	2.2	19	4	US-09-018-125-9
C 6	13	2.2	19	4	US-09-495-052-4
C 7	13	2.2	20	1	US-08-171-718-3
C 8	13	2.2	20	3	US-08-882-501-5
C 9	13	2.2	20	3	US-08-478-087-3
C 10	13	2.2	20	3	US-09-418-641-46
C 11	13	2.2	20	3	US-09-280-803-41
C 12	13	2.2	20	4	US-09-861-159-78
C 13	13	2.2	20	4	US-09-679-299A-100
C 14	12	2.0	14	1	US-08-375-116A-122
C 15	12	2.0	15	1	US-07-962-569A-1
C 16	12	2.0	15	1	US-08-242-664-27
C 17	12	2.0	15	1	US-08-484-138-27
C 18	12	2.0	15	1	US-08-464-148-10
C 19	12	2.0	15	1	US-08-385-500-10
C 20	12	2.0	15	1	US-08-846-784-10
C 21	12	2.0	15	2	US-08-889-291-35
C 22	12	2.0	15	3	US-09-098-244-35
C 23	12	2.0	15	4	US-09-375-314-35
C 24	12	2.0	15	4	US-09-767-395-35
C 25	12	2.0	15	5	PTC-US95-06379-27
C 26	12	2.0	16	3	US-08-817-145-8
C 27	12	2.0	16	4	US-09-629-222A-41

ALIGNMENTS

RESULT 1

US-09-422-978-10030/c
; Sequence 10030, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET-020CPI

; CURRENT APPLICATION NUMBER: US/09/422,978

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 10030

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: primer_bind

; LOCATION: 1..20

; OTHER INFORMATION: downstream amplification primer 99-8910 for SEQ 2165, in comple

US-09-422-978-10030

Query Match

Best Local Similarity

Score 15; DB 4; Length 20;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Indels 0; Gaps 0;

Oy 24 GAGGAGTTCCTTTA 38

Db 15 GAGGAGTTCCTTTA 1

RESULT 2

US-08-651-692-1

; Sequence 1, Application US/08651692

; Patent No. 5856099

; GENERAL INFORMATION:

; APPLICANT: Loren Miraglia, Thomas Geiger,

; APPLICANT: Clarence Frank Bennett and Nicholas M. Dean

; TITLE OF INVENTION: Compositions and Methods for

; TITLE OF INVENTION: Modulating Type I Interleukin-1 Receptor Expression

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS: 42

; ADDRESSEE: Law Offices of Jane Massey Licata

STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,692
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-651-692-1

Query Match 2.3%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 GGCGTCGGCGGCT 386
Db 7 GGCGTCGGCGGCT 20

RESULT 3
US-08-651-692-2
Sequence 2, Application US/08651692
Patent No. 5856099
GENERAL INFORMATION:
APPLICANT: Loren Miraglia, Thomas Geiger,
APPLICANT: Clarence Frank Bennett and Nicholas M. Dean
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Modulating Type I Interleukin-1 Receptor Expression
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,692
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-651-692-2

Query Match 2.3%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 GGCGTCGGCGGCT 386
Db 2 GGCGTCGGCGGCT 15

RESULT 4
US-09-357-072-30/c
Sequence 30, Application US/09357072
Patent No. 6015712
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Brenda F. Baker
APPLICANT: Hong Zhang
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF PADD EXPRESSION
FILE REFERENCE: R1S-0027
CURRENT APPLICATION NUMBER: US/09/357,072
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 30
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-072-30

Query Match 2.2%; Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 CTGCACTTTGGTT 142
Db 14 CTGCACTTTGGTT 2

RESULT 5
US-09-018-125-9
Sequence 9, Application US/09018125A
Patent No. 6468983
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Kondo, Seiji
APPLICANT: Cowell, John K.
APPLICANT: Li, Guiying
APPLICANT: Torrence, Paul F.
TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES
TITLE OF INVENTION: EFFECTIVE TO TREAT TELOMERASE-EXPRESSING MALIGNANCIES
FILE REFERENCE: 8656-022
CURRENT APPLICATION NUMBER: US/09/018,125A
CURRENT FILING DATE: 1999-02-03
EARLIER APPLICATION NUMBER: 60/044,507
EARLIER FILING DATE: 1997-04-21

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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-018-125-9

Query Match          2.2%; Score 13; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CCGGGGTGCAAAAT 407
Db 3 CCGGGGTGCAAAAT 15

RESULT 6
US-09-495-052-4/c
; Sequence 4, Application US/09495052
; Patent No. 6479258
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES
; FILE REFERENCE: DIVER1460-11
; CURRENT APPLICATION NUMBER: US/09/495,052
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-09-495-052-4

Query Match          2.2%; Score 13; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 GTTCGTCTTCCA 520
Db 15 GTTCGTCTTCCA 3

RESULT 7
US-08-171-718-3
; Sequence 3, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-018-125-9

Query Match          2.2%; Score 13; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CCGGGGTGCAAAAT 407
Db 3 CCGGGGTGCAAAAT 15

RESULT 6
US-09-495-052-4/c
; Sequence 4, Application US/09495052
; Patent No. 6479258
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES
; FILE REFERENCE: DIVER1460-11
; CURRENT APPLICATION NUMBER: US/09/495,052
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-09-495-052-4

Query Match          2.2%; Score 13; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 GTTCGTCTTCCA 520
Db 15 GTTCGTCTTCCA 3

RESULT 7
US-08-171-718-3
; Sequence 3, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-171-718-3

Query Match          2.2%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 ACATCCTTTTCAC 130
Db 8 ACATCCTTTTCAC 20

RESULT 8
US-08-882-501-5/c
; Sequence 5, Application US/08882501
; Patent No. 6054269
; GENERAL INFORMATION:
; APPLICANT: GARNIER, Fabien
; APPLICANT: GERBAUD, Guy
; APPLICANT: GALIMAND, Marc
; APPLICANT: COURVALIN, Patrice
; APPLICANT: DUKTA-MALEN, Sylvie
; APPLICANT: CHARLES, Murielle
; APPLICANT: EVERS, Stefan
; APPLICANT: CASADEWALL, Barbara
; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR
; TITLE OF INVENTION: DETECTING ENTEROCOCCI AND STREPTOCOCCI BACTERIAL STRAINS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882.501
; FILING DATE: 25-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDowell, Leslie A.
; REGISTRATION NUMBER: 34,872
; REFERENCE/DOCKET NUMBER: 03495.0155-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-882-501-5

Query Match      2.2%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      335 GCCTCTACTTCTG 347
Db      15 GCCTCTACTTCTG 3

RESULT 9
US-08-478-087-3
; Sequence 3, Application US/08478087
; Patent No. 6077685
; GENERAL INFORMATION:
; APPLICANT: Trofater, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,087
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,718
; FILING DATE: 22-DEC-1993
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
```

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; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-478-087-3

Query Match      2.2%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      116 ACATCCTTTTTCAC 130
Db      8 ACATCCTTTTTCAC 20

RESULT 10
US-09-418-641-46/c
; Sequence 46, Application US/09418641A
; Patent No. 6124133
; GENERAL INFORMATION:
; APPLICANT: Jennifer K. Taylor
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF FRA-1 EXPRESSION
; FILE REFERENCE: RTS-0105
; CURRENT APPLICATION NUMBER: US/09/418,641A
; CURRENT FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-418-641-46

Query Match      2.2%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GAACCGGAGGAAG 30
Db      13 GAACCGGAGGAAG 1

RESULT 11
US-09-280-805-41/c
; Sequence 41, Application US/09280805
; Patent No. 6184212
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
; APPLICANT: Graham, Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 271
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
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RESULT 15
US-07-962-569A-1
; Sequence 1, Application US/07962569A
: Patent No. 5391497

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RESULT 13
US-09-679-299A-100
; Sequence 100, Application US/09679299A
; Patent No. 6566135
; GENERAL INFORMATION:
; APPLICANT: Vickie L. Brown-Driver
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 6 EXPRESSION
; FILE REFERENCE: RTS-0187
; CURRENT APPLICATION NUMBER: US/09/679,299A
; CURRENT FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 164

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GENERAL INFORMATION:
APPLICANT: MENON, RAVI S.
APPLICANT: JEFFERS, KATHLEEN F.
APPLICANT: CHANG, YING-FON
APPLICANT: HAM, RICHARD G.
TITLE OF INVENTION: HUMAN K-CASEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH. D.
STREET: 11545 W. BERNARDO COURT, STE. 302
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92127
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/962,569A
FILING DATE: 19921013
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 920224.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 451-1120
TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..15
US-07-962-569A-1

Query Match 2.0%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 16
US-08-242-664-27/c
Sequence 27, Application US/08242664
Patent No. 5571937
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-138-27

Query Match 2.0%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: MENON, RAVI S.
APPLICANT: JEFFERS, KATHLEEN F.
APPLICANT: CHANG, YING-FON
APPLICANT: HAM, RICHARD G.
TITLE OF INVENTION: HUMAN K-CASEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH. D.
STREET: 11545 W. BERNARDO COURT, STE. 302
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92127
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/962,569A
FILING DATE: 19921013
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 920224.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 451-1120
TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..15
US-07-962-569A-1

Query Match 2.0%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 16
US-08-242-664-27/c
Sequence 27, Application US/08242664
Patent No. 5571937
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-138-27

Query Match 2.0%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCTC 186
13 TTGCTCTTCTC 2

RESULT 18
US-08-464-148-10
; Sequence 10, Application US/08464148
; Patent No. 5710026
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,148
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/385,500
; FILING DATE: 08-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..15
; OTHER INFORMATION: /standard_name="ZC2683"
US-08-464-148-10

Query Match 2.0%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No.1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 19
US-08-385-500-10
; Sequence 10, Application US/08385500
; Patent No. 5712117
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,784
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/385,500
; FILING DATE: 08-FEB-1995
; ATTORNEY/AGENT INFORMATION:

ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,500
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..15
OTHER INFORMATION: /standard_name="ZC2683"
US-08-385-500-10

Query Match 2.0%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No.1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 20
US-08-846-784-10
; Sequence 10, Application US/08846784
; Patent No. 5747645
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,784
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/385,500
; FILING DATE: 08-FEB-1995
; ATTORNEY/AGENT INFORMATION:


```

; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..15
; OTHER INFORMATION: /standard_name="ZC2683"
US-08-846-784-10

Query Match      2.0%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      246 CTCCTGGAGCCC 257
Db      3 CTCCTGGAGCCC 14

RESULT 21
US-08-889-291-35
; Sequence 35, Application US/08889291
; Patent No. 594519
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane K
; APPLICANT: Derbyshire, Elaine J
; APPLICANT: McCafferty, John G
; APPLICANT: Vaughan, Tristan J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Labelling and selection of molecules
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,291
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: PC/GB97/01835
; FILING DATE: 08-JUL-1997
; APPLICATION NUMBER: GB 9614292.2
; FILING DATE: 08-JUL-1996
; APPLICATION NUMBER: GB 9624880.2
; FILING DATE: 29-NOV-1996
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: GB 9624880.2
; FILING DATE: 18-JUN-1997
; APPLICATION NUMBER: GB 9712818.5
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/34063
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-098-244-35

Query Match      2.0%; Score 12; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      246 CTCCTGGAGCCC 257
Db      3 CTCCTGGAGCCC 14

RESULT 22
US-09-098-244-35
; Sequence 35, Application US/09098244
; Patent No. 6180336
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane K
; APPLICANT: Derbyshire, Elaine J
; APPLICANT: McCafferty, John G
; APPLICANT: Vaughan, Tristan J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Labelling and selection of molecules
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,244
; FILING DATE: 17-JUN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/889,291
; FILING DATE: 08-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PC/GB97/01835
; FILING DATE: 08-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9614292.2
; FILING DATE: 08-JUL-1996
; APPLICATION NUMBER: GB 9624880.2
; FILING DATE: 29-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9712818.5
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/34800
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-098-244-35

Query Match      2.0%; Score 12; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      246 CTCCTGGAGCCC 257
Db      3 CTCCTGGAGCCC 14
```

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 23
US-09-375-314-35
; Sequence 35, Application US/09375314
; Patent No. 6342588
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane K
; APPLICANT: Derbyshire, Elaine J
; APPLICANT: McCafferty, John G
; APPLICANT: Vaughan, Tristan J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Labelling and selection of molecules
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,314
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/889,291
; FILING DATE: 08-JUL-1997
; APPLICATION NUMBER: PCT/GB97/01835
; FILING DATE: 08-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9614292.2
; FILING DATE: 08-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9624880.2
; FILING DATE: 29-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/34063
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-375-314-35

Query Match 2.0%; Score 12; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 24
US-09-767-395-35
; Sequence 35, Application US/09767395
```

```
; Patent No. 6489123
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane K
; APPLICANT: Derbyshire, Elaine J
; APPLICANT: McCafferty, John G
; APPLICANT: Vaughan, Tristan J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Labelling and selection of molecules
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/767,395
; FILING DATE: 23-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/098,244
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/GB97/01835
; FILING DATE: 08-JUL-1997
; APPLICATION NUMBER: GB 9614292.2
; FILING DATE: 08-JUL-1996
; APPLICATION NUMBER: GB 9624880.2
; FILING DATE: 29-NOV-1996
; APPLICATION NUMBER: GB 9712818.5
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/34800
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-767-395-35

Query Match 2.0%; Score 12; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 25
PCT-US95-06379-27/c
; Sequence 27, Application PCT/US9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Wei, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
```

```
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06379
; FILING DATE: May 13, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-27

Query Match          2.0%; Score 12; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      175 TTGCTCTTCTCT 186
Db      13 TTGCTCTTCTCT 2

RESULT 26
US-08-817-145-8
; Sequence 8, Application US/08817145
; Patent No. 6025329
; GENERAL INFORMATION:
; APPLICANT: UTSUMI, Jun
; APPLICANT: SUDO, Tetsuo
; APPLICANT: TANAKA, Yasuhiko
; APPLICANT: MATSUI, Mizuo
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR OPHTHALMIC
; TITLE OF INVENTION: DISEASES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP.
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,145
; FILING DATE: 02-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 760-230P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic Primer"
US-08-817-145-8

Query Match          2.0%; Score 12; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      246 CTCCTGGAGCCC 257
Db      2 CTCCTGGAGCCC 13

RESULT 27
US-09-629-222A-41/c
; Sequence 41, Application US/09629222A
; Patent No. 6599700
; GENERAL INFORMATION:
; APPLICANT: Bellacosa, Alfonso
; TITLE OF INVENTION: Methods for Detection of Transition
; TITLE OF INVENTION: Single-Nucleotide Polymorphisms
; FILE REFERENCE: FCCC 96-21
; CURRENT APPLICATION NUMBER: US/09/629,222A
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/463,891
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US98/15828
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/053,936
; PRIOR FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-629-222A-41

Query Match          2.0%; Score 12; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      116 CTACATCTCTTT 127
Db      15 CTACATCTCTTT 4

RESULT 28
US-08-152-313-59
; Sequence 59, Application US/08152313
; Patent No. 5561041
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; TITLE OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,313
```

```

; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
; US-08-152-313-59

Query Match      2.0%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCATGAA 501
Db 5 GGGCTGCATGAA 16

RESULT 29
US-08-050-073-138
; Sequence 138, Application US/08050073
; Patent No. 5567809
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Begovich, Ann B.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
; APPLICANT: Scharf, Stephen J.
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
; NUMBER OF SEQUENCES: 315
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,073
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8769
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2977
; TELEFAX: (510) 814-2974
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; APPLICATION NUMBER: US/08/050-073-159

Query Match      2.0%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGAGC 255
Db 1 ACCTCTGGAGC 12

RESULT 30
US-08-050-073-159
; Sequence 159, Application US/08050073
; Patent No. 5567809
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Begovich, Ann B.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
; APPLICANT: Scharf, Stephen J.
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
; NUMBER OF SEQUENCES: 315
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,073
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8769
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2977
; TELEFAX: (510) 814-2974
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; APPLICATION NUMBER: US/08/050-073-159

Query Match      2.0%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGAGC 255
Db 1 ACCTCTGGAGC 12

RESULT 31
US-08-579-223-59
; Sequence 59, Application US/08579223
; Patent No. 5726019
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
```

;; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
;; TITLE OF INVENTION: ANALYSIS OF SPUTUM
;; NUMBER OF SEQUENCES: 128
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Spensley Horn Jubas & Lubitz
;; STREET: 1880 Century Park East, Suite 500
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: USA
;; ZIP: 90067
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/579,223
;; FILING DATE: 28-DEC-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/152,313
;; FILING DATE: 12-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wetherell, Jr., Ph.D., John R.,
;; REGISTRATION NUMBER: 31,678
;; REFERENCE/DOCKET NUMBER: PD-2912
;; TELEPHONE: (619) 455-5100
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 59:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..17
;; US-08-579-223-59

Query Match 2.0%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 490 GGCTGCATGAA 501
Db 5 GGCTGCATGAA 16

RESULT 32
US-08-758-306-1283/c
; Sequence 1283, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: FastSeq Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/758,306
;; FILING DATE: December 3, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 212/132
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1283:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-758-306-1283

Query Match 2.0%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 248 CCTGGAGCCCT 259
Db 13 CCTGGAGCCCT 2

RESULT 33
US-08-181-664-46
; Sequence 46, Application US/08181664
; Patent No. 6025127
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION IN
; HISTOLOGIC TISSUE
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/181,664
; FILING DATE: JANUARY 14, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3055
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
US-08-181-664-46

Query Match          2.0%; Score 12; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 490 GGCGTCGATGAA 501
Db 5 GGCGTCGATGAA 16

RESULT 34
US-09-866-108A-7364
; Sequence 7364, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7365
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7365

Query Match          2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGTT 510
Db 5 GAAATTCAGTT 16

RESULT 36
US-09-866-108A-7366
; Sequence 7366, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
```

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7366
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7366

Query Match      2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
Db 4 GAAATTCAGTT 15

RESULT 37
US-09-866-108A-7367, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7366
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7366

Query Match      2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
Db 4 GAAATTCAGTT 15

RESULT 37
US-09-866-108A-7367, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
```

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; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7367
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7367

Query Match      2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
Db 3 GAAATTCAGTT 14

RESULT 38
US-09-866-108A-7368, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7368
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7368

Query Match      2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
Db 2 GAAATTCAGTT 13

RESULT 39
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US-09-866-108A-7369
; Sequence 7369, Application US/09866108A
; Patent No. 6866188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Shaaron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6866188
; SEQ ID NO 7369
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7369

Query Match          2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      499 GAAATTCAGTT 510
Db      1 GAAATTCAGTT 12

RESULT 40
PCT-US94-12947A-59
; Sequence 59, Application PC/TUS9412947A
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; TITLE OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12947A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
PCT-US94-12947A-59

Query Match          2.0%; Score 12; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      490 GGGCTGCATGAA 501
Db      5 GGGCTGCATGAA 16

RESULT 41
US-09-178-002-9
; Sequence 9, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide sense primer
US-09-178-002-9

Query Match          2.0%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      94 GTAGTGAAGAGG 105
Db      6 GTAGTGAAGAGG 17

RESULT 42
US-08-050-073-121
; Sequence 121, Application US/08050073
; Patent No. 5567809
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Begovich, Ann B.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
```


APPLICANT: Scharf, Stephen J.
TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
NUMBER OF SEQUENCES: 315
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,073
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-050-073-121
Query Match 2.0%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 244 ACCTCCTGGAGC 255
Db 2 ACCTCCTGGAGC 13
RESULT 43
US-08-050-073-158/c
Sequence 158, Application US/08050073
Patent No. 5567809
GENERAL INFORMATION:
APPLICANT: Apple, Raymond J.
APPLICANT: Begovich, Ann B.
APPLICANT: Bugawan, Teodorica L.
APPLICANT: Erlich, Henry A.
APPLICANT: Griffith, Robert L.
APPLICANT: Scharf, Stephen J.
TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
NUMBER OF SEQUENCES: 315
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,073

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-050-073-158
Query Match 2.0%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 244 ACCTCCTGGAGC 255
Db 17 ACCTCCTGGAGC 6
RESULT 44
US-09-197-378-17
Sequence 17, Application US/09197378
Patent No. 5959097
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF MEK2 EXPRESSION
FILE REFERENCE: RTS-0017
CURRENT APPLICATION NUMBER: US/09/197,378
CURRENT FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 17
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-197-378-17
Query Match 2.0%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130 CTGGACTTTGGT 141
Db 6 CTGGACTTTGGT 17
RESULT 45
US-09-205-860-28
Sequence 28, Application US/09205860
Patent No. 5981732
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
FILE REFERENCE: RTS-0031
CURRENT APPLICATION NUMBER: US/09/205,860
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 28
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide

US-09-205-860-28

Query Match 2.0%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330
|||||
Db 7 AGGATCTTCACC 18

RESULT 46

US-09-256-496-13

Sequence 13, Application US/09256496
Patent No. 5998206
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF G-AFLHA-12 EXPRESSION
FILE REFERENCE: RTS-0056
CURRENT APPLICATION NUMBER: US/09/256,496
CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 13
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide

US-09-256-496-13

Query Match 2.0%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330
|||||
Db 3 AGGATCTTCACC 14

RESULT 47

US-08-696-497B-15

Sequence 15, Application US/08696497B
Patent No. 6007231
GENERAL INFORMATION:
APPLICANT: Vijs, Jan and Bishop, Robert
TITLE OF INVENTION: Method of Computer Aided
TITLE OF INVENTION: Diagnostic DNA Test Design, and Apparatus Therefor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rines & Rines
STREET: 81 No. 6007231th State Street
CITY: Concord
STATE: NH
COUNTRY: USA
ZIP: 03301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: IBM PC
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft No. 6007231lepad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,497B
FILING DATE: 14-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA: No. 6007231e
ATTORNEY/AGENT INFORMATION:
NAME: Rines, Robert H.
REGISTRATION NUMBER: 15,932
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 228-0121
TELEFAX: (603) 228-0210
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

US-08-696-497B-15

Query Match 2.0%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
|||||
Db 3 TCGTCTCTCCAG 14

RESULT 48

US-08-180-470-45

Sequence 45, Application US/08180470
Patent No. 6045994
GENERAL INFORMATION:
APPLICANT: ZABEAU, Marc
APPLICANT: VOS, Pieter
TITLE OF INVENTION: SELECTIVE RESTRICTION FRAGMENT
TITLE OF INVENTION: AMPLIFICATION: A GENERAL METHOD FOR DNA
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: The George Mason Bldg., Washington & Prince
STREET: Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,470
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/950,011
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-180-470-45

Query Match 2.0%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-205-860-28

Query Match 2.0%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330
|||||
Db 7 AGGATCTTCACC 18

RESULT 46

US-09-256-496-13

Sequence 13, Application US/09256496
Patent No. 5998206
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF G-AFLHA-12 EXPRESSION
FILE REFERENCE: RTS-0056
CURRENT APPLICATION NUMBER: US/09/256,496
CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 13
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide

US-09-256-496-13

Query Match 2.0%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330
|||||
Db 3 AGGATCTTCACC 14

RESULT 47

US-08-696-497B-15

Sequence 15, Application US/08696497B
Patent No. 6007231
GENERAL INFORMATION:
APPLICANT: Vijs, Jan and Bishop, Robert
TITLE OF INVENTION: Method of Computer Aided
TITLE OF INVENTION: Diagnostic DNA Test Design, and Apparatus Therefor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rines & Rines
STREET: 81 No. 6007231th State Street
CITY: Concord
STATE: NH
COUNTRY: USA
ZIP: 03301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: IBM PC
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft No. 6007231lepad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,497B
FILING DATE: 14-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA: No. 6007231e
ATTORNEY/AGENT INFORMATION:
NAME: Rines, Robert H.
REGISTRATION NUMBER: 15,932
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 228-0121
TELEFAX: (603) 228-0210
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

US-08-696-497B-15

Query Match 2.0%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
|||||
Db 3 TCGTCTCTCCAG 14

RESULT 48

US-08-180-470-45

Sequence 45, Application US/08180470
Patent No. 6045994
GENERAL INFORMATION:
APPLICANT: ZABEAU, Marc
APPLICANT: VOS, Pieter
TITLE OF INVENTION: SELECTIVE RESTRICTION FRAGMENT
TITLE OF INVENTION: AMPLIFICATION: A GENERAL METHOD FOR DNA
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: The George Mason Bldg., Washington & Prince
STREET: Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,470
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/950,011
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-180-470-45

Query Match 2.0%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: ORES-5003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "probe"
US-08-649-991-33

Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCCTC 186
DB 4 TTGCTCTTCCTC 15

RESULT 51
US-08-649-991-34
Sequence 34, Application US/08649991
Patent No. 5919462
GENERAL INFORMATION:
APPLICANT: Narwa, Remy
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS DERIVED FROM THE
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR
TITLE OF INVENTION: APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF
TITLE OF INVENTION: MATERNOFETAL TRANSMISSION OF HIV-1
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,991
FILING DATE: 17-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9505914
FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: ORES-5003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "probe"
US-08-649-991-34

QY 36 TTACCAATTCAA 47
DB 6 TTACCAATTCAA 17

RESULT 49
US-09-972-115A-17
Sequence 17, Application US/09972115A
Patent No. 6593728
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Mieczyslaw, Piatyszek A.
APPLICANT: Walter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patent in version 3.1
SEQ ID NO 17
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-972-115A-17

Query Match 2.0%; Score 12; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
DB 3 CTCCTGGAGCCC 14

RESULT 50
US-08-649-991-33
Sequence 33, Application US/08649991
Patent No. 5919462
GENERAL INFORMATION:
APPLICANT: Narwa, Remy
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS DERIVED FROM THE
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR
TITLE OF INVENTION: APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF
TITLE OF INVENTION: MATERNOFETAL TRANSMISSION OF HIV-1
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,991
FILING DATE: 17-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9505914
FILING DATE: 18-MAY-1995

Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 TTGCTCTTCCTC 186
Db 4 TTGCTCTTCCTC 15
RESULT 52
US-08-649-991-35
Sequence 35 Application US/08649991
Patent No. 5919462
GENERAL INFORMATION:
APPLICANT: Narwa, Remy
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS DERIVED FROM THE
TITLE OF INVENTION: HIV-1 VIRUS GENOME. CORRESPONDING PEPTIDES AND THEIR
TITLE OF INVENTION: APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF
TITLE OF INVENTION: MATERNOFETAL TRANSMISSION OF HIV-1
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/649,991
APPLICATION NUMBER: US/08/649,991
FILING DATE: 17-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9505914
FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: ORES-5003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "probe"
US-08-649-991-35
Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 TTGCTCTTCCTC 186
Db 3 TTGCTCTTCCTC 14
RESULT 53
US-09-422-978-11302/c
Sequence 11302 Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET 020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1993-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 11302
LENGTH: 19
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..19
OTHER INFORMATION: downstream amplification primer 99-4077 for SEQ 3437, in comple
US-09-422-978-11302
Query Match 2.0%; Score 12; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 TGCTCTTCCTCC 187
Db 15 TGCTCTTCCTCC 4
RESULT 54
US-08-388-381-8
Sequence 8, Application US/08388381
Patent No. 5552283
GENERAL INFORMATION:
APPLICANT: Diamandis, Eleftherios
APPLICANT: Dunn, James M.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
TITLE OF INVENTION: and targeted Screening for p53 Mutations
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,381
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/271,946
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN-P-003-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20

NAME/KEY: primer for exon 5 of human p53 gene
US-08-388-381-8
Query Match 2.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 510 TCGTCTCTCCAG 521
Db 9 TCGTCTCTCCAG 20
RESULT 55
US-08-388-381-9/c
Sequence 9, Application US/08388381
Patent No. 5552283
GENERAL INFORMATION:
APPLICANT: Diamandis, Eleftherios
APPLICANT: Dunn, James M.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
TITLE OF INVENTION: and Targeted Screening for p53 Mutations
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,381
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/271,946
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE: human
FEATURE:

NAME/KEY: primer for exon 6 of human p53 gene
US-08-388-381-9
Query Match 2.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 510 TCGTCTCTCCAG 521
Db 18 TCGTCTCTCCAG 7
RESULT 56
US-08-375-116A-123/c
Sequence 123, Application US/08375116A
Patent No. 5631146
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Huizenga, David E.
TITLE OF INVENTION: DNA APAMERS AND CATALYSTS THAT BIND
TITLE OF INVENTION: ADENOSINE AND/OR ADENOSINE-5'-PHOSPHATES AND METHODS FOR
TITLE OF INVENTION: ISOLATION THEREOF
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,116A
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/266001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 9617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-375-116A-123
Query Match 2.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 180 CTTCTCTCGCTA 191
Db 16 CTTCTCTCGCTA 5
RESULT 57
US-09-205-860-3
Sequence 3, Application US/09205860
Patent No. 5981732
GENERAL INFORMATION:
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
FILE REFERENCE: RTS-0031
CURRENT APPLICATION NUMBER: US/09/205,860

; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-205-860-3

Query Match 2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 9 AGGATCTTCACC 20

RESULT 58
US-08-630-019A-37
; Sequence 37, Application US/08630019A
; Patent No. 6015710
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David
; APPLICANT: No. 6015710ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630, 019A
; FILING DATE: 09-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "peptide nucleic acid (PNA),
; DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by
; DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
; DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"
US-08-630-019A-37

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 9 AGGATCTTCACC 20

RESULT 59
US-08-630-019A-42
; Sequence 42, Application US/08630019A
; Patent No. 6015710
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David
; APPLICANT: No. 6015710ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630, 019A
; FILING DATE: 09-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "phosphorothioate (PS) nucleic acid"

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 9 AGGATCTTCACC 20

RESULT 60
US-08-838-545-42
; Sequence 42, Application US/08838545
; Patent No. 6046307
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David R.
; APPLICANT: No. 6046307ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
US-08-630-019A-37

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 9 AGGATCTTCACC 20

Db 1 AGGATCTTCACC 12

RESULT 59
US-08-630-019A-42
; Sequence 42, Application US/08630019A
; Patent No. 6015710
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David
; APPLICANT: No. 6015710ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630, 019A
; FILING DATE: 09-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "phosphorothioate (PS) nucleic acid"

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 1 AGGATCTTCACC 12

RESULT 60
US-08-838-545-42
; Sequence 42, Application US/08838545
; Patent No. 6046307
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David R.
; APPLICANT: No. 6046307ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
US-08-630-019A-42

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 1 AGGATCTTCACC 12

RESULT 60
US-08-838-545-42
; Sequence 42, Application US/08838545
; Patent No. 6046307
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David R.
; APPLICANT: No. 6046307ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
US-08-630-019A-42

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 1 AGGATCTTCACC 12

RESULT 60
US-08-838-545-42
; Sequence 42, Application US/08838545
; Patent No. 6046307
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David R.
; APPLICANT: No. 6046307ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
US-08-630-019A-42

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 1 AGGATCTTCACC 12

RESULT 60
US-08-838-545-42
; Sequence 42, Application US/08838545
; Patent No. 6046307
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David R.
; APPLICANT: No. 6046307ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
US-08-630-019A-42

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 1 AGGATCTTCACC 12

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,545
FILING DATE: 09-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "peptide nucleic acid (PNA),
DESCRIPTION: where (deoxy(ribose-phosphate linkages are replaced by
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
DESCRIPTION: glycine amino N through a methylenecarbonyl linker"
US-08-838-545-42

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330
|||||
DB 1 AGGATCTTCACC 12

RESULT 61
US-08-838-545-47
Sequence 47, Application US/08838545
Patent No. 6046307
GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Piatyszek, Mieczyslaw A.
APPLICANT: Corey, David R.
APPLICANT: No. 6046307ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,545
FILING DATE: 09-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "phosphorothioate (PS)
DESCRIPTION: nucleic acid"
US-08-838-545-47

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330
|||||
DB 1 AGGATCTTCACC 12

RESULT 62
US-08-765-626-8
Sequence 8, Application US/08765626
Patent No. 6071726
GENERAL INFORMATION:
APPLICANT: Visible Genetics Inc.
APPLICANT: Diamandis, Eleftherios
APPLICANT: Dunn, James M.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
TITLE OF INVENTION: and Targeted Screening for p53 Mutations
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,626
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08605
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/388,381
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252

```
;
; TELEFAX: (914) 962-4330
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 5 of human p53 gene
;
US-08-765-626-8
;
Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
Db 9 TCGTCTCTCCAG 20

RESULT 63
US-08-765-626-9/c
; Sequence 9, Application US/08765626
; Patent No. 6071726
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Diamandis, Eleftherios
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,626
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08605
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 5 of human p53 gene
;
US-08-765-626-8
;
Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
Db 9 TCGTCTCTCCAG 20
```

```
;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 6 of human p53 gene
;
US-08-765-626-9
;
Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
Db 18 TCGTCTCTCCAG 7

RESULT 64
US-08-777-266A-14
; Sequence 14, Application US/08777266A
; Patent No. 6077833
; GENERAL INFORMATION:
; APPLICANT: Clarence Frank Bennett
; APPLICANT: Timothy A. Vickers
; TITLE OF INVENTION: Oligonucleotide Compositions and
; TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,266A
; FILING DATE: December 31, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 14:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
;
US-08-777-266A-14
;
Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258
Db 6 TCCTGGAGCCCC 17
```


RESULT 65

US-09-101-886B-15
; Sequence 15, Application US/09101886B
; Patent No. 6197507
; GENERAL INFORMATION:
; APPLICANT: BERG, THOMAS
; APPLICANT: TOLLERSUD, OLE K
; APPLICANT: NILSEN, OIVIND
; TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BARBARA G. ERNST
; STREET: 555 13TH STREET, NW SUITE 701E
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101.886B
; FILING DATE: 29-JANUARY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/00109
; FILING DATE: 12-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-240
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-09-101-886B-15

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

378 GCGGCGGCTGCA 389

Db 7 GCGGCGGCTGCA 18
|||||

RESULT 66

US-09-290-640-21/c
; Sequence 21, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcuson, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-290-640-21

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGAATGCTCTT 182

Db 20 GGAATGCTCTT 9
|||||

RESULT 67

US-08-943-731-546
; Sequence 546, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: KALA-KOKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; STREET: FLR
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 546:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-546

```
Query Match      2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 201 CTGGGACCTAGA 212
Db 3 CTGGGACCTAGA 14

RESULT 68
US-09-349-532-42
; Sequence 42, Application US/09349532
; Patent No. 6294650
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David R.
; APPLICANT: No. 6294650ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/838,545
; FILING DATE: 09-APR-1997
; APPLICATION NUMBER: US 08/630,019
; FILING DATE: 09-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "peptide nucleic acid (PNA)",
; DESCRIPTION: where (deoxy(ribose-phosphate linkages are replaced by
; DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
; DESCRIPTION: glycine amino N through a methylenecarbonyl linker"
US-09-349-532-42

Query Match      2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 319 AGGATCTTCACC 330
Db 1 AGGATCTTCACC 12

RESULT 70
US-09-326-186B-14
; Sequence 14, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0376
; CURRENT APPLICATION NUMBER: US/09/326,186B
; CURRENT FILING DATE: 1999-06-04
```

; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-326-186B-14

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258
|||
Db 6 TCCTGGAGCCCC 17

RESULT 71
US-09-326-186B-198
; Sequence 198, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: ISPH-0376
; CURRENT APPLICATION NUMBER: US/09/326,186B
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 198
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-326-186B-198

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258
|||
Db 5 TCCTGGAGCCCC 16

RESULT 72
US-09-662-235-1
; Sequence 1, Application US/09662235
; Patent No. 6372436
; GENERAL INFORMATION:
; APPLICANT: Pouzyrev, Anatoli Timofeyevich
; APPLICANT: Riddle, Donald Lee
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF CDNA LIBRARIES ENRICHED IN CLONES
; FILE REFERENCE: 2733/61965
; CURRENT APPLICATION NUMBER: US/09/662,235
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Sequence

; OTHER INFORMATION: Oligonucleotide Primer
US-09-662-235-1

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
|||
Db 1 CTCCTGGAGCCC 12

RESULT 73
US-09-659-845A-172
; Sequence 172, Application US/09659845A
; Patent No. 6492170
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION
; FILE REFERENCE: RTS-0183
; CURRENT APPLICATION NUMBER: US/09/659,845A
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 172
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-845A-172

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCGGAGGAGCTT 32
|||
Db 5 CCGGAGGAGCTT 16

RESULT 74
US-09-622-277-6
; Sequence 6, Application US/09622277
; Patent No. 6521407
; GENERAL INFORMATION:
; APPLICANT: Warenius, Hilmar Meek
; APPLICANT: Seabra, Laurence Anthony
; TITLE OF INVENTION: METHODS FOR DETERMINING CHEMOSENSITIVITY OF CANCER CELLS BASED
; FILE REFERENCE: 1417-188
; CURRENT APPLICATION NUMBER: US/09/622,277
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00500
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: GB 9903035.5
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: GB 9814545.1
; PRIOR FILING DATE: 1998-07-03
; PRIOR APPLICATION NUMBER: GB 9812151.0
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: GB 9803447.3
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: GB 9803446.5
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR and DNA sequencing primer for exon 5 antisense

US-09-622-277-6

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
|||||
DB 9 TCGTCTCTCCAG 20

RESULT 75

US-09-422-978-11732/c
; Sequence 11732, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11732
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-4029 for SEQ 3867, in compleme
US-09-422-978-11732

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 CGTCTCTCCAGA 522
|||||
DB 14 CGTCTCTCCAGA 3

RESULT 76

US-09-198-452A-1338
; Sequence 1338, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1338
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1338

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 CTGAGGATCTTC 327

Db

|||||
9 CTGAGGATCTTC 20

RESULT 77

US-09-601-144-14
; Sequence 14, Application US/09601144
; Patent No. 6566514
; GENERAL INFORMATION:
; APPLICANT: Wright, Jim A.
; APPLICANT: Young, Aiping H.
; APPLICANT: Lee, Yoon S.
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES COMPLEMENTARY TO THIOREDOXIN
; TITLE OF INVENTION: AND THIOREDOXIN REDUCTASE GENES AND METHODS OF USING
; FILE REFERENCE: 683-112US-A
; CURRENT APPLICATION NUMBER: US/09/601,144
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/073,196
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-601-144-14

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 TGGATATCTTTT 453
|||||
DB 7 TGGATATCTTTT 18

RESULT 78

US-09-665-615B-21/c
; Sequence 21, Application US/09665615B
; Patent No. 6653133
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-665-615B-21

Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGAATTGCTCTT 182
|||||
DB 20 GGAATTGCTCTT 9

RESULT 79

US-09-860-473-93/c
; Sequence 93, Application US/09860473

```
; Patent No. 6656732
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
; FILE REFERENCE: RTS-0222
; CURRENT APPLICATION NUMBER: US/09/860,473
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 169
; SEQ ID NO 93
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-860-473-93

Query Match      2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 GTGGCGGACTTT 291
DB 15 GTGGCGGACTTT 4

RESULT 80
US-09-890-010A-1/c
; Sequence 1, Application US/09890010A
; Patent No. 6664042
; GENERAL INFORMATION:
; APPLICANT: Posnett, David N
; TITLE OF INVENTION: DETERMINING VIRAL LOAD IN DOUBLE NEGATIVE T CELLS
; FILE REFERENCE: 19603/2732
; CURRENT APPLICATION NUMBER: US/09/890,010A
; CURRENT FILING DATE: 2001-11-23
; PRIOR APPLICATION NUMBER: PCT/US00/01959
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-890-010A-1

Query Match      2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328
DB 17 TGAGGATCTTCA 6

RESULT 81
US-09-980-052-61
; Sequence 61, Application US/09980052
; Patent No. 6670130
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Chaeol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/09/980,052
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29

; Patent No. 6656732
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
; FILE REFERENCE: RTS-0222
; CURRENT APPLICATION NUMBER: US/09/860,473
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 169
; SEQ ID NO 93
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-860-473-93

Query Match      2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AGGTCGCGCGTG 76
DB 5 AGGTCGCGCGTG 16

RESULT 82
PCT-US95-08605-8
; Sequence 8, Application PC/TUS9508605
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Diamandis, Eleftherios
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for p53 Mutations
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08605
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,946
; FILING DATE: 08-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/388,381
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
```

TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE: human
ORGANISM: human
FEATURE:
NAME/KEY: primer for exon 5 of human p53 gene
PCT-US95-08605-8

Query Match 2.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
| | | | | | | | | |
DB 9 TCGTCTCTCCAG 20

RESULT 83
PCT-US95-08605-9/c
Sequence 9, Application PC/TUS9508605
GENERAL INFORMATION:
APPLICANT: Visible Genetics Inc.
APPLICANT: Diamandis, Eleftherios
APPLICANT: Dunn, James M.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
NUMBER OF INVENTIONS: and Targeted Screening for p53 Mutations
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08605
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/271,946
FILING DATE: 08-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/388,381
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marina I. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE: human

FEATURE:
NAME/KEY: primer for exon 6 of human p53 gene
PCT-US95-08605-9

Query Match 2.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
| | | | | | | | | |
DB 18 TCGTCTCTCCAG 7

RESULT 84
US-08-441-887A-269
Sequence 269, Application US/08441887A
Patent No. 5837832
GENERAL INFORMATION:
APPLICANT: Chee, Mark
APPLICANT: Cronin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Hubbell, Earl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
NUMBER OF INVENTIONS: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-326-2400
TELEFAX: 650-326-2422
TELEX:
INFORMATION FOR SEQ ID NO: 269:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (probe)
US-08-441-887A-269

Query Match 1.8%; Score 11; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	462	CCATGAAGAA	472
Db	2	CCATGAAGAA	12
<p>INFORMATION FOR SEQ ID NO: 1:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 14 base pairs</p> <p>TYPE: nucleic acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: cdna</p> <p>HYPOTHETICAL: NO</p> <p>ANTI-SENSE: NO</p> <p>FRAGMENT TYPE:</p> <p>ORIGINAL SOURCE:</p> <p>US-08-239-431A-1</p>			
<p>Query Match 1.8%; Score 11; DB 1; Length 14;</p> <p>Best Local Similarity 100.0%; Pred. No. 4e+04;</p> <p>Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>			
QY	246	CTCCTGGAGCC	256
Db	3	CTCCTGGAGCC	13
<p>RESULT 87</p> <p>US-09-267-423-1</p> <p>Sequence 1, Application US/09267423</p> <p>Patent No. 6395878</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Regan, John W.</p> <p>APPLICANT: Gil, Daniel W.</p> <p>APPLICANT: Woodward, David F.</p> <p>TITLE OF INVENTION: NO. 6395878el Human Prostaglandin EP Receptor</p> <p>FILE REFERENCE: 17023 DIV CIP</p> <p>CURRENT APPLICATION NUMBER: US/09/267.423</p> <p>CURRENT FILING DATE: 1999-03-12</p> <p>EARLIER APPLICATION NUMBER: 09/019,393</p> <p>EARLIER FILING DATE: 1998-02-05</p> <p>EARLIER APPLICATION NUMBER: 08/239,431</p> <p>EARLIER FILING DATE: 1994-05-05</p> <p>NUMBER OF SEQ ID NOS: 10</p> <p>SOFTWARE: FastSeq for Windows Version 3.0</p> <p>SEQ ID NO 1</p> <p>LENGTH: 14</p> <p>TYPE: DNA</p> <p>ORGANISM: Homo sapiens</p> <p>US-09-267-423-1</p>			
<p>Query Match 1.8%; Score 11; DB 4; Length 14;</p> <p>Best Local Similarity 100.0%; Pred. No. 4e+04;</p> <p>Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>			
QY	246	CTCCTGGAGCC	256
Db	3	CTCCTGGAGCC	13
<p>RESULT 88</p> <p>US-08-140-797-4/c</p> <p>Sequence 4, Application US/08140797</p> <p>Patent No. 5578714</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Poso, Angel Oscar; Chaudhuri, Asok</p> <p>TITLE OF INVENTION: THE CLONING OF DUFFY BLOOD GROUP ANTIGEN</p> <p>NUMBER OF SEQUENCES: 16</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Sprung Horn Kramer & Woods</p> <p>STREET: 660 White Plains Road</p> <p>CITY: Tarrytown</p> <p>STATE: New York</p> <p>COUNTRY: USA</p> <p>ZIP: 10591-5144</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage</p> <p>COMPUTER: Apole Macintosh</p>			

```

; OPERATING SYSTEM: System 7.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/140,797
; FILING DATE: October 21, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: NYBC 265-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-140-797-4

Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 CAAGCCCTGGG 487
DB 15 CAAGCCCTGGG 5

RESULT 89
US-08-182-968A-32/c
; Sequence 32, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-32

Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
DB 13 AGGCTGAGCCC 3

RESULT 90
US-08-319-492B-440/c
; Sequence 440, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 440:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-319-492B-440

Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 441 CTGGATACTT 451
```


DB	CTGGAATCTT	DB	CTGGAATCTT
Db	12 CTGGAATCTT 2	Db	11 CTGGAATCTT 1
RESULT 91		RESULT 92	
US-08-319-492B-441/c		US-08-319-492B-442/c	
Sequence 441, Application US/08319492B		Sequence 442, Application US/08319492B	
Patent No. 5616488		Patent No. 5616488	
GENERAL INFORMATION:		GENERAL INFORMATION:	
APPLICANT: Sullivan, Sean M.		APPLICANT: Sullivan, Sean M.	
APPLICANT: Draper, Kenneth G.		APPLICANT: Draper, Kenneth G.	
APPLICANT: McSwiggen, James		APPLICANT: McSwiggen, James	
APPLICANT: Stinchcomb, Dan T.		APPLICANT: Stinchcomb, Dan T.	
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES		TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES	
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS		TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS	
NUMBER OF SEQUENCES: 751		NUMBER OF SEQUENCES: 751	
CORRESPONDENCE ADDRESS:		CORRESPONDENCE ADDRESS:	
ADDRESSER: Lyon & Lyon		ADDRESSER: Lyon & Lyon	
STREET: 633 West Fifth Street		STREET: 633 West Fifth Street	
CITY: Los Angeles		CITY: Los Angeles	
STATE: California		STATE: California	
COUNTRY: U.S.A.		COUNTRY: U.S.A.	
ZIP: 90071		ZIP: 90071	
COMPUTER READABLE FORM:		COMPUTER READABLE FORM:	
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb		MEDIUM TYPE: 3.5" Diskette, 1.44 Mb	
MEDIUM TYPE: storage		MEDIUM TYPE: storage	
COMPUTER: IBM Compatible		COMPUTER: IBM Compatible	
OPERATING SYSTEM: IBM P.C. DOS 5.0		OPERATING SYSTEM: IBM P.C. DOS 5.0	
SOFTWARE: Word Perfect 5.1		SOFTWARE: Word Perfect 5.1	
CURRENT APPLICATION DATA:		CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/08/319,492B		APPLICATION NUMBER: US/08/319,492B	
FILING DATE: October 7, 1994		FILING DATE: October 7, 1994	
PRIOR APPLICATION DATA:		PRIOR APPLICATION DATA:	
PRIOR APPLICATION DATA: including application		PRIOR APPLICATION DATA: including application	
PRIOR APPLICATION DATA: described below:		PRIOR APPLICATION DATA: described below:	
APPLICATION NUMBER: 08/008,895		APPLICATION NUMBER: 08/008,895	
FILING DATE: January 19, 1993		FILING DATE: January 19, 1993	
APPLICATION NUMBER: 07/989,849		APPLICATION NUMBER: 07/989,849	
FILING DATE: December 7, 1992		FILING DATE: December 7, 1992	
ATTORNEY/AGENT INFORMATION:		ATTORNEY/AGENT INFORMATION:	
NAME: Warburg, Richard		NAME: Warburg, Richard	
REGISTRATION NUMBER: 32,327		REGISTRATION NUMBER: 32,327	
REFERENCE/DOCKET NUMBER: 209/276		REFERENCE/DOCKET NUMBER: 209/276	
TELECOMMUNICATION INFORMATION:		TELECOMMUNICATION INFORMATION:	
TELEPHONE: (213) 489-1600		TELEPHONE: (213) 489-1600	
TELEFAX: (213) 955-0440		TELEFAX: (213) 955-0440	
TELEX: 67-3510		TELEX: 67-3510	
INFORMATION FOR SEQ ID NO: 441:		INFORMATION FOR SEQ ID NO: 441:	
SEQUENCE CHARACTERISTICS:		SEQUENCE CHARACTERISTICS:	
LENGTH: 15 base pairs		LENGTH: 15 base pairs	
TYPE: nucleic acid		TYPE: nucleic acid	
STRANDEDNESS: single		STRANDEDNESS: single	
TOPOLOGY: linear		TOPOLOGY: linear	
US-08-319-492B-441		US-08-319-492B-441	
Query Match	1.8%; Score 11; DB 1; Length 15;	Query Match	1.8%; Score 11; DB 1; Length 15;
Best Local Similarity	100.0%; Pred. No. 4e+04;	Best Local Similarity	100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	441 CTGGAATCTT 451	QY	441 CTGGAATCTT 451
Db	11 CTGGAATCTT 1	Db	11 CTGGAATCTT 1
RESULT 93		RESULT 93	
US-08-486-670A-4/c		US-08-486-670A-4/c	
Sequence 4, Application US/08486670A		Sequence 4, Application US/08486670A	
Patent No. 5583696		Patent No. 5583696	
GENERAL INFORMATION:		GENERAL INFORMATION:	
APPLICANT: Pogo, Angel Oscar; Chaudhuri, Asok		APPLICANT: Pogo, Angel Oscar; Chaudhuri, Asok	
TITLE OF INVENTION: THE CLONING OF DUFFY BLOOD GROUP ANTIGEN		TITLE OF INVENTION: THE CLONING OF DUFFY BLOOD GROUP ANTIGEN	
NUMBER OF SEQUENCES: 16		NUMBER OF SEQUENCES: 16	
CORRESPONDENCE ADDRESS:		CORRESPONDENCE ADDRESS:	
ADDRESSER: Sprung Horn Kramer & Woods		ADDRESSER: Sprung Horn Kramer & Woods	
STREET: 660 White Plains Road		STREET: 660 White Plains Road	
CITY: Tarrytown		CITY: Tarrytown	
STATE: New York		STATE: New York	
COUNTRY: USA		COUNTRY: USA	
ZIP: 10591-5144		ZIP: 10591-5144	
COMPUTER READABLE FORM:		COMPUTER READABLE FORM:	
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage		MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage	
COMPUTER: Apple Macintosh		COMPUTER: Apple Macintosh	

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; OPERATING SYSTEM: System 7.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.670A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/140.797
; FILING DATE: October 21, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: NYBC 265-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-486-670A-4
;
Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 54.5%; Pred. NO. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 CAACGCTGGG 487
DB 15 CAACGCTGGG 5

RESULT 94
US-08-363-240A-651
; Sequence 651, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELETYPE: 67-3510
; INFORMATION FOR SEQ ID NO: 652:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-363-240A-652
;
Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 54.5%; Pred. NO. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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; OPERATING SYSTEM: System 7.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.670A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/140.797
; FILING DATE: October 21, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: NYBC 265-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-486-670A-4
;
Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. NO. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 CAACGCTGGG 487
DB 15 CAACGCTGGG 5

RESULT 94
US-08-363-240A-651
; Sequence 651, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
;
US-08-363-240A-652
;
Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 54.5%; Pred. NO. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Qy 337 CTCTACTCTG 347
|:|:|:|:|:
Db 1 CUCUACUUCG 11

RESULT 96

US-08-292-620A-499
; Sequence 499, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 499:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-292-620A-499

Query Match 1.8%; Score 11; DB 2; Length 15;

Best Local Similarity 81.8%; Pred. No. 4e+04;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 244 ACCTCCTGGAG 254

||||:|:|:|

Db 4 ACCUCCUGGAG 14

RESULT 97

US-08-292-620A-688

; Sequence 688, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 688:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-292-620A-688

Query Match 1.8%; Score 11; DB 2; Length 15;

Best Local Similarity 81.8%; Pred. No. 4e+04;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 244 ACCTCCTGGAG 254

||||:|:|:|

Db 4 ACCUCCUGGAG 14

RESULT 98

US-08-292-620A-736

; Sequence 736, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

two

two

```
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 736:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-736

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCCTCTGAG 254
DB 4 ACCUCCUGAG 14

RESULT 99
US-08-774-306A-32/c
; Sequence 32, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California

APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 736:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-736

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCCTCTGAG 254
DB 4 ACCUCCUGAG 14

RESULT 99
US-08-774-306A-32/c
; Sequence 32, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
```

two

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COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,306A
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-306A-32

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
DB 13 AGGCTGAGCCC 3

RESULT 100
US-08-585-684B-622
; Sequence 622, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
```

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 622:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-622

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428
DB 4 ACCUCAAAGA 14

RESULT 101
US-08-585-684B-623
Sequence 623, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: January 16, 1996
PRIOR APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 623:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-623

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 624:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-624

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428
DB 4 ACCUCAAAGA 14

RESULT 102
US-08-585-684B-624
Sequence 624, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: January 16, 1996
PRIOR APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 624:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-624

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428
DB 4 ACCUCAAAGA 14

RESULT 103
US-08-585-684B-625
Sequence 625, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale

APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/585,684B

FILING DATE: January 16, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/000,951

FILING DATE: July 7, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/078

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 625:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-585-684B-625

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTCAAGA 428

Db 3 ACCUCAAAGA 13

RESULT 104

US-08-585-684B-1821

Sequence 1821, Application US/08585684B

Patent No. 5877021

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Jarvis, Thale

APPLICANT: McSwiggen, James

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

INDUCTION OF GRAFT TOLERANCE

TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

NUMBER OF SEQUENCES: 2751

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/585,684B

FILING DATE: January 16, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/000,951

FILING DATE: July 7, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/078

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1821:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-585-684B-1821

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 72.7%; Pred. No. 4e+04;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAT 51

Db 5 AAUUCAAAAU 15

RESULT 105

US-08-585-684B-1822

Sequence 1822, Application US/08585684B

Patent No. 5877021

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Jarvis, Thale

APPLICANT: McSwiggen, James

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

INDUCTION OF GRAFT TOLERANCE

TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

NUMBER OF SEQUENCES: 2751

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/585,684B

FILING DATE: January 16, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/000,951

FILING DATE: July 7, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/078

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1822:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-1822

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 72.7%; Pred. No. 4e+04;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAAT 51
||:|||||:
DB 5 AAUUCAAAAU 15

RESULT 106
US-08-585-684B-1823
Sequence 1823, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast-SEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1823:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-1823

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 72.7%; Pred. No. 4e+04;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAAT 51
||:|||||:
DB 5 AAUUCAAAAU 15

RESULT 107
US-08-422-560A-31
Sequence 31, Application US/08422560A
Patent No. 5910626
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
METHODS FOR USE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,560A
FILING DATE: 14-APR-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/956,700
FILING DATE: 02-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:152/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-422-560A-31

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 72.7%; Pred. No. 4e+04;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 555 GGTGTGTGACT 565
||:|||||:
DB 4 GGUGAUGACT 14

RESULT 108
US-09-064-156A-32/c
Sequence 32, Application US/09064156A
Patent No. 6132966
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 498
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,156A
FILING DATE: April 21, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/774,306
FILING DATE: December 26, 1996
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-064-156A-32

Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
DB 13 AGGCTGAGCCC 3
RESULT 109
US-09-071-845-499
Sequence 499, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 499:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-499
Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTCGAG 254
DB 4 ACCUCGUGAG 14
RESULT 110
US-09-071-845-688
Sequence 688, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993

APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 688:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-688

Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254
DB 4 ACCUCCUGGAG 14

RESULT 112
US-09-038-073-622
Sequence 622, Application US/09038073
Patent No. 6194150
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 622:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-038-073-622

Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428

APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 688:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-688

Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254
DB 4 ACCUCCUGGAG 14

RESULT 111
US-09-071-845-736
Sequence 736, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:

Db ||||:|||||
 4 ACCUCAAAGA 14

RESULT 113

US-09-038-073-623
; Sequence 623, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 623:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-038-073-623

Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAAGA 428
 ||||:|||||
Db 4 ACCUCAAAGA 14

RESULT 114

US-09-038-073-624
; Sequence 624, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 624:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-038-073-624

Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAAGA 428
 ||||:|||||
Db 4 ACCUCAAAGA 14

RESULT 115

US-09-038-073-625
; Sequence 625, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073

```
;
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 625:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-038-073-625
;
; Query Match 1.8%; Score 11; DB 3; Length 15;
; Best Local Similarity 81.8%; Pred. No. 4e+04; Indels 0;
; Matches 9; Conservative 2; Mismatches 0; Gaps 0;
;
; QY 418 ACCTTCAAGA 428
; Db 3 ACCUCAAAGA 13
;
; RESULT 116
; US-09-038-073-1821
; Sequence 1821, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1821:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-038-073-1821
;
; Query Match 1.8%; Score 11; DB 3; Length 15;
; Best Local Similarity 81.8%; Pred. No. 4e+04; Indels 0;
; Matches 9; Conservative 2; Mismatches 0; Gaps 0;
;
; QY 418 ACCTTCAAGA 428
; Db 3 ACCUCAAAGA 13
;
; RESULT 117
; US-09-038-073-1822
; Sequence 1822, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1822:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-038-073-1822
;
; Query Match 1.8%; Score 11; DB 3; Length 15;
; Best Local Similarity 72.7%; Pred. No. 4e+04; Indels 0;
; Matches 8; Conservative 3; Mismatches 0; Gaps 0;
;
; QY 41 AATTCAAAAAT 51
; Db 5 AAUUCAAAAAU 15
;
; RESULT 118
; US-09-038-073-1823
; Sequence 1823, Application US/09038073
```

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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-038-073-1821
;
; Query Match 1.8%; Score 11; DB 3; Length 15;
; Best Local Similarity 72.7%; Pred. No. 4e+04; Indels 0;
; Matches 8; Conservative 3; Mismatches 0; Gaps 0;
;
; QY 41 AATTCAAAAAT 51
; Db 5 AAUUCAAAAAU 15
;
; RESULT 117
; US-09-038-073-1822
; Sequence 1822, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1822:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-038-073-1822
;
; Query Match 1.8%; Score 11; DB 3; Length 15;
; Best Local Similarity 72.7%; Pred. No. 4e+04; Indels 0;
; Matches 8; Conservative 3; Mismatches 0; Gaps 0;
;
; QY 41 AATTCAAAAAT 51
; Db 5 AAUUCAAAAAU 15
;
; RESULT 118
; US-09-038-073-1823
; Sequence 1823, Application US/09038073
```

```
/ Patent No. 6194150
/ GENERAL INFORMATION:
/ APPLICANT: Stinchcomb, Daniel T.
/ APPLICANT: Jarvis, Thale
/ APPLICANT: McSwiggan, James
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
/ TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
/ NUMBER OF SEQUENCES: 2751
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/038,073
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/585,684
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/078
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 1823:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-038-073-1823

Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 72.7%; Pred. No. 4e+04;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAT 51
Db 5 AAUUCAAAAT 15

RESULT 119
US-07-879-647A-31
/ Sequence 31, Application US/07879647A
/ Patent No. 5266689
/ GENERAL INFORMATION:
/ APPLICANT: Chakraborty, P.R.
/ APPLICANT: Dashkevich, M.
/ APPLICANT: Elbrecht, A.
/ APPLICANT: Feigner, S.D.
/ APPLICANT: Liberator, P.A.
/ APPLICANT: Profous-Juchelka, H.
/ TITLE OF INVENTION: Eimeria Maxima DNA
/ TITLE OF INVENTION: Probes
/ NUMBER OF SEQUENCES: 50
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Merck & Co., Inc.
/ STREET: 126 Lincoln Avenue
/ CITY: Rahway
/ STATE: New Jersey
/ ZIP: 07065
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
/ MEDIUM TYPE: storage
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 6.0.4
/ SOFTWARE: Microsoft Word 4.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/879,584A
/ FILING DATE: 19920512
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/706,717
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/ COUNTRY: USA
/ ZIP: 07065
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
/ MEDIUM TYPE: storage
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 6.0.4
/ SOFTWARE: Microsoft Word 4.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/879,647A
/ FILING DATE: 19920512
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/706,628
/ FILING DATE: 29-MAY-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Tribble, Jack L.
/ REGISTRATION NUMBER: 32,633
/ REFERENCE/DOCKET NUMBER: 184201A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (908) 594-5321
/ TELEFAX: (908) 594-4720
/ TELEX: 138825
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 bases
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-07-879-647A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 120
US-07-879-584A-31
/ Sequence 31, Application US/07879584A
/ Patent No. 5278298
/ GENERAL INFORMATION:
/ APPLICANT: Chakraborty, P.R.
/ APPLICANT: Dashkevich, M.
/ APPLICANT: Elbrecht, A.
/ APPLICANT: Feigner, S.D.
/ APPLICANT: Liberator, P.A.
/ APPLICANT: Profous-Juchelka, H.
/ TITLE OF INVENTION: Eimeria Brunetti DNA
/ TITLE OF INVENTION: Probes
/ NUMBER OF SEQUENCES: 50
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Merck & Co., Inc.
/ STREET: 126 Lincoln Avenue
/ CITY: Rahway
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07065
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
/ MEDIUM TYPE: storage
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 6.0.4
/ SOFTWARE: Microsoft Word 4.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/879,584A
/ FILING DATE: 19920512
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/706,717
```

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; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184191A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-584A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 121
US-07-879-470A-31
; Sequence 31, Application US/07879470A
; Patent No. 528845
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevicz, M.
; APPLICANT: Eibrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Necatrix DNA
; TITLE OF INVENTION: Probes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,470A
; FILING DATE: 19920512
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,351
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184221A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-470A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 123
US-07-879-640A-31
; Sequence 31, Application US/07879644A
; Patent No. 529813
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevicz, M.
; APPLICANT: Eibrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Acervulina DNA
; TITLE OF INVENTION: Probes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,644A
; FILING DATE: 19920512
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,817
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184181A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-644A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 123
US-07-879-640A-31
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```

; TOPOLOGY: linear
; US-07-879-470A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 122
US-07-879-644A-31
; Sequence 31, Application US/07879644A
; Patent No. 529813
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevicz, M.
; APPLICANT: Eibrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Acervulina DNA
; TITLE OF INVENTION: Probes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,644A
; FILING DATE: 19920512
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,817
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184181A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-644A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 123
US-07-879-640A-31
```

; Sequence 31, Application US/07879640A
; Patent No. 5359050
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Elbrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Mitis DNA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,640A
; FILING DATE: 19920512
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,355
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184211A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-640A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGA 365
Db 3 CGCAGGCTGA 13
RESULT 124
US-07-879-594A-31
; Sequence 31, Application US/07879594A
; Patent No. 5449768
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Elbrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Fraeox DNA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.

; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,594A
; FILING DATE: 19920512
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,360
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184231A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-594A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGA 365
Db 3 CGCAGGCTGA 13
RESULT 125
US-07-879-469A-31
; Sequence 31, Application US/07879469A
; Patent No. 5563256
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Elbrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Tenella DNA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,469A
; FILING DATE: 19920512

US-08-050-073-145

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255
|||
Db 1 CCTCCTGGAGC 11

RESULT 127

US-08-050-073-152/C
; Sequence 152, Application US/08050073
; Patent No. 5567809
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Begovich, Ann B.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
; APPLICANT: Scharf, Stephen J.
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 315
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,073
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petty, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8769
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-050-073-152

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255
|||
Db 16 CCTCCTGGAGC 6

RESULT 128

US-08-050-073-154
; Sequence 154, Application US/08050073
; Patent No. 5567809
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Begovich, Ann B.

US-09-966-880a-7_copy_80_676.Oligo.rni

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,362
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tridble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: 184241A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-879-469A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGA 365
|||
Db 3 CGCAGGCTGA 13

RESULT 126

US-08-050-073-145
; Sequence 145, Application US/08050073
; Patent No. 5567809
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Begovich, Ann B.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
; APPLICANT: Scharf, Stephen J.
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 315
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,073
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petty, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8769
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA

APPLICANT: Bugawan, Teodorica L.
APPLICANT: Erlich, Henry A.
APPLICANT: Griffith, Robert L.
APPLICANT: Scharf, Stephen J.
TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
TITLE OF INVENTION: Typing
NUMBER OF SEQUENCES: 315
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,073
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-050-073-154

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCTGGAGC 255
Db 1 CCTCTGGAGC 11

RESULT 129
US-07-695-201B-4/c
Sequence 4, Application US/07695201B
Patent No. 5994056
GENERAL INFORMATION:
APPLICANT: Higuchi, Russell H.
TITLE OF INVENTION: Homogeneous Methods for Nucleic Acid
TITLE OF INVENTION: Amplification and Detection
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-third Street
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/695,201B
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Sias, Stacey R. 32,630
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 2599
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 420-3197
TELEFAX: (415) 658-5239
TELEX: 4992659
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-695-201B-4

Query Match 1.8%; Score 11; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 CCGCTGCTACC 229
Db 11 CCGCTGCTACC 1

RESULT 130
US-08-470-532-4/c
Sequence 4, Application US/08470532
Patent No. 6171785
GENERAL INFORMATION:
APPLICANT: Higuchi, Russell H.
TITLE OF INVENTION: Homogeneous Methods for Nucleic Acid
TITLE OF INVENTION: Amplification and Detection
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,532
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sias, Stacey R. 32,630
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 9012A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-470-532-4

Query Match 1.8%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 CCGCTGCTACC 229
Db 11 CCGCTGCTACC 1

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELEPHONE: (213) 489-1500
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 682:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-390-850-682

Query Match 1.8%; Score 11; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 129 ACTGGACTTGG 139
DB 1 ACUGGACUUUG 11

RESULT 134
US-08-435-634-682
Sequence 682, Application US/08435634
Patent No. 5731295
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Gustofson, John
APPLICANT: Stinchcomb, Dan T.

TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
OF ARTHRITIC CONDITIONS
NUMBER OF SEQUENCES: 1151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,634
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,850
FILING DATE: February 17, 1995
APPLICATION NUMBER: 08/354,920
FILING DATE: December 13, 1994
APPLICATION NUMBER: 08/152,487
FILING DATE: No. 5731295, September 12, 1993
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1500
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 682:
SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-634-682

Query Match 1.8%; Score 11; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 129 ACTGGACTTGG 139
DB 1 ACUGGACUUUG 11

RESULT 135
US-08-758-306-405
Sequence 405, Application US/08758306
Patent No. 5807743

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 405:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-758-306-405

Query Match 1.8%; Score 11; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTTGGCCC 547
DB 6 CCUUUGCCCC 16

```
RESULT 136
US-08-758-306-407
; Sequence 407, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-407

Query Match 1.8%; Score 11; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTGGCCCC 547
DB 5 CCUUUGCCCC 15

RESULT 137
US-08-758-306-409
; Sequence 409, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-409

Query Match 1.8%; Score 11; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTGGCCCC 547
DB 5 CCUUUGCCCC 15
```

```
RESULT 138
US-08-292-620A-1635
; Sequence 1635, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOSOME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 409:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-409

Query Match 1.8%; Score 11; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTGGCCCC 547
DB 4 CCUUUGCCCC 14
```

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1635:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1635

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186
Db 5 UGCUUCUCCUC 15

RESULT 139
US-08-292-620A-1691
Sequence 1691, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
INTRACELLULAR ADHESION
MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

two

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1691:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1691

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186
Db 5 UGCUUCUCCUC 15

RESULT 140
US-08-292-620A-1770
Sequence 1770, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
INTRACELLULAR ADHESION
MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

two

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1770:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1770

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186
Db 3 USCUCUCCUC 13

RESULT 141
US-08-292-620A-1830
Sequence 1830, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

two

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1830:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1830

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGAG 254
Db 5 ACCUCCUGGAG 15

RESULT 142
US-08-292-620A-1836
Sequence 1836, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

two

INFORMATION FOR SEQ ID NO: 1836:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-292-620A-1836

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGAG 254

Db 5 ACCUCCUGGAG 15

RESULT 143

US-08-292-620A-1891
; Sequence 1891, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 MB

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1891:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-292-620A-1891

Query Match

Best Local Similarity 1.8%; Score 11; DB 2; Length 17;

Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db

RESULT 144

US-08-292-620A-1894

; Sequence 1894, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 MB

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1894:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-292-620A-1894

Query Match

Best Local Similarity 1.8%; Score 11; DB 2; Length 17;

Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186

Db 2 UGCUCUCCUC 12

RESULT 145

US-08-292-620A-1968

; Sequence 1968, Application US/08292620A

two

two

```

; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1968:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-1968

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGAG 254
Db 5 ACCUCUGGAG 15

RESULT 146
US-08-292-620A-1981
; Sequence 1981, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:

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two

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; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1981:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-1981

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186
Db 5 UGCUCUCCUC 15

RESULT 147
US-08-292-620A-1984
; Sequence 1984, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:

```

two

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292.620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1984:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1984

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186
:|:|:|:|:|:
Db 2 UGCUCUCCUC 12

RESULT 148
US-08-292-620A-1986
; Sequence 1986, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James Mcswiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

two

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292.620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1986:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1986

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186
:|:|:|:|:|:
Db 5 UGCUCUCCUC 15

RESULT 149
US-08-532-896-51
; Sequence 51, Application US/08532896
; Patent No. 6124115
; GENERAL INFORMATION:
; APPLICANT: LIU-THIE, Van
; APPLICANT: LARIE, Fernand
; TITLE OF INVENTION: PRODUCTION AND USE OF ISOLATED TYPE 5
; TITLE OF INVENTION: 17B-HYDROXYSTEROID DEHYDROGENASE
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,896
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/1259-313
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-532-896-51

Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 GGGTGCACAAATA 408
|||||
DB 6 GGGTGCACAAATA 16

RESULT 150
US-09-071-845-1635
; Sequence 1635, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1635:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1635

Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186
|||||
DB 5 UGCUUCCUC 15

RESULT 151
US-09-071-845-1691
; Sequence 1691, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1691:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1691

Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TGCTCTTCCTC 186
Db 5 UGCUUCUCC 15

RESULT 152

US-09-071-845-1770
; Sequence 1770, Application US/09071845
; Patent No. 6132967

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1770:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1770

Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TGCTCTTCCTC 186
Db 3 UGCUUCUCC 13

RESULT 153

US-09-071-845-1830
; Sequence 1830, Application US/09071845
; Patent No. 6132967

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1830:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1830

Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 244 ACCTCTCGAG 254
Db 5 ACCUCCUGAG 15

RESULT 154

US-09-071-845-1836
; Sequence 1836, Application US/09071845
; Patent No. 6132967

GENERAL INFORMATION:

```

; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1836:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1836
;
; Query Match 1.8%; Score 11; DB 3; Length 17;
; Best Local Similarity 81.8%; Pred. No. 4e+04;
; Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; QY 244 ACCTCCTGGAG 254
; DB |||||:||||
; 5 ACCUCCUGGAG 15
;
; RESULT 155
; US-09-071-845-1891
; Sequence 1891, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

```

```

; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1891:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1891
;
; Query Match 1.8%; Score 11; DB 3; Length 17;
; Best Local Similarity 54.5%; Pred. No. 4e+04;
; Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
;
; QY 176 TGCTCTTCCTC 186
; DB |||||:||||
; 5 UGCUCUCCUC 15
;
; RESULT 156
; US-09-071-845-1894
; Sequence 1894, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

```

```

; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1894:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1894

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Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Qy 176 TGCTCTTCCTC 186
   |||:|:|:|
Db 2 UGCUUCUCCUC 12

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RESULT 157
US-09-071-845-1968
; Sequence 1968, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

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; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1968:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1968

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Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 244 ACCTCCTGGAG 254
   |||:|:|:|
Db 5 ACCUCCUGGAG 15

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RESULT 158
US-09-071-845-1981
; Sequence 1981, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 1981:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1981
;
; Query Match 1.8%; Score 11; DB 3; Length 17;
; Best Local Similarity 54.5%; Pred. No. 4e-04;
; Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Qy 176 TGCTCTTCCTC 186
Db 5 UGCUUCCUC 15

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```

RESULT 159
US-09-071-845-1984
; Sequence 1984, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 1981:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1981
;
; Query Match 1.8%; Score 11; DB 3; Length 17;
; Best Local Similarity 54.5%; Pred. No. 4e-04;
; Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 1984:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1984
;
; Query Match 1.8%; Score 11; DB 3; Length 17;
; Best Local Similarity 54.5%; Pred. No. 4e-04;
; Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

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Qy 176 TGCTCTTCCTC 186
Db 2 UGCUUCCUC 12

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RESULT 160
US-09-071-845-1986
; Sequence 1986, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 1984:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1984
;
; Query Match 1.8%; Score 11; DB 3; Length 17;
; Best Local Similarity 54.5%; Pred. No. 4e-04;
; Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```



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QY 586 TTGGGACTTTG 596
Db 6 TTGGGACTTTG 16

RESULT 165
US-08-962-690-17/c
; Sequence 17, Application US/08962690
; Patent No. 6214805
; GENERAL INFORMATION:
; APPLICANT: Torrence, Paul F. H.
; APPLICANT: Silverman, Robert H.
; APPLICANT: Cirino, Nick M.
; APPLICANT: Li, Guiying
; APPLICANT: Xiao, Wei
; APPLICANT: Player, Mark R.
; TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 8656-019
; CURRENT APPLICATION NUMBER: US/08/962,690
; EARLIER FILING DATE: 1997-11-03
; EARLIER APPLICATION NUMBER: 08/801,896
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 60/011,725
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-08-962-690-17

Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 540 TTGGCCCTGT 550
Db 14 TTGGCCCTGT 4

RESULT 166
US-08-584-040-5442
; Sequence 5442, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064

QY 342 CTTCTGTGAGG 352
Db 7 CUUCUGAGG 17

RESULT 167
US-08-584-040-5443
; Sequence 5443, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
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SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5442:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-5442

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 342 CTTCTGTGAGG 352
Db 7 CUUCUGAGG 17

RESULT 167
US-08-584-040-5443
; Sequence 5443, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5443:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-5443

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 342 CTTCTGTGAGG 352
Db 6 CUUCUGAGG 16

RESULT 168
US-09-474-432B-592/c
Sequence 592, Application US/09474432B
Patent No. 6528640
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
FILE REFERENCE: MBHB00-831-B (247/276)
CURRENT APPLICATION NUMBER: US/09/474,432B
PRIOR FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: Patent in version 3.0
SEQ ID NO 592
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-474-432B-592

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243' CACCTCCTGGA 253
Db 11 CACCTCCTGGA 1

RESULT 169
US-09-474-432B-700/c
Sequence 700, Application US/09474432B
Patent No. 6528640
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex

APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
FILE REFERENCE: MBHB00-831-B (247/276)
CURRENT APPLICATION NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: Patent in version 3.0
SEQ ID NO 700
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-474-432B-700

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 GGAGCCCTGC 261
Db 13 GGAGCCCTGC 3

RESULT 170
US-09-535-012A-12/c
Sequence 12, Application US/09535012A
Patent No. 6531281
GENERAL INFORMATION:
APPLICANT: Elf Exploration Production
TITLE OF INVENTION: Method of Detecting Sulphate-Reducing Bacteria
FILE REFERENCE: 111628-00114
CURRENT APPLICATION NUMBER: US/09/535,012A
CURRENT FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 9903637
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 12
LENGTH: 17
TYPE: DNA
ORGANISM: Desulfovibrio vulgaris
FEATURE:
OTHER INFORMATION: asp02 primer
US-09-535-012A-12

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GAACCGGAGGA 28
Db 17 GAACCGGAGGA 7

RESULT 171
US-09-371-772B-2336
Sequence 2336, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Resulting from the Infection of the Blood with the Bacterium *Brucella abortus*

APPLICANT: KIDDOYNE, Shauna
APPLICANT: Beigelman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, Dave
APPLICANT: Zinner, Shawn

; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MH000-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 591
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-591

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 CACCTCTCTGGA 253
Db 11 CACCTCTCTGGA 1

RESULT 176
US-09-476-387-699/c
; Sequence 699, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinner, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MH000-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 699
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-699

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 GGAGCCCTCTGC 261
Db 13 GGAGCCCTCTGC 3

RESULT 177
US-09-827-998-183
; Sequence 183, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDH0RF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 183
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-183

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 426 AGATTATTTT 436
Db 7 AGATTATTTT 17

RESULT 178
US-09-827-998-184
; Sequence 184, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDH0RF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 184
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-184

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 426 AGATTATTTT 436
Db 6 AGATTATTTT 16

RESULT 179
US-09-827-998-185
; Sequence 185, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong

```
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 185
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-185

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      426 AGATTATTTT 436
Db      |||||
        5 AGATTATTTT 15

RESULT 180
US-09-827-998-186
; Sequence 186, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 186
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-186

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      426 AGATTATTTT 436
Db      |||||
        4 AGATTATTTT 14

RESULT 181
US-09-827-998-187
; Sequence 187, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 187
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-187

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      426 AGATTATTTT 436
Db      |||||
        3 AGATTATTTT 13

RESULT 182
US-09-827-998-188
; Sequence 188, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 188
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-188

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      426 AGATTATTTT 436
Db      |||||
        2 AGATTATTTT 12

RESULT 183
US-09-827-998-189
; Sequence 189, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 189
; LENGTH: 17
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-189

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AAGATTATTTT 436
   |||||
Db 1 AAGATTATTTT 11

RESULT 184
US-09-827-998-345
; Sequence 345, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 345
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-345

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
   |||||
Db 7 AAGATTATTTT 17

RESULT 185
US-09-827-998-346
; Sequence 346, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 346
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-346

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
   |||||
Db 5 AAGATTATTTT 15

RESULT 186
US-09-827-998-347
; Sequence 347, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 347
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-347

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
   |||||
Db 5 AAGATTATTTT 15

RESULT 187
US-09-827-998-348
; Sequence 348, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 348
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-348

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
   |||||
Db 4 AAGATTATTTT 14

RESULT 188
```

US-09-827-998-349
; Sequence 349, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 351
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-351
Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 425 AAGATTATTTT 435
DB 1 AAGATTATTTT 11
RESULT 191
US-09-827-998-648/c
; Sequence 648, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 648
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-648
Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 81 CTACCTGTGCT 91
DB 17 CTACCTGTGCT 7
RESULT 192
US-09-827-998-649/c
; Sequence 649, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

US-09-827-998-349
; Sequence 349, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 349
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-349
Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 425 AAGATTATTTT 435
DB 3 AAGATTATTTT 13
RESULT 189
US-09-827-998-350
; Sequence 350, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 350
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-350
Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 425 AAGATTATTTT 435
DB 2 AAGATTATTTT 12
RESULT 190
US-09-827-998-351
; Sequence 351, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

```
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 649
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-649

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      81 CTACCTGTGCT 91
Db      16 CTACCTGTGCT 6

RESULT 193
US-09-827-998-650/c
; Sequence 650, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 650
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-650

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      81 CTACCTGTGCT 91
Db      15 CTACCTGTGCT 5

RESULT 194
US-09-827-998-651/c
; Sequence 651, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 651
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-651

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      81 CTACCTGTGCT 91
Db      13 CTACCTGTGCT 3

RESULT 196
US-09-827-998-653/c
; Sequence 653, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 653
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-653

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      81 CTACCTGTGCT 91
```


;; CURRENT APPLICATION NUMBER: US/09/749,233
;; CURRENT FILING DATE: 2000-12-27
;; PRIOR APPLICATION NUMBER: 09/411,578
;; PRIOR FILING DATE: 1999-10-04
;; PRIOR APPLICATION NUMBER: 98203457.1
;; PRIOR FILING DATE: 1998-10-16
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 21
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Eimeria tenella
US-09-749-233-21

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 586 TTGGGACTTTC 596
Db 6 TTGGGACTTTC 16

RESULT 202
US-09-866-108A-932
;; Sequence 932, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharron G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wensheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;; FILE REFERENCE: AEOICA-7
;; CURRENT APPLICATION NUMBER: US/09/866,108A
;; CURRENT FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aecomica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 932
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-932

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 586 TTGGGACTTTC 596
Db 6 TTGGGACTTTC 16

RESULT 204
US-09-866-108A-934
;; Sequence 934, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharron G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wensheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

Qy 359 AGGCTGAGCCC 369
Db 7 AGGCTGAGCCC 17

RESULT 203
US-09-866-108A-933
;; Sequence 933, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharron G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wensheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;; FILE REFERENCE: AEOICA-7
;; CURRENT APPLICATION NUMBER: US/09/866,108A
;; CURRENT FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aecomica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 933
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-933

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 359 AGGCTGAGCCC 369
Db 6 AGGCTGAGCCC 16

RESULT 204
US-09-866-108A-934
;; Sequence 934, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharron G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wensheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 934
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-934

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
Db 5 AGGCTGAGCCC 15

RESULT 205
US-09-866-108A-935
; Sequence 935, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 935
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-936

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: PCT/US01/00668
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 935
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-935

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
Db 4 AGGCTGAGCCC 14

RESULT 206
US-09-866-108A-936
; Sequence 936, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 936
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-936

QY 359 AGGCTGAGCCC 369
|||||
Db 3 AGGCTGAGCCC 13

RESULT 207

US-09-866-108A-937
; Sequence 937, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 937
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-938

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
|||||
Db 2 AGGCTGAGCCC 12

RESULT 208
US-09-866-108A-938
; Sequence 938, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

QY 359 AGGCTGAGCCC 369
|||||
Db 2 AGGCTGAGCCC 12

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
|||||
Db 2 AGGCTGAGCCC 12

US-09-866-108A-937
; Sequence 937, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 938
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-938

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
|||||
Db 1 AGGCTGAGCCC 11

RESULT 209

US-09-866-108A-1462
; Sequence 1462, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 937
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-937

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
|||||
Db 2 AGGCTGAGCCC 12

RESULT 208
US-09-866-108A-938
; Sequence 938, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1462
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1462

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGGG 492
Db 7 CCTGGGAAGGG 17

RESULT 210
US-09-866-108A-1463
; Sequence 1463, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00685
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1463
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1463

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 482 CCTGGGAAGGG 492
Db 6 CCTGGGAAGGG 16

RESULT 211
US-09-866-108A-1464
; Sequence 1464, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00685
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1464
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1464

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 482 CCTGGGAAGGG 492
Db 5 CCTGGGAAGGG 15

RESULT 212
US-09-866-108A-1465
; Sequence 1465, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng

```
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1465
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1465

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CTTGGGAAGGG 492
Db 4 CTTGGGAAGGG 14

RESULT 213
US-09-866-108A-1466
; Sequence 1466, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1465
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1465

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CTTGGGAAGGG 492
Db 4 CTTGGGAAGGG 14

RESULT 214
US-09-866-108A-1467
; Sequence 1467, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1467
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1467
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; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1466
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1466

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CTTGGGAAGGG 492
Db 3 CTTGGGAAGGG 13

RESULT 214
US-09-866-108A-1467
; Sequence 1467, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1467
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1467

Query Match 1.8%; Score 11; DB 4; Length 17;
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Best Local Similarity 100.0%; Pred. No. 4e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGG 492

Db 2 CCTGGGAAGG 12

RESULT 215

US-09-866-108A-1468
; Sequence 1468, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15735
; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1468
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1468

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGG 492

Db 1 CCTGGGAAGG 11

RESULT 216

US-09-866-108A-7363
; Sequence 7363, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEMICA-7
CURRENT APPLICATION NUMBER: US/09/866.108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15735
SOFTWARE: Aemica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 7363
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-7363

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGT 509

Db 7 GAAATTCAGT 17

RESULT 217

US-09-866-108A-7370
; Sequence 7370, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Acmica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 7370
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-7370

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 AAAATTTCAGTT 510
Db 1 AAAATTTCAGTT 11

RESULT 218
US-09-866-108A-9635/c
;; Sequence 9635, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharron G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wensheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;; FILE REFERENCE: AEWICA-7
;; CURRENT APPLICATION NUMBER: US/09/866,108A
;; CURRENT FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Acmica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 9635
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-9635

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCTCCG 188
Db 17 CTCCTCTCCG 7

RESULT 219
US-09-866-108A-9636/c
;; Sequence 9636, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharron G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wensheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;; FILE REFERENCE: AEWICA-7
;; CURRENT APPLICATION NUMBER: US/09/866,108A
;; CURRENT FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Acmica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 9636
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-9636

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCTCCG 188
Db 16 CTCCTCTCCG 6

RESULT 220
US-09-866-108A-9637/c
;; Sequence 9637, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharron G.
;; APPLICANT: HANZEL, David K.

```

; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9637
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9637

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Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 178 CTCCTCTCTCCG 188
Db 15 CTCCTCTCTCCG 5

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RESULT 221
US-09-866-108A-9638/c
; Sequence 9638, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9638
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9638

```

```

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 178 CTCCTCTCTCCG 188
Db 14 CTCCTCTCTCCG 4

```

```

RESULT 222
US-09-866-108A-9639/c
; Sequence 9639, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9639
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9639

```

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCCTCTCCG 188
Db 13 CTCCTCTCCG 3

RESULT 223

US-09-866-108A-9640/c
; Sequence 9640, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9640
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-866-108A-9640

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCCTCTCCG 188
Db 12 CTCCTCTCCG 2

RESULT 224

US-09-866-108A-9641/c
; Sequence 9641, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.

APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 9641
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens

US-09-866-108A-9641

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCCTCTCCG 188
Db 11 CTCCTCTCCG 1

RESULT 225

US-08-248-848-56/c
; Sequence 56, Application US/08248848
; Patent No. 5523217
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R.
; APPLICANT: Versalovic, James
; APPLICANT: Koeuth, Thearith
; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using
; TITLE OF INVENTION: Repetitive DNA Sequence Amplification
; Patent No. 5523217
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,848

; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/781,424
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5394
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5325
 ; TELEFAX: 713/651-5246
 ; TELEX: 762829
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: YES
 ; US-08-248-848-56

Query Match 1.8%; Score 11; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 CGGACTGGGAC 207
 |||||
 Db 17 CGGACTGGGAC 7

RESULT 226
 US-08-248-848-57
 ; Sequence 57, Application US/08248848
 ; Patent No. 5523217
 ; GENERAL INFORMATION:
 ; APPLICANT: Lupski, James R.
 ; APPLICANT: Versalovic, James
 ; APPLICANT: Koeuth, Thearith
 ; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using
 ; TITLE OF INVENTION: Repetitive DNA Sequence Amplification
 ; Patent No. 5523217
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski
 ; STREET: 1301 McKinney, Suite 5100
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77010-3095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/248,848
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/781,424
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5394
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5325
 ; TELEFAX: 713/651-5246
 ; TELEX: 762829
 ; INFORMATION FOR SEQ ID NO: 57:
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: YES
 ; US-08-248-848-57

Query Match 1.8%; Score 11; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 CGGACTGGGAC 207
 |||||
 Db 2 CGGACTGGGAC 12

RESULT 227
 US-08-050-073-190/c
 ; Sequence 190, Application US/08050073
 ; Patent No. 5567809
 ; GENERAL INFORMATION:
 ; APPLICANT: Apple, Raymond J.
 ; APPLICANT: Begovich, Ann B.
 ; APPLICANT: Bugawan, Teodorica L.
 ; APPLICANT: Erlich, Henry A.
 ; APPLICANT: Griffith, Robert L.
 ; APPLICANT: Schaff, Stephen J.
 ; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
 ; TITLE OF INVENTION: Typing
 ; NUMBER OF SEQUENCES: 315
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hoffmann-La Roche Inc.
 ; STREET: 340 Kingsland Street
 ; CITY: Nutley
 ; STATE: New Jersey
 ; COUNTRY: U.S.A.
 ; ZIP: 07110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/050,073
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Petty, Douglas A.
 ; REGISTRATION NUMBER: 35,321
 ; REFERENCE/DOCKET NUMBER: 8769
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 814-2974
 ; TELEFAX: (510) 814-2977
 ; INFORMATION FOR SEQ ID NO: 190:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: genomic DNA
 ; US-08-050-073-190

Query Match 1.8%; Score 11; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGGAG 254
 |||||
 Db 17 ACTCTGGGAG 7

RESULT 228

US-08-480-547A-18/c
; Sequence 18, Application US/08480547A
; Patent No. 5652131
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharon H.
; APPLICANT: Kadlec, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marchall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,547A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5652131and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32791
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-480-547A-18
Query Match 1.8%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 317 TGAGGATCTTC 327
DB 15 TGAGGATCTTC 5
RESULT 229
US-08-111-077-56/c
; Sequence 56, Application US/08111077
; Patent No. 5691136
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R.
; APPLICANT: Versalovic, James
; APPLICANT: Koeuth, Thearith
; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using
; TITLE OF INVENTION: Repetitive DNA Sequence Amplification
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/111,077
; FILING DATE: 19930824
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5394
; TELECOMMUNICATION INFORMATION:

CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/111,077
FILING DATE: 19930824
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
US-08-111-077-56
Query Match 1.8%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 197 CGGACTGGGAC 207
DB 17 CGGACTGGGAC 7
RESULT 230
US-08-111-077-57
; Sequence 57, Application US/08111077
; Patent No. 5691136
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R.
; APPLICANT: Versalovic, James
; APPLICANT: Koeuth, Thearith
; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using
; TITLE OF INVENTION: Repetitive DNA Sequence Amplification
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/111,077
; FILING DATE: 19930824
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5394
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
US-08-111-077-57

Query Match 1.8%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 CGGACTGGGAC 207
DB 2 CGGACTGGGAC 12

RESULT 231
US-08-250-847B-18/c
; Sequence 18, Application US/08250847B
; Patent No. 5702936
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecek, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,847B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5702936and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-250-847B-18

Query Match 1.8%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTC 327
DB 15 TGAGGATCTTC 5

RESULT 232
US-08-363-240A-1234/c
; Sequence 1234, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaler, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1234:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-1234

Query Match 1.8%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 ACCTCAGTCTG 318
DB 16 ACCTCAGTCTG 6

RESULT 233
US-08-465-095-3/c
; Sequence 9, Application US/08465095

Patent No. 5949534
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Iida, Naoka
TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,095
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,656
FILING DATE: 07-JAN-1994
APPLICATION NUMBER: 08/001,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/472,377
FILING DATE: 01-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GZI-003C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-465-095-9

Query Match 1.8%; Score 11; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 465 TGAAGAAGCTT 475
Db 15 TGAAGAAGCTT 5

RESULT 234
US-09-205-922-30/c
Sequence 30, Application US/09205922
Patent No. 5951455
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-11 EXPRESSION
FILE REFERENCE: RTS-0030
CURRENT APPLICATION NUMBER: US/09/205,922
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 30
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-922-30

Query Match 1.8%; Score 11; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 322 ATCTTCACGCG 332
Db 13 ATCTTCACGCG 3

RESULT 235
US-09-205-922-62
Sequence 62, Application US/09205922
Patent No. 5951455
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-11 EXPRESSION
FILE REFERENCE: RTS-0030
CURRENT APPLICATION NUMBER: US/09/205,922
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 62
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-922-62

Query Match 1.8%; Score 11; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 180 CTTCTCCGCT 190
Db 7 CTTCTCCGCT 17

RESULT 236
US-08-463-949A-18/c
Sequence 18, Application US/08463949A
Patent No. 5955583
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Corbin, Jackie D.
APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecsek, Ann
APPLICANT: Loughney, Kate
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,949A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993

ATTORNEY/AGENT INFORMATION:
NAME: No. 595583and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-463-949A-18

Query Match 1.8%; Score 11; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTC 327
Db 15 TGAGGATCTTC 5

RESULT 237

US-08-928-692-41
Sequence 41, Application US/08928692
Patent No. 5958727
GENERAL INFORMATION:

APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 59587270 No. 5958727disk of No. 5958727th America, Inc.

STREET: 405 Lexington Avenue
CITY: New York
STATE: NY

COUNTRY: USA

ZIP: 10174

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,692

FILING DATE: 12-SEPT-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4944.200-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-928-692-41

Query Match 1.8%; Score 11; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 GGATCTTCACC 330
Db 1 GGATCTTCACC 11

RESULT 238

US-09-156-979-44/c

Sequence 44, Application US/09156979

Patent No. 5962672

GENERAL INFORMATION:

APPLICANT: Cowsett, Lex M.

TITLE OF INVENTION: ANTISENSE MODULATION OF RHOB EXPRESSION

FILE REFERENCE: RTS-0013

CURRENT APPLICATION NUMBER: US/09/156,979

CURRENT FILING DATE: 1998-09-18

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 44

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-156-979-44

Query Match 1.8%; Score 11; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGCTGC 165
Db 14 AGAACGGCTGC 4

RESULT 239

US-09-156-979-45/c

Sequence 45, Application US/09156979

Patent No. 5962672

GENERAL INFORMATION:

APPLICANT: Cowsett, Lex M.

TITLE OF INVENTION: ANTISENSE MODULATION OF RHOB EXPRESSION

FILE REFERENCE: RTS-0013

CURRENT APPLICATION NUMBER: US/09/156,979

CURRENT FILING DATE: 1998-09-18

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 45

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-156-979-45

Query Match 1.8%; Score 11; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGCTGC 165
Db 17 AGAACGGCTGC 7

RESULT 240

US-09-256-496-15

Sequence 15, Application US/09256496

Patent No. 5998206

GENERAL INFORMATION:

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION

FILE REFERENCE: RTS-0056

CURRENT APPLICATION NUMBER: US/09/256,496

CURRENT FILING DATE: 1999-02-23

NUMBER OF SEQ ID NOS: 86

SEQ ID NO 15

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-496-15

Query Match      1.8%; Score 11; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCAC 329
      |||||
Db 8 AGGATCTTCAC 18

RESULT 241
US-09-255-893-40/c
; Sequence 40, Application US/09255893A
; Patent No. 6008344
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2 GROUP IV EXPRESSION
; FILE REFERENCE: RTS-0055
; CURRENT APPLICATION NUMBER: US/09/255,893A
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-893-40

Query Match      1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 GGAAGGGCTG 495
      |||||
Db 17 GGAAGGGCTG 7

RESULT 242
US-09-358-381-16
; Sequence 16, Application US/09358381
; Patent No. 6020199
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION
; FILE REFERENCE: RTS-0079
; CURRENT APPLICATION NUMBER: US/09/358,381
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-358-381-16

Query Match      1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GAACGGCTGCC 166
      |||||
Db 6 GAACGGCTGCC 16
```

```
RESULT 243
US-08-464-410A-18/c
; Sequence 18, Application US/08464410A
; Patent No. 6037119
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecik, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,410A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037119and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-464-410A-18

Query Match      1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTC 327
      |||||
Db 15 TGAGGATCTTC 5

RESULT 244
US-09-255-912-9
; Sequence 9, Application US/09255912
; Patent No. 6037142
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTS-0044
; CURRENT APPLICATION NUMBER: US/09/255,912
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 9
```

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-912-9

Query Match 1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ACAGCCTCTTG 15
Db 3 ACAGCCTCTTG 13

RESULT 245

US-08-180-470-44
; Sequence 44, Application US/08180470
; Patent No. 6045994
; GENERAL INFORMATION:
; APPLICANT: ZABEAU, Marc
; APPLICANT: VOS, Pieter
; TITLE OF INVENTION: SELECTIVE RESTRICTION FRAGMENT
; TITLE OF INVENTION: AMPLIFICATION: A GENERAL METHOD FOR DNA
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swacker & Mathis
; STREET: The George Mason Bldg., Washington & Prince
; STREET: Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22133-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,470
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/950,011
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-180-470-44

Query Match 1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 TTACCAATTC 46
Db 6 TTACCAATTC 16

RESULT 246

US-09-143-212-9

; Sequence 9, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia and Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
; FILE REFERENCE: RFS-0005
; CURRENT APPLICATION NUMBER: US/09/143,212B
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-9

Query Match 1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 TCACCTCCTGG 252
Db 2 TCACCTCCTGG 12

RESULT 247

US-09-289-466-72/c
; Sequence 72, Application US/09289466A
; Patent No. 6124272
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PDK-1 EXPRESSION
; FILE REFERENCE: RFS-0060
; CURRENT APPLICATION NUMBER: US/09/289,466A
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 72
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-289-466-72

Query Match 1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 TTTGTAGAAAA 461
Db 12 TTTGTAGAAAA 2

RESULT 248

US-09-213-719-87
; Sequence 87, Application US/09213719B
; Patent No. 6150162
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD44 EXPRESSION
; FILE REFERENCE: RFS-0006
; CURRENT APPLICATION NUMBER: US/09/213,719B
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 87
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-213-719-87

Query Match 1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 CCACCTCAGT 315
DB 1 CCACCTCAGT 11

RESULT 249

US-09-156-856-7
Sequence 7, Application US/09156856A
Patent No. 6221591

GENERAL INFORMATION:
APPLICANT: Aerts, Johannes M.

TITLE OF INVENTION: Determination of a genetic risk factor for infection
TITLE OF INVENTION: and other diseases, and detection of activated
TITLE OF INVENTION: phagocytes
FILE REFERENCE: Sequence 1-20

Patent No. 6221591

CURRENT APPLICATION NUMBER: US/09/156,856A

CURRENT FILING DATE: 1998-09-18

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 18

TYPE: DNA

ORGANISM: Homo sapiens

US-09-156-856-7

Query Match 1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 GCAAGCTGAG 366
DB 5 GCAAGCTGAG 15

RESULT 250

US-09-038-637-141
Sequence 141, Application US/09038637
Patent No. 6235470

GENERAL INFORMATION:
APPLICANT: Sidransky, David

TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
NUMBER OF SEQUENCES: 195

CORRESPONDENCE ADDRES:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/038,637

FILING DATE: 10-MAR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/579,233

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/152,313

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/146001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 141:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

US-09-038-637-141

Query Match 1.8%; Score 11; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 CGCTGGGCTAA 65
DB 2 CGCTGGGCTAA 12

RESULT 251

US-09-338-907-414/c

Sequence 414, Application US/09338907

Patent No. 6265546

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Ilya, Chumakov

APPLICANT: Bougueret, Lydie

TITLE OF INVENTION: PROSTATE CANCER GENE

FILE REFERENCE: GENSET.18CF1CP

CURRENT APPLICATION NUMBER: US/09/338,907

CURRENT FILING DATE: 1999-06-23

EARLIER APPLICATION NUMBER: 08/996,306

EARLIER FILING DATE: 1997-12-22

EARLIER APPLICATION NUMBER: 60/099,658

EARLIER FILING DATE: 1998-09-09

EARLIER APPLICATION NUMBER: 09/218,207

EARLIER FILING DATE: 1998-12-22

NUMBER OF SEQ ID NOS: 578

SOFTWARE: Patent.pm

SEQ ID NO 414

LENGTH: 18

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..18

OTHER INFORMATION: downstream amplification primer for SEQ 250, SEQ 327

US-09-338-907-414

Query Match 1.8%; Score 11; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GTTTCCTTACC 40
DB 18 GTTTCCTTACC 8

RESULT 252

US-09-630-706-33/c

Sequence 33, Application US/09630706

Patent No. 6277640

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION

FILE REFERENCE: RTS-0053

CURRENT APPLICATION NUMBER: US/09/630,706

CURRENT FILING DATE: 2000-08-01

NUMBER OF SEQ ID NOS: 94


```
; SEQ ID NO 33
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-630-706-33

Query Match
Best Local Similarity 100.0%; Score 11; DB 3; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACAGGCTCTTG 15
Db 17 ACAGGCTCTTG 7

RESULT 253
US-09-577-902-16
; Sequence 16, Application US/09577902
; Patent No. 6284538
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION
; FILE REFERENCE: ISPR-0463
; CURRENT APPLICATION NUMBER: US/09/577,902
; CURRENT FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/358,381
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US99/29594,
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-577-902-16

Query Match
Best Local Similarity 100.0%; Score 11; DB 3; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GAACGGCTGCC 166
Db 6 GAACGGCTGCC 16

RESULT 254
US-09-339-972-41
; Sequence 41, Application US/09339972
; Patent No. 6323002
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6323002disk of No. 6323002th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/339,972
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,692
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-339-972-41

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 GGATCTTACC 330
Db 1 GGATCTTACC 11

RESULT 255
US-09-218-207-414/c
; Sequence 414, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CP1
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 414
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer for SEQ 250, SEQ 327
US-09-218-207-414

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GTTCTTTACC 40
Db 18 GTTCTTTACC 8

RESULT 256
US-08-584-040-8335
```

```

; Sequence 8335, Application US/08564040
; Patent No. 634698
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwigger, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT OF DISEASES OF THE VASCULAR SYSTEM
; TITLE OF INVENTION: CONDITIONS RELATING TO THE TREATMENT OF DISEASES OF THE VASCULAR SYSTEM
; TITLE OF INVENTION: OF VASCULAR ENDOGENOUS GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8335:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PS-08-584-040-8335

```

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Query Match      1.8%; Score 11; DB 4; Length 18;
Best Local Similarity 90.9%; Pred. No. 4e+04;
Matches 10; Conservative 1; Mismatches 0; Indels
```

Qy 156 GAACGGCTGCC 166
|||||:||||
Db 3 GAACGGCTGCC 13

RESULT 257
US - 08-679-645-1167/c
Sequence 1167, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwaggen, James A.
; APPLICANT: Merlo, Patricia Ann Owe
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.

```

, TITLE OF INVENTION: COMPOSITION AND METHODS FOR
,
, TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
,
, TITLE OF INVENTION: IN PLANTS
,
, NUMBER OF SEQUENCES: 1263
,
, CORRESPONDENCE ADDRESS:
,
, ADDRESSEE: Lyon & Lyon
,
, STREET: 633 West Fifth Street
,
, CITY: Suite 4700
,
, CITY: Los Angeles
,
, STATE: California
,
, COUNTRY: U.S.A.
,
, ZIP: 90071-2066
,
, COMPUTER READABLE FORM:
,
, MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
,
, MEDIUM TYPE: storage
,
, COMPUTER: IBM Compatible
,
, OPERATING SYSTEM: IBM P.C. DOS 5.0
,
, SOFTWARE: Word Perfect 5.1
,
, CURRENT APPLICATION DATA:
,
, APPLICATION NUMBER: US/08/679,645
,
, FILING DATE: July 12, 1996
,
, CLASSIFICATION: 800
,
, PRIORITY APPLICATION DATA:
,
, APPLICATION NUMBER: 60/001,135
,
, FILING DATE: July 13, 1995
,
, APPLICATION NUMBER: 08/300,726
,
, FILING DATE: September 2, 1994
,
, ATTORNEY/AGENT INFORMATION:
,
, NAME: Warburg, Richard J.
,
, REGISTRATION NUMBER: 32,327
,
, REFERENCE/DOCKET NUMBER: 219/247
,
, TELECOMMUNICATION INFORMATION:
,
, TELEPHONE: (213) 489-1600
,
, TELEFAX: (213) 955-0440
,
, TELEX: 67-3510
,
, INFORMATION FOR SEQ ID NO: 1167:
,
, SEQUENCE CHARACTERISTICS:
,
, LENGTH: 18 base pairs
,
, TYPE: nucleic acid
,
, STRANDEDNESS: single
,
, TOPOLOGY: linear
,
, US-08-679-645-1167

```

```
Query Match      1.9%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 375 GCTGCGGCGGC 385
Db 18 GCTGCGGCGGC 8

```

RESULT 250
US-08-679-645-1169/c
Sequence 1169, Application US/08679645
Patent No. 6350934
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McSwiggen, James A.
APPLICANT: Merlo, Patricia Ann Owens
APPLICANT: Guo, Lining
APPLICANT: Skokut, Thomas A.
APPLICANT: Young, Scott A.
APPLICANT: Folkerts, Otto
APPLICANT: Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND
TITLE OF INVENTION: MODULATION OF GE
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street

```

STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1169:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-1169

Query Match 1.8%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GCTGCGCGCGC 385
DB 15 GCTGCGCGCGC 5

RESULT 259
US-09-167-109-145/c
; Sequence 145, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsett, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoming S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09/167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 145
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-145

Query Match 1.8%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 CTTTGGTTATC 145
DB 135 CTTTGGTTATC 145

DB 11 CTTTGGTTATC 1

RESULT 260
US-09-167-109-163
; Sequence 163, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsett, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoming S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09/167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 163
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-163

Query Match 1.8%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AAGTTTCTTTA 38
DB 7 AAGTTTCTTTA 17

RESULT 261
US-09-387-341-105/c
; Sequence 105, Application US/09387341
; Patent No. 6410323
; GENERAL INFORMATION:
; APPLICANT: Roberts, M. Luisa
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene Expression
; FILE REFERENCE: ISPH-0404
; CURRENT APPLICATION NUMBER: US/09/387,341
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: 09/156,424
; EARLIER FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 09/156,979
; EARLIER FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 09/156,807
; EARLIER FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 09/161,015
; EARLIER FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-387-341-105

Query Match 1.8%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGACGGCTGC 165
DB 14 AGACGGCTGC 4

```
RESULT 262
US-09-387-341-106/c
; Sequence 106, Application US/09387341
; Patent No. 6410323
; GENERAL INFORMATION:
; APPLICANT: Roberts, M. Luisa
; APPLICANT: Cowbert, Lex M.
; TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene
; FILE REFERENCE: ISPH-0404
; CURRENT FILING DATE: 1998-08-31
; CURRENT APPLICATION NUMBER: US/09/387,341
; EARLIER FILING DATE: 1998-09-18
; EARLIER FILING DATE: 1998-09-18
; EARLIER FILING DATE: 1998-09-18
; EARLIER FILING DATE: 1998-09-18
; EARLIER FILING DATE: 1998-09-18
; EARLIER FILING DATE: 1998-09-18
; EARLIER FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-387-341-106

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGACGGCTGC 165
Db 17 AGACGGCTGC 7

RESULT 263
US-09-394-455-16/c
; Sequence 16, Application US/09394455
; Patent No. 6531305
; GENERAL INFORMATION:
; APPLICANT: Witman, George F.
; APPLICANT: San Agustin, Jovenal
; APPLICANT: Leszyk, John D.
; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING
; FILE REFERENCE: 07917/078001
; CURRENT FILING DATE: 1999-09-10
; CURRENT APPLICATION NUMBER: US/09/394,455
; PRIOR FILING DATE: 1999-09-10
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Ovine
US-09-394-455-16

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCCAACT 311
Db 14 AACCCCAACT 4

RESULT 264
US-09-422-978-8311/c
```

```
; Sequence 8311, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT FILING DATE: 1999-10-20
; CURRENT APPLICATION NUMBER: US/09/422,978
; EARLIER FILING DATE: 1999-04-21
; EARLIER FILING DATE: 1999-04-21
; EARLIER FILING DATE: 1998-11-23
; EARLIER FILING DATE: 1998-11-23
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8311
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-1480 for SEQ 446, in complen
US-09-422-978-8311

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GTTCTTTACC 40
Db 18 GTTCTTTACC 8

RESULT 265
US-09-371-772B-3991
; Sequence 3991, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; FILE REFERENCE: MEH00,876-J (237/198)
; CURRENT FILING DATE: 1999-08-10
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3991
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3991

Query Match
Best Local Similarity 90.3%; Score 11; DB 4; Length 18;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 156 GAACGGCTGC 166
Db 3 GAACGGCTGC 13

RESULT 266
```

US-08-179-656A-9/c
; Sequence 9, Application US/08179656A
; Patent No. 6673893
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Iida, Naoka
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,656A
; FILING DATE: 07-JAN-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/001,177
; FILING DATE: 07-JAN-1993
; APPLICATION NUMBER: 07/472,377
; FILING DATE: 01-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GZI-003C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-179-656A-9

Query Match 1.8%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 TGAAGAAGACTT 475
Db 15 TGAAGAAGACTT 5

RESULT 267
PCT-US94-00300-9/c
; Sequence 9, Application PC/TUS9400300
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Iida, Naoka
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00300
; FILING DATE: 07-JAN-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/001,177
; FILING DATE: 07-JAN-1993
; APPLICATION NUMBER: 07/472,377
; FILING DATE: 01-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GZI-003C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US94-00300-9

Query Match 1.8%; Score 11; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 TGAAGAAGACTT 475
Db 15 TGAAGAAGACTT 5

RESULT 268
PCT-US94-06066-18/c
; Sequence 18, Application PC/TUS9406066
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Washington
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,051
; FILING DATE: 27-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US94-06066-18

Query Match 1.8%; Score 11; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TCAGGATCTTC 327
DB 15 TCAGGATCTTC 5

RESULT 269

US-08-271-942A-89
; Sequence 89, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0

SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/271,942A

FILING DATE: 08-JUL-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Marina T. Larson

REGISTRATION NUMBER: 32,038

REFERENCE/DOCKET NUMBER: VGEN.P-003-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (914) 245-3252

TELEFAX: (914) 962-4330

TELEX:

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:

LENGTH: 19

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: human

FEATURE:

NAME/KEY: primer for exon 8 of human Rb1 gene

US-08-271-942A-89

Query Match 1.8%; Score 11; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AGATTATTTT 435
DB 9 AGATTATTTT 19

RESULT 270

US-08-474-177-6

; Sequence 6, Application US/08474177

; Patent No. 5624819

; GENERAL INFORMATION:

; APPLICANT: Skolnick, Mark H.

; APPLICANT: Cannon-Albright, Lisa A.

; APPLICANT: Kamb, Alexander

; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

; STREET: 1201 New York Avenue, Suite 1000

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/474,177

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/03537

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/251,938

; FILING DATE: 01-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,087

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,086

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/227,369

; FILING DATE: 14-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/214,592

; FILING DATE: 18-MAR-1994

; ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348-E

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-474-177-6

Query Match 1.8%; Score 11; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ACCGAGGAG 30
Db 5 ACCGAGGAG 15

RESULT 271
US-08-487-033-6
; Sequence 6, Application US/08487033
; Patent No. 5739027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,033
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-487-033-6

Query Match 1.8%; Score 11; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04; 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ACCGAGGAG 30

Db 5 ACCGAGGAG 15

RESULT 272
US-08-431-896B-6
; Sequence 6, Application US/08431896B
; Patent No. 5773244
; GENERAL INFORMATION:
; APPLICANT: Ares, Manuel, Jr.
; APPLICANT: Ford, Ethan E.
; TITLE OF INVENTION: RNA Cyclase Ribozymes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,896B
; FILING DATE: 01-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,857
; FILING DATE: 19-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 02307E-070000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-431-896B-6

Query Match 1.8%; Score 11; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04; 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 CAAATAGCCAT 413
Db 6 CAAATAGCCAT 16

RESULT 273
US-08-480-810-6
; Sequence 6, Application US/08480810
; Patent No. 580236
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:

APPLICATION NUMBER: 08/246,985
FILING DATE: 20-MAY-1994
APPLICATION NUMBER: US 025,396
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,493
FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Primer 11F (JP)
US-08-611-757-34

Query Match 1.8%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 CTCCTGGAGCC 256
Db 9 CTCCTGGAGCC 19

RESULT 276
US-08-848-251-6
Sequence 6, Application US/08848251
Patent No. 5989815
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
TITLE OF INVENTION: 36
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCI/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-848-251-6

Query Match 1.8%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ACCGGAGGAAG 30
Db 5 ACCGGAGGAAG 15

RESULT 277
US-08-874-186-3/c
Sequence 3, Application US/08874186
Patent No. 5989885
GENERAL INFORMATION:
APPLICANT: Teng, David H-F.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Perry III, William L.
APPLICANT: Skolnick, Mark H.
TITLE OF INVENTION: SPECIFIC MUTATIONS OF MAP KINASE KINASE
IN HUMAN TUMOR CELL LINES IDENTIFY IT AS A TUMOR
SUPPRESSOR IN VARIOUS TYPES OF CANCER
TITLE OF INVENTION: 4 (MKK4)
TITLE OF INVENTION: SUPPRESSOR
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,186
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,482
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 24884-121392-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer for STS."
US-08-874-186-3

Query Match 1.8%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 TTGCAATAAG 156
DB 12 TTGCAATAAG 2

RESULT 278
US-08-538-711A-18/c
Sequence 18, Application US/08538711A
Patent No. 5994062
GENERAL INFORMATION:
APPLICANT: MULSHINE, JAMES, L.
TITLE OF INVENTION: AN EPITHELIAL PROTEIN AND
TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/538,711A
FILING DATE: 02-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 2026-4201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: nucleic acid
STRANDEDNESS: Unknown
TOPOLOGY: Linear
MOLECULE TYPE: other nucleic acid
US-08-538-711A-18

Query Match 1.8%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 552 TGAGTTGATG 562
DB 17 TGAGTTGATG 7

RESULT 279
US-08-743-637B-85/c
Sequence 85, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Pseudomonas aeruginosa
US-08-743-637B-85

Query Match 1.8%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCTTGATGAAC 21
DB 16 TCTTGATGAAC 6

RESULT 280
US-08-486-047-6
Sequence 6, Application US/08486047
Patent No. 5994095
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,047
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
; US-08-486-047-6

```

```

Query Match 1.8%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 20 ACCGGAGGAG 30
Db 5 ACCGGAGGAG 15

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```

RESULT 281
US-08-526-840B-85/c
; Sequence 85, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY

```

```

;
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OVARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas aeruginosa
;
; US-08-526-840B-85

```

```

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 11 TCTTGATGAAC 21
Db 16 TCTTGATGAAC 6

```

```

RESULT 282
US-09-120-130-6
; Sequence 6, Application US/09120130
; Patent No. 6037462
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,130
; FILING DATE:
; CLASSIFICATION:

```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/480,810
;; FILING DATE: 08/480,810
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/251,938
;; FILING DATE: 01-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/215,087
;; FILING DATE: 18-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/215,086
;; FILING DATE: 18-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/227,369
;; FILING DATE: 14-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/214,582
;; FILING DATE: 18-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ihnen, Jeffrey L.
;; REGISTRATION NUMBER: 28,957
;; REFERENCE/DOCKET NUMBER: 24884-109348
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-962-4810
;; TELEFAX: 202-962-8300
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORGANISM: Homo sapiens
US-09-120-130-6

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCGGAGGAAG 30
|||||
Db 5 ACCGGAGGAAG 15

RESULT 283
US-09-115-252-6
;; Sequence 6, Application US/09115252
;; Patent No. 6060301
;; GENERAL INFORMATION:
;; APPLICANT: Kamb, Alexander
;; TITLE OF INVENTION: MTS1 GENE
;; NUMBER OF SEQUENCES: 36
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
;; STREET: 1201 New York Avenue, Suite 1000
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/115,252
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/480,810

;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: PCT/US95/03316
;; FILING DATE: 17-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/251,938
;; FILING DATE: 01-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/215,087
;; FILING DATE: 18-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/215,086
;; FILING DATE: 18-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/227,369
;; FILING DATE: 14-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/214,582
;; FILING DATE: 18-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ihnen, Jeffrey L.
;; REGISTRATION NUMBER: 28,957
;; REFERENCE/DOCKET NUMBER: 24884-109348
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-962-4810
;; TELEFAX: 202-962-8300
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORGANISM: Homo sapiens
US-09-115-252-6

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCGGAGGAAG 30
|||||
Db 5 ACCGGAGGAAG 15

RESULT 284
US-08-779-916A-89
;; Sequence 89, Application US/08779916A
;; Patent No. 6063567
;; GENERAL INFORMATION:
;; APPLICANT: Gallie, Brenda L.
;; APPLICANT: Dunn, James M.
;; APPLICANT: Stevens, John K.
;; TITLE OF INVENTION:
;; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
;; NUMBER OF SEQUENCES: 123
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oppedahl & Larson
;; STREET: 1992 Commerce Street, Suite 309
;; CITY: Yorktown Heights
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10598-4412
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS 5.0
;; SOFTWARE: Word Perfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/779,916A

FILING DATE: 18-MAR-1994
 PRIOR APPLICATION DATA: US 08/227,369
 APPLICATION NUMBER:
 FILING DATE: 14-APR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/214,582
 FILING DATE: 18-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24884-109348
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-986-515-6

Query Match 1.8%; Score 11; DB 3; Length 19;
 Best Local Similarity 100.0%; Fred. No. 4e-04;
 Matches 11; Conservative 0; Mismatches 0; Indels

QY 20 ACCGGAGGAAG 30
 |||||
 DB 5 ACCGGAGGAAG 15

RESULT 286
 US-08-388-029A-3/c
 Sequence 3, Application US/08388029A
 Patent No. 6110665
 GENERAL INFORMATION:
 APPLICANT: FENGER, CLARA K.
 APPLICANT: GRANSTROM, DAVID R.
 APPLICANT: GALADHAR, ALVIN A.
 TITLE OF INVENTION: SARCOCYTIS NEURONA DIAGNOSTIC PRIMER
 NUMBER OF SEQUENCES: 97
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
 STREET: 99 CANAL CENTER PLAZA, SUITE 300
 CITY: ALEXANDRIA
 STATE: VIRGINIA
 COUNTRY: US
 ZIP: 22314
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/388,029A
 FILING DATE: 14-FEB-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PRICE, ROBERT L.
 REGISTRATION NUMBER: 22,685
 REFERENCE/DOCKET NUMBER: 434-046
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-684-1111
 TELEFAX: 703-684-1124
 TELEX: AMERPAT
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-388-029A-3

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGCTGA 365
DB 14 CGCAAGCTGA 4

RESULT 287

US-09-120-128-6
Sequence 6, Application US/09120128
Patent No. 6140473

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/120,128
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/251,938
FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/215,087
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/215,086
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/227,369
FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,582
FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-120-128-6

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCGAGGAG 30
DB 5 ACCGAGGAG 15

RESULT 288

US-08-974-549A-404/C
Sequence 404, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/911,312

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/912,951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618

;; FILING DATE: 01-OCT-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 404:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..19
;; OTHER INFORMATION: /note= "TCP1.30 primer"
US-08-974-549A-404

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 CTGGTTCACCT 247
DB 19 CTGGTTCACCT 9

RESULT 289
US-08-938-669A-22/c
; Sequence 22, Application US/08938669A
; Patent No. 6171788
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
; TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
; TITLE OF INVENTION: RELATED DISEASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,669A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/791,154
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mendelson, Elliot
; REGISTRATION NUMBER: P-42,878
; REFERENCE/DOCKET NUMBER: 07425-0034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-6857
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-938-669A-22

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 356 GCAAGGCTGAG 366
DB 15 GCAAGGCTGAG 5

RESULT 290
US-09-120-129-6
; Sequence 6, Application US/09120129
; Patent No. 6180776
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,129
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-120-129-6

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCGGAGGAAG 30
|||||
Db 5 ACCGGAGGAAG 15

RESULT 291
US-09-201-139-6
; Sequence 6, Application US/09201139
; Patent No. 6210949
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,139
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/508,735
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-201-139-6

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCGGAGGAAG 30
|||||

Db 5 ACCGGAGGAAG 15

RESULT 292
US-09-120-131-6
; Sequence 6, Application US/09120131
; Patent No. 6218146
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,131
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-120-131-6

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCGGAGGAAG 30
|||||

Db 5 ACCGAGGAG 15

RESULT 293

US-08-725-027-18/c

; Sequence 18, Application US/08725027

; Patent No. 6251586

; GENERAL INFORMATION:

; APPLICANT: MUSHINE, JAMES, L.

; APPLICANT: TUCKMAN, MELVIN, S.

; TITLE OF INVENTION: AN EPITHELIAL PROTEIN AND

; TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/725.027

; FILING DATE: 02-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US08/538,711

; FILING DATE: 02-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KATHRYN M. BROWN

; REGISTRATION NUMBER: 34,556

; REFERENCE/DOCKET NUMBER: 2026-4201US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 758-4800

; TELEFAX: (212) 751-6849

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19

; TYPE: nucleic acid

; STRANDEDNESS: Unknown

; TOPOLOGY: Linear

; MOLECULE TYPE: other nucleic acid

US-08-725-027-18

Query Match 1.8%; Score 11; DB 3; Length 19;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 552 TGAGTTGATG 562

|||||

Db 17 TGAGTTGATG 7

RESULT 294

US-09-338-907-507/c

; Sequence 507, Application US/09338907

; Patent No. 6265546

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Ilyia, Chumakov

; APPLICANT: Bougueleret, Lydie

; TITLE OF INVENTION: PROSTATE CANCER GENE

; FILE REFERENCE: GENSET.18CF1CP

; CURRENT APPLICATION NUMBER: US/09/338.907

; CURRENT FILING DATE: 1999-06-23

; EARLIER APPLICATION NUMBER: 08/996.306

; EARLIER FILING DATE: 1997-12-22

; EARLIER APPLICATION NUMBER: 60/099.658

; EARLIER FILING DATE: 1998-09-09

; EARLIER APPLICATION NUMBER: 09/218.207

; EARLIER FILING DATE: 1998-12-22

; NUMBER OF SEQ ID NOS: 578

; SOFTWARE: Patent.pm

; SEQ ID NO 507

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1..19

; OTHER INFORMATION: potential microsequencing oligo for 4-22-174.mis2

US-09-338-907-507

Query Match 1.8%; Score 11; DB 3; Length 19;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 TTCAAAAATGT 53

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Db 17 TTCAAAAATGT 7

RESULT 295

US-09-338-907-508/c

; Sequence 508, Application US/09338907

; Patent No. 6265546

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Ilyia, Chumakov

; APPLICANT: Bougueleret, Lydie

; TITLE OF INVENTION: PROSTATE CANCER GENE

; FILE REFERENCE: GENSET.18CF1CP

; CURRENT APPLICATION NUMBER: US/09/338.907

; CURRENT FILING DATE: 1999-06-23

; EARLIER APPLICATION NUMBER: 08/996.306

; EARLIER FILING DATE: 1997-12-22

; EARLIER APPLICATION NUMBER: 60/099.658

; EARLIER FILING DATE: 1998-09-09

; EARLIER APPLICATION NUMBER: 09/218.207

; EARLIER FILING DATE: 1998-12-22

; SOFTWARE: Patent.pm

; NUMBER OF SEQ ID NOS: 578

; SEQ ID NO 508

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1..19

; OTHER INFORMATION: potential microsequencing oligo for 4-22-176.mis2

US-09-338-907-508

Query Match 1.8%; Score 11; DB 3; Length 19;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 TTCAAAAATGT 53

|||||

Db 19 TTCAAAAATGT 9

RESULT 296

US-09-218-307-507/c

; Sequence 507, Application US/09218207

; Patent No. 6346381

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Ilyia, Chumakov

; APPLICANT: Bougueleret, Lydie

; TITLE OF INVENTION: Prostate cancer gene

```

; FILE REFERENCE: GENSET.018CP1
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 507
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: misc feature
; LOCATION: 1..19
; OTHER INFORMATION: potential microsequencing oligo for 4-22-174.mis2
US-09-218-207-507

Query Match      1.8%; Score 11; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      43  TTCAAAAATGT 53
Db      17  TTCAAAAATGT 7

RESULT 297
US-09-218-207-508/c
; Sequence 508, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilyia, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CP1
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 508
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: misc feature
; LOCATION: 1..19
; OTHER INFORMATION: potential microsequencing oligo for 4-22-176.mis2
US-09-218-207-508

Query Match      1.8%; Score 11; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      43  TTCAAAAATGT 53
Db      19  TTCAAAAATGT 9

RESULT 298
US-09-306-828-22/c
; Sequence 22, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.

```

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; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis ;
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-22

Query Match      1.8%; Score 11; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      356  GCAAGGCTGAG 366
Db      15  GCAAGGCTGAG 5

RESULT 299
US-08-912-951-171/c
; Sequence 171, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643

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; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-912-951-171

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Query Match 1.8%; Score 11; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 237 CTGGTTCACCT 247
DB 19 CTGGTTCACCT 9

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RESULT 300
US-09-336-946B-69
; Sequence 69, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 69
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-336-946B-69

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Query Match 1.8%; Score 11; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 166 CACGTGGAATT 176
DB 1 CACGTGGAATT 11

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Search completed: March 4, 2004, 23:34:15
Job time : 83 secs